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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:09:54 ; Search time 95.5625 Seconds
50.576 Million cell updates/sec

Title: US-10-632-706-198

Perfect score: 59

Sequence: 1 WQQGTTVTVSS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext. 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_21:*
- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003ab:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description | RESULT |
|------------|-------|--------------------|-------|-------------|---|
| 1 | 59 | 100.0 | 11 2 | ARR85166 | 1 AAR85166 |
| 2 | 59 | 100.0 | 11 2 | ARR85166 | 1 AAR85166 standard; protein; 11 AA. |
| 3 | 59 | 100.0 | 11 4 | Aau07452 | 1 XX |
| 4 | 59 | 100.0 | 11 5 | AAB28561 | 1 AC |
| 5 | 59 | 100.0 | 11 5 | Aau70517 | 1 XX |
| 6 | 59 | 100.0 | 11 5 | AAU70501 | 1 DT |
| 7 | 59 | 100.0 | 11 5 | AAU70585 | 1 XX |
| 8 | 59 | 100.0 | 11 5 | AUU70477 | 1 DE |
| 9 | 59 | 100.0 | 11 6 | AEO1019 | 1 Human ONS-M21 antibody; heavy variable region; chimeric protein; framework region; FR 4; medulloblastoma; brain tumour; treatment; diagnosis. |
| 10 | 59 | 100.0 | 11 6 | ABR44663 | 1 XX |
| 11 | 59 | 100.0 | 11 7 | ABO33904 | 1 OS Homo sapiens. |
| 12 | 59 | 100.0 | 11 7 | ADG75671 | 1 XX |
| 13 | 59 | 100.0 | 11 8 | ADH17860 | 1 PR 19-NOV-1993; 93UP-00291078. |
| 14 | 59 | 100.0 | 11 8 | ADH18011 | 1 XX |
| 15 | 59 | 100.0 | 11 8 | ADQ90791 | 1 PA (CHUS) CHUGAI SEIYAKU KK. |
| 16 | 59 | 100.0 | 11 8 | ADR12645 | 1 PT Ohtomo T, Sato K, Tauchiya M; |
| 17 | 59 | 100.0 | 11 8 | ADR38796 | 1 XX |
| 18 | 59 | 100.0 | 11 8 | ADR38793 | 1 DR WPI; 1995-200347/26. |
| 19 | 59 | 100.0 | 11 8 | ADR38802 | 1 XX |
| 20 | 59 | 100.0 | 11 8 | ADR38799 | 1 PT Reconstituted antibody against human medulloblastoma cells - contains high proportion of human antibody origin and has low antigenicity. |
| 21 | 59 | 100.0 | 11 8 | ADU38427 | 1 XX |
| 22 | 59 | 100.0 | 11 8 | ADU677919 | 1 PS Claim 1B; Page 102; 120pp; Japanese. |
| 23 | 59 | 100.0 | 11 9 | ADW07403 | 1 XX |
| 24 | 59 | 100.0 | 11 9 | ADW07419 | 1 Sequence 11 AA; |

AAR85163-R85166 are human antibody ONS-M21 heavy variable region framework regions (FRE). They were used in the construction of a human/murine chimeric antibody, reactive with human medulloblastoma (a brain tumour) cells. The chimeric antibody can be used in the diagnosis and treatment of this disease.

Query Match 100.0%; Score 59; DB 2; Length 11; Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WQGQTIVTVSS 11
ID ||||| | | | |
Db 1 WQGQTIVTVSS 11

RESULT 2
AAR97333
ID AAR97333 standard; peptide; 11 AA.
AC AAR97333;
XX
DT 15-OCT-1996 (first entry)
XX Humanised monoclonal antibody heavy chain framework region.
DR
XX Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complemental antibody; humanised; mouse; framework region; anti-carcinoembryonic antigen; CEA;
KW diagnosis; imaging; therapy; immune response.
KW Homo sapiens.
OS
XX WO200149713-A2.
PR
XX 12-JUL-2001.
PD
XX 29-DEC-2000; 2000WO-IT000554.
XX WO200149713-A2.
PR
XX (CNEN) ENEA ENTE NUOVE TECNOLOGIE ENERGIA.
PA (CONS-) SOC CONSORTILE METAPONTUM AGROBIOS SRL.
XX
PI Benvenuto E, Francioni R, Desiderio A, Tavladoraki P,
DR DR N-PSDB; AAS11874.
XX
PT Peptides which are able to confer stability and solubility to an antibody comprising those peptides, useful for treating pathologies (e.g. tumor) associated with accumulation of a molecule inside or outside a human, or animal cell.
XX
PS Claim 1, Page 57; 109PP; English.
XX
CC The invention relates to peptides which are able to confer stability and solubility to an antibody comprising these peptides. The peptides are especially H-FR1, H-FR2, H-FR3, HFR4, L-FR1, L-FR2, L-FR3 or L-FR4 present within a variable region of an antibody which makes the antibody soluble and stable in cytoplasm. Peptides having the sequences of HFR1 to H-FR4 are present within the variable region of the heavy chain of an antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order (H-FR1)-(H-CDR1)-(H-FR2)-(H-CDR2)-(H-FR3)-(H-CDR3) and peptides having the sequences of L-FR1 to L-FR4 are present within the variable region of the light chain of an antibody, covalently linked to the L-CDR1, L-CDR2, L-CDR3 in the order (L-FR1)-(L-CDR1)-(L-FR2)-(L-FR3)-(L-CDR3)-(L-CDR4). The antibodies and polynucleotides are useful (e.g. by gene therapy) for the manufacture of a medicament for the treatment of pathologies associated with accumulation of a molecule inside or outside a human, animal cell or plant cell. The pathologies are infectious (e.g. viral infections such as HIV, human immunodeficiency virus infections), tumour, metabolic and immune (especially auto-immune pathologies). The present sequence represents the peptide H-FR4-F8 (also known as H-FR4)
CC Sequence 11 AA;
SQ Query Match 100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WQGQTIVTVSS 11
Db 1 WQGQTIVTVSS 11

RESULT 3
AAU07452
ID AAU07452 standard; peptide; 11 AA.
AC AAU07452;
XX
DT 24-OCT-2001 (first entry)
XX
DB Synthetic peptide H-FR4-F8.

QY 1 WQGQTIVTVSS 11
ID AAE28561
AC AAE28561;
XX
DT 27-DEC-2002 (first entry)
XX scFv antibody heavy chain frame work region 4 from S18 clone.
XX
KW Human; sugar-nucleic acid interaction; single chain human antibody; scFv; L-peptide binder; D-nucleic acid binder; sugar-protein interaction; FR4;

KW frame work region 4.
 KW XX transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
 OS Homo sapiens.
 XX OS IGD; IgE; IgY; IgD; kappa; lambda; CHBP.
 PN WO200267860-A2.
 XX PD 06-SEP-2002.
 XX PP 22-FEB-2002; 2002WO-US005193.
 XX PR 22-FEB-2001; 2001US-0271377P.
 XX PA (SCRIPPS RES INST.
 XX PI Wong C;
 XX DR WPI; 2002-691633/74.
 PT Selecting L-peptide or D-nucleic acid binders that binds to enantiomers of naturally occurring carbohydrate, comprises providing enantiomers of naturally occurring carbohydrate, and screening library against enantiomers.
 XX PS Disclosure; FIG 6B; 46pp; English.
 CC The present invention relates to a novel method of selecting L-peptide or D-nucleic acid binders that bind to enantiomers of naturally occurring sugar or carbohydrate. The method involves providing enantiomers of naturally occurring sugar or carbohydrate employable for screening the library and then screening the library against the enantiomers for identifying a L-peptide binder or D-nucleic acid binder having binding activity with respect to enantiomers. The method is useful for Selecting L-peptide binder or D-nucleic acid binder that binds to enantiomer of naturally occurring sugar or carbohydrate. It is useful for selecting L-enzymatic binders and/or L-nucleic acid binders that are resistant to enzymatic degradation due to their non-naturally occurring chirality, for blocking or activating the biological function of the naturally occurring sugar or carbohydrate to which they are targeted. The naturally occurring sugars and carbohydrates include bacterial or viral cell surface sugars or carbohydrates, heparin sulphates involved in viral entry, thrombosis and angiogenesis. The method is useful for identifying D-peptides, for studying sugar-protein and sugar-nucleic acid interaction and for designing high-affinity and hydrolase resistant molecules as artificial receptors capable of binding natural carbohydrates. The immobilised enantiomers are useful for screening phage expressing a peptide library on the coat protein to identify specific clones that bind to an immobilised enantiomer. The present sequence is single chain human antibody (FcFv) heavy chain frame work region 4 (FR4) from S18 clone. This sequence is used to illustrate the method of the invention
 SQ Sequence 11 AA;

| | | | | | | | | | |
|-----------------------|--------|--------------|-----|-------|--------|------------|----|------|---|
| Query Match | 100.0% | Score | 59 | DB | 5 | Length | 11 | | |
| Best Local Similarity | 100.0% | Pred. | No. | 0.011 | ; | Mismatches | 0 | | |
| Matches | 11 | Conservative | 0 | ; | Indels | 0 | ; | Gaps | 0 |

OY 1 WGQGTIVVSS 11
 Db 1 WGQGTIVVSS 11

RESULT 5
 AAU70517
 ID AAU70517 standard; peptide; 11 AA.

AC AAU70517;
 XX 14-FEB-2002 (first entry)
 DE Mouse heavy chain immunoglobulin framework region 4 #7.

XX Immunglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarity determining region; framework region; IgBp;
 KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
 KW IGD; IgE; IgY; IgM; kappa; lambda; CHBP.
 XX OS Mus musculus.
 PN WO200181806-A1.

KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
 KW XX IGD; IgE; IgY; IgD; kappa; lambda; CHBP.
 OS Mus musculus.
 PN WO200181806-A1.

PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array.
 XX Disclosure; FIG 1B; 129pp; English.

CC The invention relates to transforming a population of cells (e.g. plant
 CC cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IgBP) polypeptides
 CC that specifically bind to a ligand or form one or more disulfide bonds
 CC with polypeptides in transfected cells, to generate an IgBP that binds to
 CC a ligand, and transformed plant cells are selected, and preparing an IgBP
 CC array in plant cells. At least one peptide sequence has at least 75%
 sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
 IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
 useful for preparing an immunoglobulin binding protein array, preferably
 heavy chain binding protein (CHBP) array in eukaryotic cells especially
 plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
 cells (e.g. insect cells or mammalian cells). The CHBP is useful for
 discovery of e.g. screening assays of IgBPs having desired
 characteristics. The present sequence is a mammalian immunoglobulin
 CC derived peptide that may be incorporated into an IgBP of the invention
 XX SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0;
 Matches 11; Conservative 0; Indels 0; Gaps 0;
 Qy 1 WGQGIFTVTVSS 11
 Db 1 WGQGIFTVTVSS 11

RESULT 9
 ABO10719
 ID ABO10719 standard; peptide: 11 AA.
 XX
 AC ABO10719;
 XX DT 20-AUG-2003 (first entry)
 XX DE Deimmunised murine J415-4 antibody framework sequence VHFR4.
 XX
 KW Modified antibody; deimmunised antibody; anti-PSMA antibody;
 KW prostate specific membrane antigen; immunogenic; CDR; murine;
 KW complementarity determining region; J591; J415; J533; B99; mouse;
 KW prostatic disorder; cancerous disorder; genitourinary inflammation;
 KW prostatitis; benign enlargement; prostatic cancer; testicular cancer;
 KW solid tumour; soft tissue tumour; metastatic lesion; pain; analgesic;
 KW antiinflammatory; cytostatic; framework region; variable heavy chain;
 KW variable light chain; VH; VL; variable region; mutant; mutein.
 XX OS Mus musculus.
 OS Synthetic.
 XX WO200298897-A2.
 XX PR 01-JUN-2001; 2001US-0295214P.
 XX PR 20-SEP-2001; 2001US-0323585P.
 XX PR 08-MAR-2002; 2002US-0362810P.
 XX PA (CORR) CORNELL RES FOUND INC.
 XX PR 30-MAY-2002; 2002WO-US017068.
 XX PR 30-MAY-2002; 2002WO-US017204.
 XX PR 20-SEP-2001; 2001US-032410P.
 XX PR 08-MAR-2002; 2002US-0362612P.
 XX PA (CORR) CORNELL RES FOUND INC.
 XX PI Bander N;
 XX DR WPI; 2003-313319/30.
 XX
 PT Ablating/killing aberrant prostate specific membrane antigen-expressing
 PT cells for treating skin disorders, by contacting the cell with an
 PT antibody that binds to the extracellular domain of prostate specific
 PT membrane antigen.
 XX PS Disclosure; Page 68; 225pp; English.
 XX CC The present invention describes a method (M1) for ablating or killing an

PT cancerous disorder, e.g. genitourinary inflammation, prostatitis, or
 PT prostatic or testicular cancer.
 XX Disclosure; Page 21; 254pp; English.

XX The present invention relates to modified (e.g. deimmunised) antibodies
 CC to prostate specific membrane antigen (PSMA). The modified anti-PSMA
 CC antibodies are less immunogenic compared to the unmodified anti-PSMA
 CC antibodies. The modified antibodies comprise complementarity determining
 CC regions (CDRs) from a non-human antibody (e.g. murine antibody J59,J415,
 CC J533 or B99), and framework sequences that are less immunogenic in humans
 CC (e.g. less antigenic than the murine frameworks in which a murine CDR
 naturally occurs). The modified antibodies bind with PSMA. Preferably
 human PSMA, with high affinity and specificity. The anti-PSMA antibodies
 CC are useful for treating or preventing a prostatic or cancerous disorder,
 e.g. genitourinary inflammation, prostatitis, benign enlargement,
 CC prostatic cancer or testicular cancer, or solid tumours, soft tissue
 CC tumours or metastatic lesions, and its associated pain. The present
 CC sequence represents a deimmunised murine framework region.
 XX SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0;
 Matches 11; Conservative 0; Indels 0; Gaps 0;
 Qy 1 WGQGIFTVTVSS 11
 Db 1 WGQGIFTVTVSS 11

RESULT 10
 ABR44663
 ID ABR44663 standard; peptide: 11 AA.
 XX
 AC ABR44663;
 XX DT 25-JUL-2003 (first entry)
 XX DE Murine J415-4 antibody VH FR4 amino acid sequence SEQ ID NO:40.
 XX KW Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytoplastic;
 KW prostate specific membrane antigen; antipsoriatic; antiarthritic;
 KW dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;
 KW epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;
 KW neoplastic disorder.
 XX OS Mus musculus.
 OS Synthetic.
 XX WO2003024388-A2.
 XX PN WO2003024388-A2.
 XX DD 27-MAR-2003.
 XX PD 27-MAR-2003.
 XX PF 30-MAY-2002; 2002WO-US017204.
 XX PR 20-SEP-2001; 2001US-032410P.
 XX PR 08-MAR-2002; 2002US-0362612P.
 XX PA (CORR) CORNELL RES FOUND INC.
 XX PI Bander N;
 XX DR WPI; 2003-313319/30.
 XX
 PT Ablating/killing aberrant prostate specific membrane antigen-expressing
 PT cells for treating skin disorders, by contacting the cell with an
 PT antibody that binds to the extracellular domain of prostate specific
 PT membrane antigen.
 XX PS Disclosure; Page 68; 225pp; English.
 XX CC The present invention describes a method (M1) for ablating or killing an

CC aberrant prostate specific membrane antigen (PSMA)-expressing cell (e.g. CC an epidermal and a dermal cell). M1 comprises contacting the cell, or a CC vascular endothelial cell proximate to the cell, with an antibody (or its CC antigen-binding fragment), which binds specifically to the extracellular CC domain of PSMA in an amount sufficient to ablate or kill the cell. The CC antibodies have anti-psoriatic, antiarthritic, dermatological, cytostatic, CC antiinflammatory and antiallergic activities, and can be used in CC vaccines. M1 is useful for treating a skin disorder in a subject, by CC administering to the subject, an amount of an antibody which binds CC specifically to the extracellular domain of PSMA (the subject is a CC mammal, preferably human and is having, or at risk of, a skin disorder). CC The skin disorder is a dermal or an epidermal disorder, and is selected CC from psoriasis (preferably chronic stationary psoriasis, psoriasis vulgaris, eruptive (glutate) psoriasis, psoriatic erythroderma, generalised pustular psoriasis (Von Zumbusch), annular pustular psoriasis, and localised pustular psoriasis), psoriatic arthritis, exfoliative dermatitis, pityriasis rubra pilaris, pityriasis rosacea, parapsoriasis, pityriasis lichenoides, lichen planus, lichen nitidus, ichthyosiform dermatosis, keratodermas, dermatosis, and prokeratosis, preferably psoriasis. M1 is useful for treating a skin disorder such as an inflammatory or neoplastic disorder of the epidermis or dermis, preferably an epithelial precancerous or cancerous lesion. M1 is also useful to treat or prevent disorders involving aberrant activity of PSMA-expressing cell, e.g. kidney, liver or brain cell. ACC69816 to ACC69837 and ABR4613 to ABR4733 represent sequences used in the exemplification of the present invention

CC SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; DB 1
OY 1 WGQGTTVTVSS 11
Db 1 WGQGTTVTVSS 11

RESULT 12 ADG75671
ID ADG75671 standard; peptide; 11 AA.
XX AC ADG75671;
XX DT 11-MAR-2004 (first entry)
XX Peptide of the human heavy chain framework region 4 SeqID135.
XX DB interleukin-9; IL-9; anti-IL-9; antibody; MH9A3; MH9D1; MH9L1;
XX KW bronchial hyperresponsiveness; asthma; atopic allergy;
XX KW mucin overproduction; chronic obstructive pulmonary disorder;
XX KW cystic fibrosis; chronic obstructive pulmonary disorder; antiallergic;
XX KW antiasthmatic; cytostatic; human.
OS Homo sapiens.
XX PN WO2003086458-A1.
XX PD 23-OCT-2003.
XX PF 11-RPR-2003; 2003MO-US01113.
XX PR 12-APR-2002; 2002US-0371683P.
XX PR 12-APR-2002; 2002US-0371728P.
XX PA (MED-) MEDIMMUNE INC.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Reed JL, Dall'acqua W, Van Snick J, Renaud J, Cormont F,
PI Uttenhoffe C,
XX DR WPI; 2003-845267/78.
XX PT New antibody or antibody fragment that specifically binds to IL-9, useful
PT for preparing a composition for preventing or treating e.g., atopic
PT allergy, asthma, mucin overproduction, chronic obstructive pulmonary
PT disorder or cystic fibrosis.

XX Disclosure; SEQ ID NO 135; 206pp; English.
XX This invention relates to novel humanised and chimeric antibody
CC molecules and functional fragments thereof, which have specificity for
CC human interleukin-9 (IL-9). Specifically, it refers to recombinant
CC antibodies derived from several mouse anti-IL-9 monoclonal antibodies,
CC namely, MH9A3, MH9D1 and MH9L1. The present invention describes using the
CC humanised and chimeric antibody molecules to treat, prevent and/or
CC ameliorate disorders including bronchial hyperresponsiveness, asthma,
CC atopic allergy, mucin overproduction, chronic obstructive pulmonary
disorder, cystic fibrosis, chronic obstructive pulmonary disorder,

PT binds to human glucose-6-phosphate isomerase.
XX
XX Claim 6; FIG 4B; 47pp; English.
XX The invention describes an immunopeptide comprising a polypeptide
CC that binds to human glucose-6-phosphate isomerase (GPI). The methods and
compositions are used for diagnosis and treatment of human autoimmune
disease, e.g., human rheumatoid arthritis. This is the amino acid
sequence of human anti-GPI-antibody heavy chain variable region framework
region
XX SQ Sequence 11 AA;
Query Match 100.0%; Score 59; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; DB 1
OY 1 WGQGTTVTVSS 11
Db 1 WGQGTTVTVSS 11

CC excessive T cell or neutrophil activity. Accordingly, these IL-9 antagonists exhibit antiallergic, antiasthmatic and cytostatic activities. This peptide sequence is a peptide from the human heavy chain framework region 4, used in an exemplification of the invention.

XX Sequence 11 AA:

Query Match 100.0%; Score 59; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011; Indels 0; Gaps 0;
CC Matches 11; Conservative 0; Mismatches 0; XX

Qy 1 WGQGTTVTVSS 11
Db 1 WGQGTTVTVSS 11

RESULT 13

ID ADH17960
XX ADH17960 standard; peptide; 11 AA.

AC

XX ADH17960;

DT

11-MAR-2004 (first entry)

DE Human modified 15H12/19D12 HCA framework region 4 peptide.

XX

KW insulin-like growth factor receptor 1; IGFR1; cytostatic; osteopathic; antiatherosclerotic; antipsoriatic; vasotropic; antidiarrhoeal; acromegaly; bladder cancer; Wilm's tumour; ovarian; pancreatic; benign prostatic hyperplasia; breast; prostate; bone; lung; colorectal; cervical; synovial sarcoma; diarrhoea; carcinoid syndrome; vasoactive intestinal peptide; gigantism; psoriasis; atherosclerosis; smooth muscle restenosis; blood vessel; microvascular proliferation; gene therapy; human; 15H12/19D12; heavy chain A; HCA; framework region.

OS Synthetic.

OS Homo sapiens.

XX

WO2003100008-A2.

PN

XX

PD 04-DEC-2003.

XX

PP 22-MAY-2003; 2003WO-US016283.

XX

PR 24-MAY-2002; 2002US-0383459P.

XX

PR 02-JUL-2002; 2002US-0393214P.

XX

PR 23-DEC-2002; 2002US-0436254P.

XX

PA (ISCHÉ) SCHERING CORP.

XX

PI Wang Y, Greenberg R, Presta L, Pachter JA, Hailey J, Brams P;

XX PI Williams D, Srinivasan M, Feingersh D;

DR WPI: 2004-042807/04.

DR DR N-PSDB; ADH17959.

XX

PT New binding composition that specifically binds to insulin-like growth factor receptor 1, useful for treating or preventing a medical condition that is mediated by elevated expression or activity of IGFR1.

XX

PS Disclosure; SEQ ID NO 69; 144P; English.

XX

CC The invention relates to a novel binding composition that specifically binds to insulin-like growth factor receptor 1 (IGFR1). The composition of the invention demonstrates cytostatic, osteopathic, antiatherosclerotic, antipsoriatic, vasotropic and antidiarrhoeal activities and may be useful for preventing or treating a medical condition selected from acromegaly, bladder cancer, Wilm's cancer, ovarian cancer, pancreatic cancer, benign prostatic hyperplasia, breast cancer, prostate cancer, bone cancer, lung cancer, colorectal cancer, cervical cancer, synovial sarcoma, diarrhoea associated with carcinoid syndrome, vasoactive intestinal peptide secreting tumours, gigantism, psoriasis, atherosclerosis, smooth muscle restenosis of blood vessels and

CC inappropriate microvascular proliferation. The composition may also have CC gene therapy applications. The current sequence is that of the human CC 15H12/19D12 heavy chain A (HCA) framework region peptide of the CC invention.

XX Sequence 11 AA:

Query Match 100.0%; Score 59; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011; Indels 0; Gaps 0;
CC Matches 11; Conservative 0; Mismatches 0; XX

Qy 1 WGQGTTVTVSS 11
Db 1 WGQGTTVTVSS 11

RESULT 14

ID ADH18011
XX ADH18011 standard; peptide; 11 AA.

AC

XX ADH18011;

DT

11-MAR-2004 (first entry)

DE Human modified 15H12/19D12 HCB framework region 4 peptide.

XX

KW insulin-like growth factor receptor 1; IGFR1; cytostatic; osteopathic; antiatherosclerotic; antipsoriatic; vasotropic; antidiarrhoeal; acromegaly; bladder cancer; Wilm's tumour; ovarian; pancreatic; benign prostatic hyperplasia; breast; prostate; bone; lung; colorectal; cervical; synovial sarcoma; diarrhoea; carcinoid syndrome; vasoactive intestinal peptide; gigantism; psoriasis; atherosclerosis; smooth muscle restenosis; blood vessel; microvascular proliferation; gene therapy; human; 15H12/19D12; heavy chain B; LCB; framework region.

OS Synthetic.

OS Homo sapiens.

XX

WO2003100008-A2.

PN

XX

PD 04-DEC-2003.

XX

PP 22-MAY-2003; 2003WO-US016283.

XX

PR 24-MAY-2002; 2002US-0383459P.

XX

PR 02-JUL-2002; 2002US-0393214P.

XX

PR 23-DEC-2002; 2002US-0436254P.

XX

PA (ISCHÉ) SCHERING CORP.

XX

PI Wang Y, Greenberg R, Presta L, Pachter JA, Hailey J, Brams P;

XX PI Williams D, Srinivasan M, Feingersh D;

DR WPI: 2004-042807/04.

DR DR N-PSDB; ADH18010.

XX

PT New binding composition that specifically binds to insulin-like growth factor receptor 1, useful for treating or preventing a medical condition that is mediated by elevated expression or activity of ISFR1.

XX

PS Disclosure; SEQ ID NO 120; 144P; English.

XX

The invention relates to a novel binding composition that specifically binds to insulin-like growth factor receptor 1 (IGFR1). The composition of the invention demonstrates cytostatic, osteopathic, antiatherosclerotic, antipsoriatic, vasotropic and antidiarrhoeal activities and may be useful for preventing or treating a medical condition selected from acromegaly, bladder cancer, Wilm's cancer, ovarian cancer, pancreatic cancer, benign prostatic hyperplasia, breast cancer, prostate cancer, bone cancer, lung cancer, colorectal cancer, cervical cancer, synovial sarcoma, diarrhoea associated with carcinoid syndrome, vasoactive intestinal peptide secreting tumours, gigantism, psoriasis, atherosclerosis, smooth muscle restenosis of blood vessels and

CC inappropriate microvascular proliferation. The composition may also have
 CC gene therapy applications. The current sequence is that of the human
 CC 15H12/19H12 heavy Chain B (HCB) framework region peptide of the
 CC invention.

SQ

Sequence 11 AA:

Query Match 100.0%; Score 59; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.011; 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGQTIVTVSS 11
 Db 1 WGQGTRIVTVSS 11

RESULT 15

ADQ90791 ADQ90791 standard; protein; 11 AA.

XX ADQ90791;

XX DT 07-OCT-2004 (first entry)

XX DB Artificially deimmunised framework sequence #14.

XX insulin-related disorder; prostate specific membrane antigen; PSMA;
 KW obesity; hyperglycaemia; hypoglycemia; hyperinsulininaemia;
 KW insulin-resistance; impaired glucose tolerance; impaired fasting glucose;
 KW Type 1 diabetes mellitus; Type 2 diabetes mellitus; gestational diabetes.
 OS Synthetic.
 XX
 PN US2004136998-A1.
 XX PD 15-JUL-2004.
 XX PP 17-OCT-2003; 2003US-00688015.
 XX PR 30-OCT-2002; 2002US-0422396P.
 PA (BAND/) BANDER N H.
 XX PI Bander NH;
 XX DR WPI; 2004-533338/51.

XX PT Use of anti-prostate specific membrane antigen antibodies for treating or
 PT preventing insulin-related disorders, e.g. obesity, hyperglycemia,
 PT hypoglycemia, hyperinsulinemia, insulin-resistance, or Type 1 or 2
 PT diabetes mellitus.

XX PS Disclosure; SEQ ID NO 40; 89pp; English.
 XX
 CC The invention relates to a method of treating or preventing an insulin-
 CC related disorder in a subject which comprises administering an antibody
 CC or its antigen-binding portion specific for prostate specific membrane
 CC antigen (PSMA). The method is useful for treating an insulin-related
 CC disorder, including obesity, hyperglycaemia, hypoglycemia,
 CC hyperinsulinaemia, insulin resistance, impaired glucose tolerance,
 CC impaired fasting glucose, Type 1 diabetes mellitus, Type 2 diabetes
 CC mellitus, and gestational diabetes. The present sequence represents an
 XX artificially deimmunised framework sequence.

SQ Sequence 11 AA:

Query Match 100.0%; Score 59; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.011; 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGQTIVTVSS 11
 Db 1 WGQGTRIVTVSS 11

Search completed: December 4, 2005, 04:45:01
 Job time : 97.5625 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:45 ; Search time 15.5833 Seconds
(without alignments)
67.918 Million cell updates/sec

Title: US-10-632-706-198
Perfect score: 59
Sequence: 1 WGQGTTVTWSS 11
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.4
1: PIR1:
2: PIR2:
3: PIR3:
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

| Result No. | Score | Query | % Match | Length | DB ID | Description |
|------------|-------|-------|---------|--------|---------|---|
| 1 | 59 | 100.0 | 74 | 2 | S226793 | Ig heavy chain V region - human |
| 2 | 59 | 100.0 | 110 | 2 | PH1655 | C;Species: Homo sapiens (man) |
| 3 | 59 | 100.0 | 113 | 2 | S55533 | C;Accession: S26793 |
| 4 | 59 | 100.0 | 113 | 2 | S55535 | R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W. |
| 5 | 59 | 100.0 | 113 | 2 | S55530 | Bur. J. Immunol. 22, 241-245, 1992 |
| 6 | 59 | 100.0 | 113 | 2 | S55534 | A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami |
| 7 | 59 | 100.0 | 113 | 2 | S55532 | A;Reference number: S26786; MUID:92111632; PMID:1730251 |
| 8 | 59 | 100.0 | 113 | 2 | S55531 | A;Accession: S26793 |
| 9 | 59 | 100.0 | 113 | 2 | S55532 | A;Status: preliminary |
| 10 | 59 | 100.0 | 114 | 2 | S46392 | A;Molecule type: mRNA |
| 11 | 59 | 100.0 | 114 | 2 | S20706 | A;Residues: 1-74 <MOR> |
| 12 | 59 | 100.0 | 115 | 2 | S20706 | C;Superfamily: immunoglobulin V region; immunoglobulin homology |
| 13 | 59 | 100.0 | 116 | 2 | S15672 | C;Keywords: heterotetramer; immunoglobulin <IMM> |
| 14 | 59 | 100.0 | 116 | 2 | S55542 | R;Hillson, J.L.; Karr, N.S.; Oppenheimer, I.R.; Mannik, M.; Sasso, E.H. |
| 15 | 59 | 100.0 | 117 | 2 | S55541 | J. Exp. Med. 178, 331-336, 1993 |
| 16 | 59 | 100.0 | 118 | 2 | PH1660 | A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo |
| 17 | 59 | 100.0 | 118 | 2 | S32786 | A;Accession: PH1642; MUID:93301610; PMID:8310388 |
| 18 | 59 | 100.0 | 119 | 2 | PH0961 | A;Molecule type: mRNA |
| 19 | 59 | 100.0 | 120 | 2 | PH1650 | A;residues: 1-110 <HL> |
| 20 | 59 | 100.0 | 120 | 2 | E94590 | A;Cross-references: UNIPARC:UPI0000176BDC |
| 21 | 59 | 100.0 | 120 | 2 | PD0008 | A;Experimental source: B cell |
| 22 | 59 | 100.0 | 120 | 2 | PD0008 | C;Superfamily: immunoglobulin V region; immunoglobulin homology |
| 23 | 59 | 100.0 | 120 | 2 | S55538 | C;Keywords: heterotetramer; immunoglobulin <IMM> |
| 24 | 59 | 100.0 | 120 | 2 | S55539 | F;7-90/Domain: immunoglobulin homology |
| 25 | 59 | 100.0 | 120 | 2 | S55537 | Query Match 100.0%; Score 59; DB 2; Length 110; |
| 26 | 59 | 100.0 | 120 | 2 | S55536 | Best Local Similarity 100.0%; Pred. No. 0.0032; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| 27 | 59 | 100.0 | 120 | 2 | S12953 | OY 1 WGQGTTVTWSS 11 |
| 28 | 59 | 100.0 | 121 | 2 | S31106 | |
| 29 | 100.0 | 121 | 2 | S55540 | | |

| Result No. | Score | Query | % Match | Length | DB ID | Description |
|------------|-------|-------|---------|--------|---------|---|
| 1 | 59 | 100.0 | 74 | 2 | S226793 | RESULT 1 |
| 2 | 59 | 100.0 | 110 | 2 | PH1655 | Ig heavy chain V region - human |
| 3 | 59 | 100.0 | 113 | 2 | S55533 | C;Species: Homo sapiens (man) |
| 4 | 59 | 100.0 | 113 | 2 | S55535 | C;Accession: S26793 |
| 5 | 59 | 100.0 | 113 | 2 | S55530 | R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W. |
| 6 | 59 | 100.0 | 113 | 2 | S55534 | Bur. J. Immunol. 22, 241-245, 1992 |
| 7 | 59 | 100.0 | 113 | 2 | S55532 | A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami |
| 8 | 59 | 100.0 | 113 | 2 | S55531 | A;Reference number: S26786; MUID:92111632; PMID:1730251 |
| 9 | 59 | 100.0 | 113 | 2 | S55532 | A;Accession: S26793 |
| 10 | 59 | 100.0 | 114 | 2 | S46392 | A;Status: preliminary |
| 11 | 59 | 100.0 | 114 | 2 | S20706 | A;Molecule type: mRNA |
| 12 | 59 | 100.0 | 115 | 2 | S20706 | A;Residues: 1-74 <HL> |
| 13 | 59 | 100.0 | 116 | 2 | S15672 | A;Cross-references: UNIPARC:UPI0000176BDC |
| 14 | 59 | 100.0 | 116 | 2 | S55542 | A;Experimental source: B cell |
| 15 | 59 | 100.0 | 117 | 2 | S55541 | C;Superfamily: immunoglobulin V region; immunoglobulin homology |
| 16 | 59 | 100.0 | 118 | 2 | PH1660 | C;Keywords: heterotetramer; immunoglobulin <IMM> |
| 17 | 59 | 100.0 | 118 | 2 | S32786 | F;7-90/Domain: immunoglobulin homology |
| 18 | 59 | 100.0 | 119 | 2 | PH0961 | Query Match 100.0%; Score 59; DB 2; Length 110; |
| 19 | 59 | 100.0 | 120 | 2 | PH1650 | Best Local Similarity 100.0%; Pred. No. 0.0032; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| 20 | 59 | 100.0 | 120 | 2 | E94590 | OY 1 WGQGTTVTWSS 11 |
| 21 | 59 | 100.0 | 120 | 2 | PD0008 | |
| 22 | 59 | 100.0 | 120 | 2 | PD0008 | |
| 23 | 59 | 100.0 | 120 | 2 | S55538 | |
| 24 | 59 | 100.0 | 120 | 2 | S55539 | |
| 25 | 59 | 100.0 | 120 | 2 | S55537 | |
| 26 | 59 | 100.0 | 120 | 2 | S55536 | |
| 27 | 59 | 100.0 | 120 | 2 | S12953 | |
| 28 | 59 | 100.0 | 121 | 2 | S31106 | |
| 29 | 100.0 | 121 | 2 | S55540 | | |

Db 100 WGQGTTVVSS 110
RESULT 3
 S5533 Ig heavy chain V region pε25 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
 C;Accession: S5533 R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
 J. Mol. Biol. 247, 932-946, 1995
 A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin
 utations in the variable region genes.
 A;Reference number: S55528; MUID:95239763; PMID:7536850
 A;Accession: S5533
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-113 <BOE>
 A;Cross-references: UNIPARC:UPI000011605; EMBL:X82594; NID:9854314; PIDN:CAA57930.1; PI
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin F;14-97/Domain: immunoglobulin homology <IMM>
 Query Match 100.0%; Score 59; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.0033; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WGQGTTVVSS 11
 Db 103 WGQGTTVVSS 113
RESULT 4
 S5535 Ig heavy chain V region pε23 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
 C;Accession: S5535 R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
 J. Mol. Biol. 247, 932-946, 1995
 A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin
 utations in the variable region genes.
 A;Reference number: S55528; MUID:95239763; PMID:7536850
 A;Accession: S5535
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-113 <BOE>
 A;Cross-references: UNIPARC:UPI00001161PC; EMBL:X82594; NID:9854292; PIDN:CAA57920.1; PI
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin F;14-97/Domain: immunoglobulin homology <IMM>
 Query Match 100.0%; Score 59; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.0033; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WGQGTTVVSS 11
 Db 103 WGQGTTVVSS 113
RESULT 5
 S5530 Ig heavy chain V region pε17 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
 C;Accession: S5530 R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
 J. Mol. Biol. 247, 932-946, 1995
 A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin
 utations in the variable region genes.
 A;Reference number: S55528; MUID:95239763; PMID:7536850
 A;Accession: S5530
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-113 <BOE>
 A;Cross-references: UNIPARC:UPI00001161FB; EMBL:X82585; NID:9854294; PIDN:CAA57921.1; PI
 A;Accession: S5529
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-113 <BOE>
 A;Cross-references: UNIPARC:UPI00001161FB; EMBL:X82583; NID:9854290; PIDN:CAA57919.1; PI
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin F;14-97/Domain: immunoglobulin homology <IMM>
 Query Match 100.0%; score 59; DB 2; length 113;
 Best Local Similarity 100.0%; Pred. No. 0.0033;

RESULT 8
 Ig heavy chain V region pel19 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Accession: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
 A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin
 utations in the variable region genes.
 A;Reference number: S55328; MUID:95239763; PMID:7536850
 A;Accession: S5532
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residue: 1-113 <BOE>
 A;Cross-references: UNIPARC:UPI00001161FF; EMBL:X82588; NID:9854300; PIDN:CAA57924.1; PI
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;14-97/Domain: immunoglobulin homology <IMM>
 Query Match 100%; Score 59; DB 2; Length 113;
 Best Local Similarity 100%; Pred. No. 0.0033;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WGQGTTVTVSS 11
 DB 103 WGQGTTVTVSS 113

RESULT 9
 Ig heavy chain V region pel18 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Accession: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
 A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin
 utations in the variable region genes.
 A;Reference number: S55328; MUID:95239763; PMID:7536850
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-113 <BOE>
 A;Cross-references: UNIPARC:UPI00001161FF; EMBL:X82587; NID:9854298; PIDN:CMA57923.1; PI
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;14-97/Domain: immunoglobulin homology <IMM>
 Query Match 100%; Score 59; DB 2; Length 113;
 Best Local Similarity 100%; Pred. No. 0.0033;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WGQGTTVTVSS 11
 DB 103 WGQGTTVTVSS 113

RESULT 10.
 Ig heavy chain V region (VH-28) - human
 C;Species: Homo sapiens (man)
 C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
 C;Accession: S46392
 R;Fugini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
 R;McBride, C.J.; Winter, G.; Griffiths, A.D.

RESULT 11
 Ig heavy chain V region - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
 A;Title: Binding specificity and variable region sequences of two monoclonal antibo
 utations in the variable region genes.
 A;Reference number: S20706
 A;Accession: S20707
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-114 <BRE>
 A;Cross-references: UNIPARC:UPI0000176837; EMBL:ZI1916
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;12-95/Domain: immunoglobulin homology <IMM>
 Query Match 100%; Score 59; DB 2; Length 114;
 Best Local Similarity 100%; Pred. No. 0.0033;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WGQGTTVTVSS 11
 DB 104 WGQGTTVTVSS 114

RESULT 12
 Ig heavy chain V region - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 A;Title: Binding specificity and variable region sequences of two monoclonal antibo
 utations in the variable region genes.
 A;Reference number: S20706
 A;Accession: S20705
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-115 <BRE>
 A;Cross-references: UNIPROT:Q8R3V9; UNIPARC:UPI0000176C45; EMBL:ZI1914
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;12-97/Domain: immunoglobulin homology <IMM>
 Query Match 100%; Score 59; DB 2; Length 115;
 Best Local Similarity 100%; Pred. No. 0.0033;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WGQGTTVTVSS 11

Db 105 WGQGTTVTVSS 115

RESULT 13

Ig heavy chain V region - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C;Accession: S15672
 R;Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris, B.
 BioTechnology 9, 266-271, 1991
 A;Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial vi
 A;Reference number: S15672; MUID:11337412; PMID:1367535
 A;Accession: S15672
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-116 <TEM>
 A;Cross-references: UNIPARC:UPI00001161F8; EMBL:X82180; NID:951978; PIDN:CAA41644.1; PI
 C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 C;Keywords: heterotetramer; immunoglobulin homology
 F;15-98/domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.0033; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WGQGTTVTVSS 11
 Db 106 WGQGTTVTVSS 116

RESULT 14

Ig heavy chain V region pε2 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
 C;Accession: S55542
 R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
 J. Mol. Biol. 247, 932-946, 1995
 A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin
 g mutations in the variable region genes
 A;Reference number: S55542; MUID:95239763; PMID:7536850
 A;Accession: S55542
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-116 <BOE>
 A;Cross-references: UNIPARC:UPI00001161F9; EMBL:X82581; NID:9854302; PIDN:CAA57917.1; PI
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.0033; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WGQGTTVTVSS 11
 Db 106 WGQGTTVTVSS 116

RESULT 15

S55541
 Ig heavy chain V region pε1 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
 C;Accession: S55541
 R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
 J. Mol. Biol. 247, 932-946, 1995
 A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin
 g mutations in the variable region genes
 A;Reference number: S55542; MUID:95239763; PMID:7536850
 A;Accession: S55541
 A;Status: preliminary

A;Molecule type: mRNA
 A;Residues: 1-117 <BOE>
 A;Cross-references: UNIPARC:UPI00001161F8; EMBL:X82180; NID:951978; PIDN:CAA57916.1; PI
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.0034; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WGQGTTVTVSS 11
 Db 107 WGQGTTVTVSS 117

Search completed: December 4, 2005, 04:53:46
 Job time : 15.5833 Secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:08:08 ; Search time 3.20833 Seconds
(without alignments)
16.417 Million cell updates/sec

Title: US-10-632-706-198
Perfect score:
Sequence: 1 WCGGTTTVVSS 11

Scoring table: BLOSUM62
Gappen 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters:

26661

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications Ab_Net:*

- 1: /cggn2_6/ptcdatal1/pupbaa/us09 NEW PUB.pep:*
- 2: /cggn2_6/ptcdatal1/pupbaa/us06 NEW PUB.pep:*
- 3: /cggn2_6/ptcdatal1/pupbaa/us07 NEW PUB.pep:*
- 4: /cggn2_6/ptcdatal1/pupbaa/us08 NEW PUB.pep:*
- 5: /cggn2_6/ptcdatal1/pupbaa/pct_new_pub.pep:*
- 6: /cggn2_6/ptcdatal1/pupbaa/us10 NEW PUB.pep:*
- 7: /cggn2_6/ptcdatal1/pupbaa/us11 NEW PUB.pep:*
- 8: /cggn2_6/ptcdatal1/pupbaa/us60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|---------------------------------------|
| 1 | 59 | 100.0 | 11 | 6 US-10-839-799-114 Sequence 114, App |
| 2 | 59 | 100.0 | 11 | 6 US-10-839-799-129 Sequence 129, App |
| 3 | 59 | 100.0 | 11 | 7 US-11-108-135-7 Sequence 7, Appl |
| 4 | 59 | 100.0 | 20 | 7 US-11-030-159-4 Sequence 4, Appl |
| 5 | 59 | 100.0 | 20 | 7 US-11-054-669-107 Sequence 107, App |
| 6 | 59 | 100.0 | 113 | 7 US-11-144-248-20 Sequence 20, Appl |
| 7 | 59 | 100.0 | 116 | 7 US-11-174-186-20 Sequence 20, Appl |
| 8 | 59 | 100.0 | 116 | 7 US-11-174-186-21 Sequence 21, Appl |
| 9 | 59 | 100.0 | 116 | 7 US-11-174-186-22 Sequence 22, Appl |
| 10 | 59 | 100.0 | 116 | 7 US-11-174-186-23 Sequence 23, Appl |
| 11 | 59 | 100.0 | 116 | 7 US-11-174-186-24 Sequence 24, Appl |
| 12 | 59 | 100.0 | 116 | 7 US-11-174-186-25 Sequence 25, Appl |
| 13 | 59 | 100.0 | 117 | 6 US-10-839-999-132 Sequence 132, App |
| 14 | 59 | 100.0 | 117 | 7 US-11-034-66-120 Sequence 120, App |
| 15 | 59 | 100.0 | 118 | 6 US-10-932-334-75 Sequence 75, Appl |
| 16 | 59 | 100.0 | 118 | 7 US-11-012-353-71 Sequence 71, Appl |
| 17 | 59 | 100.0 | 120 | 6 US-10-932-334-71 Sequence 24, Appl |
| 18 | 59 | 100.0 | 120 | 7 US-11-095-074-2 Sequence 2, Appl |
| 19 | 59 | 100.0 | 121 | 7 US-11-108-135-24 Sequence 24, Appl |
| 20 | 59 | 100.0 | 124 | 6 US-10-932-334-13 Sequence 13, Appl |
| 21 | 59 | 100.0 | 124 | 7 US-11-044-48-9 Sequence 8, Appl |
| 22 | 59 | 100.0 | 124 | 7 US-11-040-159-6 Sequence 6, Appl |
| 23 | 59 | 100.0 | 124 | 7 US-11-040-159-8 Sequence 8, Appl |
| 24 | 59 | 100.0 | 124 | 7 US-11-095-074-14 Sequence 14, Appl |
| 25 | 59 | 100.0 | 125 | 7 US-11-144-248-16 Sequence 16, Appl |

ALIGNMENTS

| | | | | |
|----|----|-------|-----|--|
| 26 | 59 | 100.0 | 125 | 7 US-11-084-554-8 Sequence 8, Appl |
| 27 | 59 | 100.0 | 136 | 6 US-10-839-799-99 Sequence 99, Appl |
| 28 | 59 | 100.0 | 138 | 6 US-10-789-723-4 Sequence 4, Appl |
| 29 | 59 | 100.0 | 143 | 7 US-11-096-074-6 Sequence 6, Appl |
| 30 | 59 | 100.0 | 143 | 7 US-11-096-074-10 Sequence 10, Appl |
| 31 | 59 | 100.0 | 143 | 7 US-11-096-074-12 Sequence 12, Appl |
| 32 | 59 | 100.0 | 143 | 7 US-11-096-074-16 Sequence 16, Appl |
| 33 | 59 | 100.0 | 143 | 7 US-11-096-074-18 Sequence 18, Appl |
| 34 | 59 | 100.0 | 145 | 6 US-10-721-763-29 Sequence 29, Appl |
| 35 | 59 | 100.0 | 154 | 6 US-10-721-763-25 Sequence 25, Appl |
| 36 | 59 | 100.0 | 174 | 7 US-11-144-484-4 Sequence 4, Appl |
| 37 | 59 | 100.0 | 237 | 6 US-10-073-301A-9 Sequence 9, Appl |
| 38 | 59 | 100.0 | 237 | 7 US-11-054-515-2104 Sequence 2104, AP |
| 39 | 59 | 100.0 | 240 | 7 US-11-054-515-2105 Sequence 2105, AP |
| 40 | 59 | 100.0 | 240 | 7 US-11-054-515-2113 Sequence 2113, AP |
| 41 | 59 | 100.0 | 243 | 7 US-11-054-515-1927 Sequence 1927, AP |
| 42 | 59 | 100.0 | 243 | 7 US-11-054-515-1945 Sequence 1945, AP |
| 43 | 59 | 100.0 | 244 | 7 US-11-054-515-2058 Sequence 2058, AP |
| 44 | 59 | 100.0 | 247 | 7 US-11-054-515-1934 Sequence 1434, AP |
| 45 | 59 | 100.0 | 248 | 7 US-11-054-515-1008 Sequence 1008, AP |

INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-10-839-799-114
SEQUENCE DESCRIPTION: SEQ ID NO: 114:

US-11-108-135-7
SEQUENCE 7, Application US/1108135
Publication No. US20050260213A1
GENERAL INFORMATION:
APPLICANT: Koenig, Scott
APPLICANT: Veri, Maria Concetta
APPLICANT: Tuailon, Nadine
APPLICANT: Bonvin, Ezio
APPLICANT: Stavenhagen, Jeffrey
APPLICANT: Rankin, Christopher
TITLE OF INVENTION: Fc-gamma-RIB-specific antibodies and methods of use thereof

RESULT 2
US-10-839-799-129
Sequence 129, Application US/10839799
Publication No. US2005249726A1
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
APPLICANT: SATO, Koh
TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHADED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 132
MEDULLOBLASTOMA CELLS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 300 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/839,799
FILING DATE: 06-May-2004
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265
FILING DATE: 09-SEP-1996

APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994

APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993

ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.

REGISTRATION NUMBER: 25-258
REFERENCE/DOCKET NUMBER: 53466/184

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: 90436

INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 129:
US-10-839-799-129

Query Match 100.0%; Score 59; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0001; Pred. No. 0.0001; Indels 0; Mismatches 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVVS 11
Db 1 WGQGTTVVS 11

RESULT 4
US-11-040-159-4
Sequence 4, Application US/11040159
Publication No. US2005025552A1
GENERAL INFORMATION:
APPLICANT: Flynn, Peter
APPLICANT: Luehrsen, Kenneth
APPLICANT: Balint, Robert F.
APPLICANT: Her, Jeng-Hsing
APPLICANT: Bebbington, Christopher R.
APPLICANT: Yarranton, Geoffrey T.
APPLICANT: Kalobios, Inc.
TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential
TITLE OF INVENTION: Binding Determinants
FILE REFERENCE: 021167-001730US
CURRENT APPLICATION NUMBER: US/11/040,159
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: US 60/537,364
PRIOR FILING DATE: 2004-01-20
PRIOR APPLICATION NUMBER: US 60/546,216
PRIOR FILING DATE: 2004-02-23
NUMBER OF SEQ ID NOS: 133
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:JH6

US-11-040-159-4
Query Match 100.0%; Score 59; DB 7; Length 20;

Query Match 100.0%; Score 59; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0001; Pred. No. 0.0001; Indels 0; Mismatches 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVVS 11
Db 1 WGQGTTVVS 11

RESULT 3

Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVVS 11
Db 10 WGQGTTVVS 20

RESULT 5
US-11-054-669-107
; Sequence 107, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Roots, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054, 669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194, 975
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 107
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 59; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVVS 11
Db 10 WGQGTTVVS 20

RESULT 6
US-11-144-248-20
; Sequence 20, Application US/11144248
; Publication No. US2005244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIbODIES TO INSULIN-LIKE GROWTH FACTOR 1 RECEPTOR
; FILE REFERENCE: ABK-PF2
; CURRENT APPLICATION NUMBER: US/11/144, 248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038, 591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259, 927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-144-248-20

Query Match 100.0%; Score 59; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00086; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVVS 11
Db 103 WGQGTTVVS 113

RESULT 7
US-11-174-186-20
; Sequence 20, Application US/11174186
; Publication No. US2005024418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174, 186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288, 564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 20
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS VH veneered
; US-11-174-186-20

Query Match 100.0%; Score 59; DB 7; length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVVS 11
Db 106 WGQGTTVVS 116

RESULT 8
US-11-174-186-21
; Sequence 21, Application US/11174186
; Publication No. US2005024418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174, 186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288, 564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 21
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS de-immunized VH1
; US-11-174-186-21

Query Match 100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVVS 11
Db 106 WGQGTTVVS 116

RESULT 9
US-11-174-186-22
; Sequence 22, Application US/11174186
; Publication No. US2005024418A1
; GENERAL INFORMATION:

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; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.3
; SEQ ID NO: 22
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS de-immunized VH2
US-11-174-186-22

Query Match          100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WGQGTTVTVSS 11
Db      106 WGQGTTVTVSS 116

RESULT 10
US-11-174-186-23
; Sequence 23, Application US/11/174,186
; Publication No. US2005024418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugui
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.3
; SEQ ID NO: 23
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS de-immunized VH3
US-11-174-186-23

Query Match          100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WGQGTTVTVSS 11
Db      106 WGQGTTVTVSS 116

RESULT 11
US-11-174-186-24
; Sequence 24, Application US/11/174,186
; Publication No. US2005024418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugui
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.3
; SEQ ID NO: 24
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS de-immunized VH4
US-11-174-186-24

Query Match          100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WGQGTTVTVSS 11
Db      106 WGQGTTVTVSS 116

RESULT 12
US-11-174-186-25
; Sequence 25, Application US/11/174,186
; Publication No. US2005024418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugui
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.3
; SEQ ID NO: 25
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS de-immunized VH5
US-11-174-186-25

Query Match          100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WGQGTTVTVSS 11
Db      106 WGQGTTVTVSS 116

RESULT 13
US-10-839-799-132
; Sequence 132, Application US/10839799
; Publication No. US20050249726A1
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; SATO, Koh
; TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:

```

US-10-932-334-75

; Sequence 75, Application US/10932334

; Publication No. US20050249728A1

; GENERAL INFORMATION:

; APPLICANT: Immunogen, Inc.

; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY

; FILE REFERENCE: A8689

; CURRENT APPLICATION NUMBER: US/10/932,334

; CURRENT FILING DATE: 2004-09-02

; PRIOR APPLICATION NUMBER: US/10/729,441

; PRIOR FILING DATE: 2003-12-08

; PRIOR APPLICATION NUMBER: 10/170,390

; PRIOR FILING DATE: 2002-06-14

; NUMBER OF SEQ ID NOS: 96

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 75

; LENGTH: 118

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: synthetic antibody structure

US-10-932-334-75

; Query Match Score 59; DB 6; Length 117;

; Best Local Similarity 100.0%; Pred. No. 0.00089;

; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Qy 1 WGQGTTVVS 11

; Db 107 WGQGTTVVS 117

RESULT 14
 US-11-054-669-120
 ; Sequence 120, Application US/11054669
 ; Publication No. US20050261480A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Foote, Jefferson
 ; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
 ; FILE REFERENCE: 30219/US/3
 ; CURRENT APPLICATION NUMBER: US/11/054,669
 ; CURRENT FILING DATE: 2005-02-08
 ; PRIOR APPLICATION NUMBER: US 10/194,975
 ; PRIOR FILING DATE: 2002-07-12
 ; PRIOR APPLICATION NUMBER: US 60/305,111
 ; PRIOR FILING DATE: 2001-07-12
 ; NUMBER OF SEQ ID NOS: 124
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO: 120
 ; LENGTH: 117
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-054-669-120

Query Match Score 59; DB 7; Length 117;

; Best Local Similarity 100.0%; Pred. No. 0.00089;

; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Qy 1 WGQGTTVVS 11

; Db 107 WGQGTTVVS 117

RESULT 15
 US-11-054-669-120
 ; Sequence 75, Application US/10932334
 ; Publication No. US20050249728A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Immunogen, Inc.
 ; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
 ; FILE REFERENCE: A8689
 ; CURRENT APPLICATION NUMBER: US/10/932,334
 ; CURRENT FILING DATE: 2004-09-02
 ; PRIOR APPLICATION NUMBER: US/10/729,441
 ; PRIOR FILING DATE: 2003-12-08
 ; PRIOR APPLICATION NUMBER: 10/170,390
 ; PRIOR FILING DATE: 2002-06-14
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 75

; LENGTH: 118

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: synthetic antibody structure

; US-10-839-799-132

Search completed: December 4, 2005, 04:37:50
 Job time : 3.20833 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2005, 04:08:08 ; Search time 3.20833 Seconds

16.417 Million cell updates/sec

Title: US-10-632-706-198
Perfect score: 59
Sequence: 1 WGQGTTVTVSS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database : Published Applications AA New:*

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6: /cgns_6/ptodata/1/pubpaas/US11_NEW_PUB_pep:*
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8: /cgns_6/ptodata/1/pubpaas/US60_NEW_PUB_pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|-------------------|
| 1 | 59 | 100.0 | 11 | US-10-839-799-114 |
| 2 | 59 | 100.0 | 11 | US-10-839-799-129 |
| 3 | 59 | 100.0 | 11 | US-11-098-074-18 |
| 4 | 59 | 100.0 | 20 | US-11-094-159-4 |
| 5 | 59 | 100.0 | 20 | US-11-054-669-107 |
| 6 | 59 | 100.0 | 113 | US-11-144-248-20 |
| 7 | 59 | 100.0 | 116 | US-11-174-186-20 |
| 8 | 59 | 100.0 | 116 | US-11-174-186-21 |
| 9 | 59 | 100.0 | 116 | US-11-174-186-22 |
| 10 | 59 | 100.0 | 116 | US-11-174-186-23 |
| 11 | 59 | 100.0 | 116 | US-11-174-186-24 |
| 12 | 59 | 100.0 | 116 | US-11-174-186-25 |
| 13 | 59 | 100.0 | 117 | US-10-839-799-132 |
| 14 | 59 | 100.0 | 117 | US-11-054-669-120 |
| 15 | 59 | 100.0 | 118 | US-10-932-334-75 |
| 16 | 59 | 100.0 | 118 | US-11-013-353-71 |
| 17 | 59 | 100.0 | 120 | US-10-932-334-71 |
| 18 | 59 | 100.0 | 120 | US-11-096-074-2 |
| 19 | 59 | 100.0 | 121 | US-11-108-135-24 |
| 20 | 59 | 100.0 | 124 | US-10-932-334-13 |
| 21 | 59 | 100.0 | 124 | US-11-144-248-8 |
| 22 | 59 | 100.0 | 124 | US-11-040-159-6 |
| 23 | 59 | 100.0 | 124 | US-11-040-159-8 |
| 24 | 59 | 100.0 | 124 | US-11-096-074-14 |
| 25 | 59 | 100.0 | 125 | US-11-144-248-16 |

ALIGNMENTS

RESULT 1
US-10-839-799-114
; Sequence 114, Application US/10839799
; Publication No. US20050249726A1
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; SATO, Ken
; TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; MELANOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/839,799
; FILING DATE: 06-May-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265
; FILING DATE: 09-SEP-1995
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; US-10-839-799-114
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 114:

; US-11-108-135-7
 ; Sequence 7, Application US/1108135

; Publication No. US20050260213A1

; GENERAL INFORMATION:

; APPLICANT: Koenig, Scott

; APPLICANT: Vari, Maria Concetta

; APPLICANT: Tuillion, Nadine

; APPLICANT: Bonvini, Ezio

; APPLICANT: Stavenhagen, Jeffrey

; APPLICANT: Rankin, Christopher

; TITLE OF INVENTION: IgG-gamma-RIB-specific antibodies and methods of use thereof

; FILE REFERENCE: 11183-014-999

; CURRENT APPLICATION NUMBER: US/11108,135

; PRIORITY NUMBER: US 60/582,045

; PRIORITY FILING DATE: 2004-06-21

; PRIORITY APPLICATION NUMBER: US 60/582,044

; PRIORITY FILING DATE: 2005-02-18

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO: 7

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Homo sapiens

; OTHER INFORMATION: Framework sequence from human germline VH1-18 and JH6 - FR4

; US-11-108-135-7

; Sequence 4, Application US/11040159

; Publication No. US2005025552A1

; GENERAL INFORMATION:

; APPLICANT: Flynn, Peter

; APPLICANT: Lubarsen, Kenneth

; APPLICANT: Balint, Robert F.

; APPLICANT: Her, Jeng-Horng

; APPLICANT: Bebbington, Christopher R.

; APPLICANT: Yarranton, Geoffrey T.

; APPLICANT: Kalobios Inc.

; TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential

; TITLE OF INVENTION: Binding Determinants

; FILE REFERENCE: 021167-001730US

; CURRENT APPLICATION NUMBER: US/11/040,159

; CURRENT FILING DATE: 2005-01-20

; PRIORITY NUMBER: US 60/537,364

; PRIORITY FILING DATE: 2004-01-20

; PRIORITY APPLICATION NUMBER: US 60/546,216

; PRIORITY FILING DATE: 2004-02-23

; NUMBER OF SEQ ID NOS: 133

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO: 4

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: Other Information: Description of Artificial Sequence:JH6

; OTHER INFORMATION: Description of Artificial Sequence:JH6

; US-11-040-159-4

; Sequence Match

; Best Local Similarity 100.0%; Score 59; DB 7; Length 11;

; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Query Match

; Best Local Similarity 100.0%; Pred. No. 0.0001; Indels 0; Gaps 0;

; Matches 11; Conservative 0; Mismatches 0;

; Query Match

; Best Local Similarity 100.0%; Pred. No. 0.0001; Indels 0; Gaps 0;

; Matches 11; Conservative 0; Mismatches 0;

; Query Match

; Best Local Similarity 100.0%; Pred. No. 0.0001; Indels 0; Gaps 0;

; Matches 11; Conservative 0; Mismatches 0;

; Query Match

; Best Local Similarity 100.0%; Pred. No. 0.0001; Indels 0; Gaps 0;

; Matches 11; Conservative 0; Mismatches 0;

; Query Match

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; Matches 11; Conservative 0; Mismatches 0;

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; Matches 11; Conservative 0; Mismatches 0;

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; Matches 11; Conservative 0; Mismatches 0;

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; Query Match

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; Matches 11; Conservative 0; Mismatches 0;

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; Matches 11; Conservative 0; Mismatches 0;

; Query Match

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; Matches 11; Conservative 0; Mismatches 0;

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; Matches 11; Conservative 0; Mismatches 0;

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; Query Match

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; Query Match

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; Matches 11; Conservative 0; Mismatches 0;

; Query Match

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; Query Match

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; Matches 11; Conservative 0; Mismatches 0;

; Query Match

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; Best Local Similarity 100.0%; Pred. No. 0.0001; Indels 0; Gaps 0;

; Matches 11; Conservative 0; Mismatches 0;

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; Matches 11; Conservative 0; Mismatches 0;

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; Matches 11; Conservative 0; Mismatches 0;

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; Matches 11; Conservative 0; Mismatches 0;

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; Best Local Similarity 100.0%; Pred. No. 0.0001; Indels 0; Gaps 0;

; Matches 11; Conservative 0; Mismatches 0;

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; Matches 11; Conservative 0; Mismatches 0;

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; Matches 11; Conservative 0; Mismatches 0;

; Query Match

; Best Local Similarity 100.0%; Pred. No. 0.0001; Indels 0; Gaps 0;

; Matches 11; Conservative 0; Mismatches 0;

; Query Match

; Best Local Similarity 100.0%; Pred. No. 0.0001; Indels 0; Gaps 0;

; Matches 11; Conservative 0; Mismatches 0;

; Query Match

; Best Local Similarity 100.0%; Pred. No. 0.0001; Indels 0; Gaps 0;

; Matches 11; Conservative 0; Mismatches 0;

; Query Match

; Best Local Similarity 100.0%; Pred. No. 0.0001; Indels 0; Gaps 0;

; Matches 11; Conservative 0; Mismatches 0;

; Query Match

Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
Db 10 WGQGTTVTVSS 20

RESULT 5

US-11-054-669-107
Sequence 107, Application US/11054669
Publication No. US20050261480A1

GENERAL INFORMATION:

APPLICANT: Foote, Jefferson
TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REFERENCE: 30219US/3

CURRENT APPLICATION NUMBER: US/11/054, 669
CURRENT FILING DATE: 2005-02-08

PRIOR APPLICATION NUMBER: US 10/194, 975
PRIOR FILING DATE: 2002-07-12

PRIOR APPLICATION NUMBER: US 60/305, 111
PRIOR FILING DATE: 2001-07-12

NUMBER OF SEQ ID NOS: 124
SOFTWARE: PatentIn version 3.3

SEQ ID NO 107
LENGTH: 20

ORGANISM: PRT

US-11-054-669-107

Query Match 100.0%; Score 59; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00018; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
Db 10 WGQGTTVTVSS 20

RESULT 6

US-11-144-248-20
Sequence 20, Application US/11144248
Publication No. US20050244408A1

GENERAL INFORMATION:

APPLICANT: Cohen, Bruce D.
TITLE OF INVENTION: ANTI-BODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2

CURRENT APPLICATION NUMBER: US/11/144, 248
CURRENT FILING DATE: 2005-06-02

PRIOR APPLICATION NUMBER: US/10/038, 591
PRIOR FILING DATE: 2002-01-04

PRIOR APPLICATION NUMBER: 60/259, 927
PRIOR FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 20
LENGTH: 113
TYPE: PRT

ORGANISM: Homo sapiens
US-11-144-248-20

Query Match 100.0%; Score 59; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00086; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
Db 103 WGQGTTVTVSS 113

RESULT 7

US-11-174-186-20
Sequence 20, Application US/11174186
Publication No. US20050244418A1

GENERAL INFORMATION:

APPLICANT: Gillies, Stephen
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019

CURRENT APPLICATION NUMBER: US/11/174, 186
CURRENT FILING DATE: 2005-07-01

PRIOR APPLICATION NUMBER: US 60/288, 564
PRIOR FILING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3

SEQ ID NO 20
LENGTH: 116
TYPE: PRT

ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: KS VH veneered

US-11-174-186-20

Query Match 100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
Db 106 WGQGTTVTVSS 116

RESULT 8

US-11-174-186-21
Sequence 21, Application US/11174186
Publication No. US20050244418A1

GENERAL INFORMATION:

APPLICANT: Lo, Kin-Ming
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019

CURRENT APPLICATION NUMBER: US/11/174, 186
CURRENT FILING DATE: 2005-07-01

PRIOR APPLICATION NUMBER: US 60/288, 564
PRIOR FILING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3

SEQ ID NO 21
LENGTH: 116
TYPE: PRT

ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: KS de-immunized VH1

US-11-174-186-21

Query Match 100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
Db 106 WGQGTTVTVSS 116

RESULT 9

US-11-174-186-22
Sequence 22, Application US/11174186
Publication No. US20050244418A1

GENERAL INFORMATION:

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; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 22
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PatentIn version 3.3
; US-11-174-186-22

Query Match          100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; MiMmatches 0;

Qy      1 WGGQTIVVSS 11
Db      106 WGQGTTVTVSS 116

RESULT 10
US-11-174-186-23
; Sequence 23, Application US/11/174,186
; Publication No. US2005024418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugui
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 23
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS de-immunized VH3
; US-11-174-186-23

Query Match          100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; MiMmatches 0;

Qy      1 WGGQTIVVSS 11
Db      106 WGQGTTVTVSS 116

RESULT 11
US-11-174-186-24
; Sequence 24, Application US/11/174,186
; Publication No. US2005024418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugui
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 24
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS- deimmunized VH4
; US-11-174-186-24

Query Match          100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; MiMmatches 0;

Qy      1 WGGQTIVVSS 11
Db      106 WGQGTTVTVSS 116

RESULT 12
US-11-174-186-25
; Sequence 25, Application US/11/174,186
; Publication No. US2005024418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugui
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 25
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS de-immunized VH5
; US-11-174-186-25

Query Match          100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; MiMmatches 0;

Qy      1 WGGQTIVVSS 11
Db      106 WGQGTTVTVSS 116

RESULT 13
US-10-839-799-132
; Sequence 132, Application US/10839799
; Publication No. US2005249726A1
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 4, 2005, 04:07:28 ; Search time 78.8333 Seconds (without alignments)

US-10-632-706-198 ; 58.302 Million cell updates/sec

Title: US-10-632-706-198

Perfect score: 59 Sequence 1 WGQGTTVTWSS 11

Sequence: 1 US-10-632-706-201

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0 Maximum Match 0%

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing First 45 summaries

Database : Published Applications AA Main:*

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2: /cgn2_6/pctodata/1/pubpaa/us08_pubcomb.pep:*

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6: /cgn2_6/pctodata/1/pubpaa/us11_pubcomb.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 59 | 100.0 | 11 | 3 | US-09-253-794-40 |
| 2 | 59 | 100.0 | 11 | 3 | US-09-828-708-78 |
| 3 | 59 | 100.0 | 11 | 3 | US-09-749-873-114 |
| 4 | 59 | 100.0 | 11 | 3 | US-09-749-873-129 |
| 5 | 59 | 100.0 | 11 | 3 | US-09-269-921-137 |
| 6 | 59 | 100.0 | 11 | 3 | US-09-563-222-157 |
| 7 | 59 | 100.0 | 11 | 3 | US-09-563-222-165 |
| 8 | 59 | 100.0 | 11 | 3 | US-09-563-222-181 |
| 9 | 59 | 100.0 | 11 | 3 | US-09-563-222-197 |
| 10 | 59 | 100.0 | 11 | 3 | US-09-509-098-179 |
| 11 | 59 | 100.0 | 11 | 4 | US-10-218-253-137 |
| 12 | 59 | 100.0 | 11 | 4 | US-10-161-351-4 |
| 13 | 59 | 100.0 | 11 | 4 | US-10-160-506-40 |
| 14 | 59 | 100.0 | 11 | 4 | US-10-310-113-26 |
| 15 | 59 | 100.0 | 11 | 4 | US-10-310-113-147 |
| 16 | 59 | 100.0 | 11 | 4 | US-10-310-113-148 |
| 17 | 59 | 100.0 | 11 | 4 | US-10-310-113-149 |
| 18 | 59 | 100.0 | 11 | 4 | US-10-310-113-150 |
| 19 | 59 | 100.0 | 11 | 4 | US-10-310-113-151 |
| 20 | 59 | 100.0 | 11 | 4 | US-10-310-113-152 |
| 21 | 59 | 100.0 | 11 | 4 | US-10-310-113-153 |
| 22 | 59 | 100.0 | 11 | 4 | US-10-310-113-154 |
| 23 | 59 | 100.0 | 11 | 4 | US-10-310-113-155 |
| 24 | 59 | 100.0 | 11 | 4 | US-10-310-113-156 |
| 25 | 59 | 100.0 | 11 | 4 | US-10-310-113-157 |
| 26 | 59 | 100.0 | 11 | 4 | US-10-310-113-158 |
| 27 | 59 | 100.0 | 11 | 4 | US-10-310-113-159 |

ALIGNMENTS

RESULT 1

US-09-253-794-40

; Sequence 40, Application US/09253794

; Patent No. US20020018750A1

; GENERAL INFORMATION:

; APPLICANT: HANSEN, Hans J.

; ATTORNEY: ARNOUR, Kathryn L.

; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED MOUSE MONOClonAL ANTIBODIES

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

SOFTWARE: PatentIn Release #1.0, Version #1.30

APPLICATION NUMBER: US/09/253,794

FILING DATE: 22-Feb-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/318,157

FILING DATE: 05-Oct-1994

ATTORNEY/AGENT INFORMATION:

NAME: SAXE, Bernhard D.

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 18733/464

TELEB COMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-253-794-40

Query Match 100.0%; Score 59; DB 3; Length 11; Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGQTIVTVSS 11
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 Db 1 WGQGTIVTVSS 11

RESULT 2
 US-09-828-708-78 Application US/09828708
 ; Sequence 78, Application US/09828708
 ; Patent No. US20030146753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ditzel, H.
 ; APPLICANT: Burton, D.
 ; APPLICANT: Schaller, M.
 ; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici-
 ; CURRENT FILING DATE: 2001-09-24
 ; NUMBER OF SEQ ID NOS: 123
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 78
 ; LENGTH: 11
 ; ORGANISM: Homo sapiens
 ; TYPE: PRT
 ; US-09-828-708-78

Query Match 100.0%; Score 59; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.01; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Type: amino acid
 QY 1 WGQGTIVTVSS 11
 Db 1 |||||
 ; US-09-749-873-114

RESULT 3
 US-09-749-873-114 Application US/09749873
 ; Sequence 114, Application US/09749873
 ; Publication No. US20030023045A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OHTOMO, Toshihiko
 ; SATO, Koh
 ; TSUCHIYA, Masayuki
 ; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
 ; NUMBER OF SEQUENCES: 132
 ; MEDIUM: MEDULLOBLASTOMA CELLS
 ; COMPUTER READABLE FORM:
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; MEDIUM TYPE: Floppy disk
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/749,873
 ; FILING DATE: 29-Dec-2000
 ; CLASSIFICATION: <Unknown>
 PROR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/646,265
 ; FILING DATE: 19-Nov-99
 ; APPLICATION NUMBER: JP 5-291078
 ; FILING DATE: 19-Nov-1993
 ATTORNEY/AGENT INFORMATION:
 ; NAME: WEGNER, Harold C.
 ; REGISTRATION NUMBER: 25,258
 ; REFERENCE/DOCKET NUMBER: S3466/184
 TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 672-5300
 ; TELEFAX: (202) 672-5399
 ; TELEX: 904136

INFORMATION FOR SEQ ID NO: 129:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 TOPology: linear
 MOLECULE TYPE: Peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 129:
 ; US-09-749-873-114

Query Match 100.0%; Score 59; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.01; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Type: amino acid
 TOPology: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 114:
 ; US-09-749-873-114

Query Match 100.0%; Score 59; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.01; Indels 0; Gaps 0;

QY 1 WGQGTTVTVSS 11
1 ||||||| 11
1 WGQGTTVTVSS 11

RESULT 5
US-09-269-921-137
; Sequence 137, Application US/09269921
; Publication No. US20030045691A1

GENERAL INFORMATION:
APPLICANT: Ono, Koichiro

APPLICANT: Ohomo, Toshihiko
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yoshimura, Yasushi
APPLICANT: Koishihara, Yasuo

TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
FILE REFERENCE: 35029-20007.00

CURRENT APPLICATION NUMBER: US/09/269,921
CURRENT FILING DATE: 1999-04-01
EARLIER APPLICATION NUMBER: PCT/JP97/03553

EARLIER FILING DATE: 1997-10-03
EARLIER APPLICATION NUMBER: JP 8-264756

NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 137
LENGTH: 11

TYPE: PRT
ORGANISM: Unknown

FEATURE:
OTHER INFORMATION: Description of Unknown Organism: JHG

PUBLICATION INFORMATION:
AUTHORS: Ravetch, J. et al.
JOURNAL: CELL

VOLUME: 27
PAGES: 583-591
DATE: 1981

US-09-269-921-137

RESULT 6
Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGQGTTVTVSS 11
1 ||||||| 11
1 WGQGTTVTVSS 11

Db US-09-563-222-165

QY 1 WGQGTTVTVSS 11
1 ||||||| 11
1 WGQGTTVTVSS 11

RESULT 7
US-09-563-222-165
; Sequence 165, Application US/09563222
; Publication No. US20030079253A1

GENERAL INFORMATION:
APPLICANT: Hiatt, Andrew

APPLICANT: Hein, Mich B.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN EUKARYOTIC CELLS
FILE REFERENCE: 310098.406

CURRENT APPLICATION NUMBER: US/09/563,222
CURRENT FILING DATE: 2000-05-02

NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 181
LENGTH: 11

TYPE: PRT
ORGANISM: Mus musculus

US-09-563-222-181

RESULT 8
Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGQGTTVTVSS 11
1 ||||||| 11
1 WGQGTTVTVSS 11

Db US-09-563-222-181

QY 1 WGQGTTVTVSS 11
1 ||||||| 11
1 WGQGTTVTVSS 11

RESULT 9
US-09-563-222-197
; Sequence 197, Application US/09563222
; Publication No. US20030079253A1

GENERAL INFORMATION:
APPLICANT: Hiatt, Andrew

APPLICANT: Hein, Mich B.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN EUKARYOTIC CELLS
FILE REFERENCE: 310098.406

CURRENT APPLICATION NUMBER: US/09/563,222
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 157
LENGTH: 11
TYPE: PRT
ORGANISM: Mus musculus
US-09-563-222-157

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CURRENT APPLICATION NUMBER: US/09/563,222
 CURRENT FILING DATE: 2000-05-02
 NUMBER OF SEQ ID NOS: 137
 SEQ ID NO: 137
 LENGTH: 11
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 197
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-563-222-197

Query Match 100 %; Score 59; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
 Db 1 WGQGTTVTVSS 11

RESULT 10
 US-09-509-098-179

Sequence 179, Application US/09509098
 Publication No. US20030103970A1

GENERAL INFORMATION:

APPLICANT: TSUCHIYA, MASAYUKI
 TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
 FILE REFERENCE: 034660274
 CURRENT APPLICATION NUMBER: US/09/509,098
 CURRENT FILING DATE: 2000-03-22
 PRIORITY APPLICATION NUMBER: PCT/JP98/04469
 PRIORITY FILING DATE: 1998-10-02
 PRIORITY FILING DATE: JPN 9-271726
 NUMBER OF SEQ ID NOS: 203
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 179
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Amino acid
 OTHER INFORMATION: Description of the H chain V-region JH6
 US-09-509-098-179

Query Match 100 %; Score 59; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
 Db 1 WGQGTTVTVSS 11

RESULT 11
 US-10-218-253-137

Sequence 137, Application US/10218253
 Publication No. US20030129105A1

GENERAL INFORMATION:

APPLICANT: Ono, Koichiro
 APPLICANT: Ohtomo, Toshihiko
 APPLICANT: Tsuchiya, Masayuki
 APPLICANT: Yoshimura, Yasushi
 APPLICANT: Koishihara, Yasuo
 TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
 CURRENT FILING DATE: 2002-11-21
 PRIORITY NUMBER: US/09/269, 921
 PRIORITY FILING DATE: 1999-04-01
 PRIORITY APPLICATION NUMBER: PCT/JP97/03553
 PRIORITY APPLICATION NUMBER: JP 8-264756
 PRIORITY FILING DATE: 1996-10-04

Query Match 100 %; Score 59; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
 Db 1 WGQGTTVTVSS 11

RESULT 12
 US-10-169-351-4

Sequence 4, Application US/10169351
 Publication No. US20030157090A1

GENERAL INFORMATION:

APPLICANT: BENVENTO, EUGENIO
 APPLICANT: FRANCONI, ROSELLA
 APPLICANT: DESIDERIO, ANGIOIA
 APPLICANT: TAVLADOURAKI, PARASKEVI
 TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES
 FILE REFERENCE: 4161-4
 CURRENT APPLICATION NUMBER: US/10/169, 351
 CURRENT FILING DATE: 2002-10-29
 PRIORITY APPLICATION NUMBER: PCT/IT00/00554
 PRIORITY FILING DATE: 2000-12-29
 PRIORITY APPLICATION NUMBER: IT RM99A000803
 PRIORITY FILING DATE: 1999-12-30
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 4
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: peptide
 US-10-169-351-4

Query Match 100 %; Score 59; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
 Db 1 WGQGTTVTVSS 11

RESULT 13
 US-10-160-506-40

Sequence 40, Application US/10160506
 Publication No. US20030161832A1

GENERAL INFORMATION:

APPLICANT: Bader, Neil H.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
 TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR
 TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
 FILE REFERENCE: 10448-162001

CURRENT APPLICATION NUMBER: US/10/160,506
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/324,100
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/342,612
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 40
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deimmunized heavy chain J415-4
; US-10-160-506-40

Query Match 100.0%; Score 59; DB 4; Length 11;
; Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Oy 1 WGQGTTVTVSS 11
; Db 1 WGQGTTVTVSS 11

RESULT 14
; US-10-310-113-26
; Sequence 26, Application US/10310113
; Publication No. US2003017664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; TITLE OF INVENTION: THROMBOSES
; FILE REFERENCE: 58122/7175B
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/443,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-310-113-26

Query Match 100.0%; Score 59; DB 4; Length 11;
; Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Oy 1 WGQGTTVTVSS 11
; Db 1 WGQGTTVTVSS 11

Search completed: December 4, 2005, 04:37:44
; Job time : 79.8333 secs

RESULT 15
; US-0-310-113-147
; Sequence 147, Application US/10310113
; Publication No. US2003017664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.

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GenCore version 5.1.6

Run on: December 4, 2005, 03:59:51 ; Search time 23.6042 Seconds

(without alignments)
38.528 Million cell updates/sec

OM protein - protein search, using sw model

Run on: December 4, 2005, 03:59:51 ; Search time 23.6042 Seconds

(without alignments)
38.528 Million cell updates/sec

Title: US-10-632-706-198

Perfect score: 59

Sequence: 1 WQGTTTVSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext. 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA,*

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2: /cgnt_6/prodata/1/iaa/6_COMB.pep: *
3: /cgnt_6/prodata/1/iaa/H_COMB.pep: *
4: /cgnt_6/prodata/1/iaa/PCTUS_COMB.pep: *
5: /cgnt_6/prodata/1/iaa/RE_COMB.pep: *
6: /cgnt_6/prodata/1/iaa/backfilesl.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Length | DB ID | Description |
|------------|-------|-------|--------|----------------------|--------------------|
| 1 | 59 | 100.0 | 11 | 1 US-08-471-780C-120 | Sequence 120, App |
| 2 | 59 | 100.0 | 11 | 1 US-08-467-282B-120 | Sequence 120, App |
| 3 | 59 | 100.0 | 11 | 1 US-08-471-282A-120 | Sequence 120, App |
| 4 | 59 | 100.0 | 11 | 1 US-08-318-157B-40 | Sequence 40, App |
| 5 | 59 | 100.0 | 11 | 1 US-08-466-710C-120 | Sequence 120, App |
| 6 | 59 | 100.0 | 11 | 2 US-08-468-739C-120 | Sequence 120, App |
| 7 | 59 | 100.0 | 11 | 2 US-08-646-265A-114 | Sequence 114, App |
| 8 | 59 | 100.0 | 11 | 2 US-08-646-265A-129 | Sequence 129, App |
| 9 | 59 | 100.0 | 11 | 2 US-09-253-794-40 | Sequence 40, App |
| 10 | 59 | 100.0 | 11 | 2 US-09-563-222C-146 | Sequence 146, App |
| 11 | 59 | 100.0 | 11 | 2 US-09-563-222C-169 | Sequence 169, App |
| 12 | 59 | 100.0 | 11 | 2 US-09-269-921-137 | Sequence 137, App |
| 13 | 59 | 100.0 | 11 | 2 US-09-293-769A-120 | Sequence 120, App |
| 14 | 59 | 100.0 | 13 | 6 51891-7-14 | Patent No. 5189147 |
| 15 | 59 | 100.0 | 15 | 1 US-08-765-179B-8 | Sequence 8, Appl |
| 16 | 59 | 100.0 | 15 | 6 51891-7-20 | Patent No. 5189147 |
| 17 | 59 | 100.0 | 16 | 4 PCT-US91-03942-91 | Sequence 91, Appl |
| 18 | 59 | 100.0 | 20 | 2 US-10-194-975-107 | Sequence 107, App |
| 19 | 59 | 100.0 | 22 | 4 PCT-US91-03942-100 | Sequence 100, App |
| 20 | 59 | 100.0 | 29 | 1 US-08-053-131-73 | Sequence 73, Appl |
| 21 | 59 | 100.0 | 29 | 1 US-08-645-641-73 | Sequence 73, Appl |
| 22 | 59 | 100.0 | 29 | 1 US-07-853-408B-73 | Sequence 73, Appl |
| 23 | 59 | 100.0 | 29 | 1 US-08-096-762-73 | Sequence 73, Appl |
| 24 | 59 | 100.0 | 29 | 1 US-08-308-665-73 | Sequence 73, Appl |
| 25 | 59 | 100.0 | 29 | 2 US-09-042-353-270 | Sequence 270, Appl |
| 26 | 59 | 100.0 | 29 | 2 US-08-758-17A-118 | Sequence 118, Appl |
| 27 | 59 | 100.0 | 29 | 4 PCT-US92-10983-73 | Sequence 73, Appl |

ALIGNMENTS

| | |
|----------|--|
| RESULT 1 | US-08-471-780C-120 |
| | Sequence 120, Application US/08471780C |
| | Patent No. 5759808 |
| | GENERAL INFORMATION: |
| | APPLICANT: Casterman, Cecile |
| | TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains |
| | NUMBER OF SEQUENCES: 130 |
| | CORRESPONDENCE ADDRESS: |
| | ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner |
| | STREET: 1300 I Street, N.W. |
| | CITY: Washington |
| | STATE: D.C. |
| | COUNTRY: USA |
| | ZIP: 20005-3315 |
| | COMPUTER READABLE FORM: |
| | COMPUTER: IBM PC compatible |
| | OPERATING SYSTEM: PC-DOS/MS-DOS |
| | CURRENT APPLICATION DATA: |
| | APPLICATION NUMBER: US/08/471,780C |
| | FILING DATE: 06-JUN-1995 |
| | CLASSIFICATION: 530 |
| | PRIOR APPLICATION DATA: |
| | APPLICATION NUMBER: US 08/106,944 |
| | FILING DATE: 17-AUG-1993 |
| | APPLICATION NUMBER: FR 92402326.0 |
| | FILING DATE: 21-AUG-1992 |
| | PRIOR APPLICATION DATA: |
| | APPLICATION NUMBER: FR 933401310.3 |
| | FILING DATE: 21-MAY-1993 |
| | ATTORNEY/AGENT INFORMATION: |
| | NAME: Potter, Jane E.R. |
| | REGISTRATION NUMBER: 33,332 |
| | REFERENCE/DOCKET NUMBER: 04958.0008-00000 |
| | TELECOMMUNICATION INFORMATION: |
| | TELEPHONE: 202-408-4000 |
| | TELEFAX: 202-408-4400 |
| | INFORMATION FOR SEQ ID NO: 120: |
| | SEQUENCE CHARACTERISTICS: |
| | LENGTH: 11 amino acids |
| | TYPE: amino acid |
| | TOPOLOGY: linear |
| | MOLECULE TYPE: peptide |
| | US-08-471-780C-120 |

Query Match 100.0%; Score 59; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;

RESULT 2
US-08-467-282B-120
; Sequence 120, Application US/08467282B
; Patent No. 5840583
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/471,282A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; FILING DATE: 21-AUG-1992
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-471-282A-120
; Query Match Score 59; DB 1; Length 11;
; Best Local Similarity 100.0%; Pred. No. 0.0017;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Qy 1 WGQGTTVSS 11
; Db 1 WGQGTTVSS 11
; RESULT 3
US-08-471-282A-120
; Sequence 120, Application US/08471282A
; Patent No. 5840583
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulines Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,157B
; FILING DATE: 05-OCT-1994

APPLICANT: ORTOMO, Toshihiko
 APPLICANT: SATO, Koh
 APPLICANT: TSUCHIYA, Masayuki.
 TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
 TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
 NUMBER OF SEQUENCES: 132
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,265A
 FILING DATE: 09-SEP-1996
 CLASSIFICATION: 435
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,265A
 FILING DATE: 09-SEP-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/JP94/01763
 FILING DATE: 19-OCT-1994
 PRIORITY/AGENT INFORMATION:
 NAME: WEGNER, Harold C.
 REGISTRATION NUMBER: 25,258
 REFERENCE/DOCKET NUMBER: 53466/184
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5300
 FILING DATE: 19-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: WEGNER, Harold C.
 REGISTRATION NUMBER: 25,258
 REFERENCE/DOCKET NUMBER: 53466/184
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5399
 FAX: 904136
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 114:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 TOPOLogy: Linear
 MOLECULE TYPE: peptide
 US-08-646-265A-114
 RESULT 8
 Query Match 100.0%; Score 59; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0017; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WGQGTTVTVSS 11
 Db 1 WGQGTTVTVSS 11
 RESULT 9
 US-09-253-794-40
 Sequence 40, Application US/09253794
 Patent No. 6676934
 GENERAL INFORMATION:
 APPLICANT: HANSEN, Hans J.
 TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
 TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
 NUMBER OF SEQUENCES: 58
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/253,794
 FILING DATE: 22-Feb-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/318,157
 FILING DATE: 05-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Saxe, Bertrand D.
 REGISTRATION NUMBER: 28,665
 REFERENCE/DOCKET NUMBER: 18733/464
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5300

RESULT 8
 US-08-646-265A-129
 Sequence 129, Application US/08646265A
 Patent No. 6214973
 GENERAL INFORMATION:
 APPLICANT: ORTOMO, Toshihiko
 APPLICANT: SATO, Koh
 APPLICANT: TSUCHIYA, Masayuki.
 TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
 TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
 NUMBER OF SEQUENCES: 132
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/253,794
 FILING DATE: 22-Feb-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/318,157
 FILING DATE: 05-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Saxe, Bertrand D.
 REGISTRATION NUMBER: 28,665
 REFERENCE/DOCKET NUMBER: 18733/464
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5300

MEDIUM TYPE: Floppy disk

TELEFAX: (202) 672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 STRANDEDNESS: <Unknown>
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 40:
 US-09-253-794-40

| Qy | 1 WGQGTTVTVSS 11 | 1 WGQGTTVTVSS 11 |
|----|------------------|------------------|
| Db | 1 WGQGTTVTVSS 11 | 1 WGQGTTVTVSS 11 |

Query Match 100.0%; Score 59; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0017; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
 US-09-563-222C-146
 ; Sequence 146, Application US/09563222C
 Patent No. 6696620
 GENERAL INFORMATION:
 APPLICANT: EPICYTE PHARMACEUTICALS, INC.
 APPLICANT: HIATT, ANDREW C.
 APPLICANT: HEIN, MICH B.
 TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
 FILE REFERENCE: 068904-0501
 CURRENT APPLICATION NUMBER: US/09/563, 222C
 CURRENT FILING DATE: 2000-05-02
 PRIOR APPLICATION NUMBER: PCT/US01/14349
 PRIOR FILING DATE: 2001-05-02
 PRIOR APPLICATION NUMBER: 09/563, 222
 PRIOR FILING DATE: 2000-05-02
 NUMBER OF SEQ ID NOS: 182
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 146
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-563-222C-146

| Qy | 1 WGQGTTVTVSS 11 | 1 WGQGTTVTVSS 11 |
|----|------------------|------------------|
| Db | 1 WGQGTTVTVSS 11 | 1 WGQGTTVTVSS 11 |

Query Match 100.0%; Score 59; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0017; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 US-09-563-222C-169
 ; Sequence 169, Application US/09563222C
 Patent No. 6696620
 GENERAL INFORMATION:
 APPLICANT: HIATT, ANDREW C.
 APPLICANT: EPICYTE PHARMACEUTICALS, INC.
 APPLICANT: HEIN, MICH B.
 TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
 FILE REFERENCE: 068904-0501
 CURRENT APPLICATION NUMBER: US/09/563, 222C
 CURRENT FILING DATE: 2000-05-02
 PRIOR APPLICATION NUMBER: PCT/US01/14349
 PRIOR FILING DATE: 2001-05-02
 PRIOR APPLICATION NUMBER: 09/563, 222
 PRIOR FILING DATE: 2000-05-02
 NUMBER OF SEQ ID NOS: 182
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 169

RESULT 12
 US-09-269-921-137
 ; Sequence 137, Application US/09269921
 Patent No. 6699374
 GENERAL INFORMATION:
 APPLICANT: Ono, Kochiro
 APPLICANT: Ohtomo, Toshihiko
 APPLICANT: Tsuchiya, Masayuki
 APPLICANT: Yoshimura, Yasuo
 TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
 FILE REFERENCE: 35029-20007.00
 CURRENT APPLICATION NUMBER: US/09/269, 921
 CURRENT FILING DATE: 1999-04-01
 EARLIER APPLICATION NUMBER: PCT/JP97/03553
 EARLIER FILING DATE: 1997-10-03
 EARLIER APPLICATION NUMBER: JP 8-264756
 EARLIER FILING DATE: 1996-10-04
 NUMBER OF SEQ ID NOS: 137
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 137
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: Description of Unknown Organism: JH6
 PUBLICATION INFORMATION:
 AUTHORS: Ravech, J. et al.
 JOURNAL: CELL
 VOLUME: 27
 PAGES: 583-591
 DATE: 1981
 US-09-269-921-137

| Qy | 1 WGQGTTVTVSS 11 | 1 WGQGTTVTVSS 11 |
|----|------------------|------------------|
| Db | 1 WGQGTTVTVSS 11 | 1 WGQGTTVTVSS 11 |

Query Match 100.0%; Score 59; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0017; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
 US-09-293-769A-120
 ; Sequence 120, Application US/09293769A
 Patent No. 6765087
 GENERAL INFORMATION:
 APPLICANT: CASTERMAN, CECELIE
 APPLICANT: HAMERS, RAYMOND
 TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
 FILE REFERENCE: 04958.0008-07000
 CURRENT APPLICATION NUMBER: US/09/293, 769A
 CURRENT FILING DATE: 1999-04-19
 PRIOR APPLICATION NUMBER: 08/471, 284
 PRIOR FILING DATE: 1995-06-05
 PRIOR APPLICATION NUMBER: 07/106, 944
 PRIOR FILING DATE: 1987-10-15
 PRIOR APPLICATION NUMBER: EPO 92402326.0

```

; PRIOR FILING DATE: 1992-08-21
; PRIOR APPLICATION NUMBER: EPO 93401310.3
; PRIOR FILING DATE: 1993-01-21
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn Ver. 2.1
; SBQ ID NO 120
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-293-769A-120

Query Match 100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017; Mismatches 0;
Matches 11; Conservative 0; Indels 0; Gaps 0;
Qy 1 WGQGTTVTVSS 11
Db 1 WGQGTTVTVSS 11

RESULT 14
5189147-14
; Patent No. 5189147
; APPLICANT: SATO, HARUO; KRANZ, DAVID M.; ELSEN, HERMAN N. ;
; TONEGAWA, SUSumu
; ANTIBODY
; TITLE OF INVENTION: METERODIMERIC T LYMPHOCYTE RECEPTOR
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/271,216
; FILING DATE: 14-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 666,988
; FILING DATE: 31-OCT-1984
; APPLICATION NUMBER: 670,122
; FILING DATE: 13-JUN-1984
; SEQ ID NO:14:
; LENGTH: 13
; 5189147-14

Query Match 100.0%; Score 59; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0023; Mismatches 0;
Matches 11; Conservative 0; Indels 0; Gaps 0;
Qy 1 WGQGTTVTVSS 11
Db 5 WGQGTTVTVSS 15

; US-08-765-179B-8
; Search completed: December 4, 2005, 04:09:45
; Job time : 24.6042 SECs
; FILING DATE: 14-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/02626
; FILING DATE: 06-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 25 115 .7
; FILING DATE: 15-JUL-1994
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-765-179B-8

Query Match 100.0%; Score 59; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0023; Mismatches 0;
Matches 11; Conservative 0; Indels 0; Gaps 0;
Qy 1 WGQGTTVTVSS 11
Db 5 WGQGTTVTVSS 15

; Search completed: December 4, 2005, 04:09:45
; Job time : 24.6042 SECs
; FILING DATE: 14-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/02626
; FILING DATE: 06-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 25 115 .7
; FILING DATE: 15-JUL-1994
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-765-179B-8

RESULT 15
US-08-765-179B-8
; Sequence 8, Application US/08765179B
; Patent No. 5854027
; GENERAL INFORMATION:
; APPLICANT: STELPE, Boris
; APPLICANT: STEINBACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
; TITLE OF INVENTION: OF ANTIBODIES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESS: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,179B
; APPLICATION NUMBER: US/08/765,179B

```


CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulinum
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain variable region complementarity determining
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.
 XX SQ Sequence 11 AA;

Query Match 100.0%; Score 60; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LATYYFFGLDV 11
 Db 1 LATYYFFGLDV 11

RESULT 2

ADR38725

ID ADR38725 standard; peptide; 11 AA.

XX AC ADR38725;

XX DT 02-DEC-2004 (first entry)

XX DE Mouse heavy chain variable region CDR3 seqid 127.

XX KW antibacter; antibody; botulinum neurotoxin type A; BONT/A;

XX KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;

XX KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;

XX KW heavy chain variable region; complementarity determining region; CDR3.

OS Mus sp.

XX US2004175385-A1.

XX PD 09-SEP-2004.

XX PR 01-AUG-2003; 2003US-00632706.

XX PR 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Marks JD, Ameredorfer P;

XX DR WPI; 2004-652009/63.

XX PT New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.

XX PS Example 3, SEQ ID NO 127; 110pp; English.

XX CC The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 (BONT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, IC6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WRI(V), WRI(M), 3-1,

CC 3-8, 3-10 and ING1, where (I) binds to and neutralises botulinum
 CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
 CC comprising BONT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain variable region complementarity determining
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.
 XX SQ Sequence 11 AA;

Query Match 100.0%; Score 60; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LATYYFFGLDV 11
 Db 1 LATYYFFGLDV 11

RESULT 3

AEB45960

ID AEB45960 standard; protein; 122 AA.

XX AC AEB45960;

XX DT 06-OCT-2005 (first entry)

XX DE Human monoclonal anti-MadCAM antibody related protein #4.

XX KW Monoclonal antibody; mucosal addressin cell adhesion molecule; MadCAM1

KW inflammation; inflammatory bowel disease; Crohn's disease;

KW ulcerative colitis; diverticular disease; gastritis; liver disease;

KW primary biliary cirrhosis; primary sclerosing cholangitis;

KW insulin dependent diabetes; graft versus host disease; antiinflammatory;

KW gastrointestinal-gen.; antiulcer; hepatotropic; antidiabetic;

KW immunosuppressive; antibody.

XX OS Homo sapiens.

XX PN WO2005067620-A2.

XX PD 28-JUL-2005.

XX PR 07-JAN-2005; 2005WO-US000370.

XX PR 09-JAN-2004; 20044US-0535490P.

XX PT (PFIZ) PFIZER INC.

PA (ABGENIX INC.

PA (PFIZ) PFIZER LTD.

XX DI Pullen N, Molloy E, Kellermann S, Green LI, Haak-Frendscho M;

XX DR WPI; 2005-554958/56.

XX PT New antibody to Mucosal Adressin Cell Adhesion Molecule, useful for
 PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel
 PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or
 PT graft versus host disease.

PS Example 5; Fig 1, 167pp; English.

XX The invention relates to a human monoclonal antibody or its antigen-binding portion that specifically binds to mucosal addressin cell adhesion molecule (MadCAM). The invention also relates to a hybridoma cell line that produces the human monoclonal antibody, a pharmaceutical composition comprising an amount of the monoclonal antibody or its antigen-binding portion and a pharmaceutical carrier, a method of treating inflammatory disease in a subject, an isolated cell line that produces the monoclonal antibody or its antigen-binding portion or the heavy chain or light chain of the antibody or of its portion, an isolated nucleic acid molecule comprising a nucleotide sequence encoding the heavy chain or its antigen-binding portion or the light chain or its antigen-binding portion of an antibody described above, a vector comprising the nucleic acid molecule, where the vector optionally comprises an expression control sequence operably linked to the nucleic acid molecule, a host cell comprising the vector or the nucleic acid molecule above, a method of producing a human monoclonal antibody or its antigen-binding portion that specifically binds MadCAM, a method of isolating an antibody or its antigen-binding portion that specifically binds to MadCAM, a method of treating a subject in need of a human antibody or its antigen-binding portion that specifically binds to MadCAM and inhibits binding to alpha4beta7, a method of inhibiting alpha4beta7 binding to cells expressing human MadCAM, a method of inhibiting MadCAM-mediated leukocyte -endothelial cell adhesion, migration and infiltration into tissues, a method of inhibiting alpha4beta7/MadCAM-dependent cellular adhesion, inhibiting the MadCAM-mediated recognition of lymphocytes to gastrointestinal lymphoid tissue, a method of diagnosing a disorder characterized by circulating soluble human MadCAM and detecting inflammation in a subject. The antibody, composition and methods are useful for diagnosing and treating inflammatory disease, e.g., CC intestinal bowel disease, Crohn's disease, ulcerative colitis, diverticular disease, gastritis, liver disease, primary biliary cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and graft versus host disease. This sequence represents a human monoclonal anti-MadCAM antibody related protein of the invention.

XX Sequence 122 AA;

SQ

Query Match

Best Local Similarity

Score

DB

Matches

Pred.

No.

2.5;

Mismatches

1;

Indels

0;

Gaps

0;

XX The present invention describes a method for classifying a B-cell as malignant or normal comprising: (a) isolating a sequence representing an immunoglobulin (Ig) variable region from the B cell; (b) detecting the presence of a glycosylation site; and (c) classifying the cell as malignant or normal on the basis of the presence or absence of a glycosylation site. Also described: (1) treating a patient suffering from risk of having lymphoma; (2) screening for substances capable of inhibiting glycosylation of the Ig variable region of the B cell receptor ; and (3) screening for substances (S) capable of inhibiting the interaction between Lectins of the type found in the germinal centre and N-glycans found on the surface of Ig of lymphoma cells. (S) has cytostatic activity, and can be used in gene therapy, and as a malignant or normal. The glycosylation inhibitor is useful in preparing a medicament for treating non-Hodgkin's lymphoma. The present sequence exemplification of the present invention.

XX Sequence 114 AA;

SQ

Query Match

Best Local Similarity

Score

DB

Matches

Pred.

No.

3.4;

Mismatches

0;

Indels

0;

Gaps

0;

XX The present invention describes a method for classifying a B-cell as malignant or normal comprising: (a) isolating a sequence representing an immunoglobulin (Ig) variable region from the B cell; (b) detecting the presence of a glycosylation site and classifying the cell as malignant or normal.

XX Disclosure; Fig 3; 61pp; English.

PT

Zhu D, Stevenson P;

DR

WPI; 2003-902720/82.

XX

PT

Classifying a B-cell as malignant or normal by isolating a sequence

PT

representing an Ig variable region from the B cell, detecting the

PT

presence of a glycosylation site and classifying the cell as malignant or

PT

normal.

XX

PS

The present invention describes a method for classifying a B-cell as

CC

malignant or normal comprising: (a) isolating a sequence representing an

CC

immunoglobulin (Ig) variable region from the B cell; (b) detecting the

CC

presence of a glycosylation site; and (c) classifying the cell as

CC

malignant or normal on the basis of the presence or absence of a

CC

glycosylation site. Also described: (1) treating a patient suffering from

CC

risk of having lymphoma; (2) screening for substances capable of

CC

inhibiting glycosylation of the Ig variable region of the B cell receptor

XX The present invention describes a method for classifying a B-cell as malignant or normal comprising: (a) isolating a sequence representing an immunoglobulin (Ig) variable region from the B cell; (b) detecting the presence of a glycosylation site; and (c) classifying the cell as malignant or normal on the basis of the presence or absence of a glycosylation site. Also described: (1) treating a patient suffering from risk of having lymphoma; (2) screening for substances capable of inhibiting glycosylation of the Ig variable region of the B cell receptor ; and (3) screening for substances (S) capable of inhibiting the interaction between Lectins of the type found in the germinal centre and N-glycans found on the surface of Ig of lymphoma cells. (S) has cytostatic activity, and can be used in gene therapy, and as a malignant or normal. The glycosylation inhibitor is useful in preparing a medicament for treating non-Hodgkin's lymphoma. The present sequence exemplification of the present invention.

XX Sequence 114 AA;

SQ

Query Match

Best Local Similarity

Score

DB

Matches

Pred.

No.

3.4;

Mismatches

0;

Indels

0;

Gaps

0;

XX The present invention describes a method for classifying a B-cell as malignant or normal comprising: (a) isolating a sequence representing an immunoglobulin (Ig) variable region from the B cell; (b) detecting the presence of a glycosylation site; and (c) classifying the cell as malignant or normal on the basis of the presence or absence of a glycosylation site. Also described: (1) treating a patient suffering from risk of having lymphoma; (2) screening for substances capable of inhibiting glycosylation of the Ig variable region of the B cell receptor ; and (3) screening for substances (S) capable of inhibiting the interaction between Lectins of the type found in the germinal centre and N-glycans found on the surface of Ig of lymphoma cells. (S) has cytostatic activity, and can be used in gene therapy, and as a malignant or normal. The glycosylation inhibitor is useful in preparing a medicament for treating non-Hodgkin's lymphoma. The present sequence exemplification of the present invention.

XX Sequence 122 AA;

SQ

Query Match

Best Local Similarity

Score

DB

Matches

Pred.

No.

2.5;

Mismatches

1;

Indels

0;

Gaps

0;

CC PA83, edema factor or lethal factor with an antibody that has binding
 CC affinity for the molecule, where the presence of elevated levels of the
 CC antibody correlates with the presence of a disease associated with B.
 CC anthracis. Alternatively, the method involves assaying for the presence
 CC of an antibody to a cell receptor, Pa63, Pa63 heptamer, Pa83, edema
 factor or lethal factor with a secondary antibody having binding affinity
 CC for the antibody, where the presence of elevated levels of the secondary
 CC antibody correlates with the presence of B. anthracis in a subject. In
 all cases, the antibody (full-length or functional fragment) may comprise
 a heavy chain variable region selected from a group of sequences ADV8610
 -ADV8627, a light chain kappa region selected from a group of sequences
 CC ADV8628-ADV8635 and a light chain lambda region selected from a group
 of sequences ADV8636-ADV8687. Diagnostic kits are provided. A claimed
 vaccine comprises a multimer of anthrax toxin Pa63. The methods and
 compositions of the present invention are also useful for producing anti-
 toxins or anti-infectives to infective agents such as anthrax, botulinum,
 smallpox, Venezuelan equine encephalomyelitis and West Nile virus. The
 present sequence is that of the heavy chain variable region of a human
 Fab (designated J K 2e G pro) with positive reactivity to anthrax
 proteins Pa63 and Pa83. Phage libraries were developed from mRNA isolated
 from blood and bone marrow samples of donors who had been vaccinated
 against anthrax. The libraries were panned against Pa83 and Pa63, and
 sequence analysis was performed on positive responders. Neutralization of
 anthrax toxin activity by purified Fabs was demonstrated.

XX Sequence 134 AA;

Query Match 78.3%; Score 47; DB 9; Length 134;

Best Local Similarity 77.8%; Pred. No. 4; Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TYYVFGLDV 11
DB 110 TYYVGMDV 118

RESULT 8

ADR28082 ID ADR28082 standard; protein; 244 AA.

AC ADR28082; DT 07-OCT-2004 (first entry)

DB NPB polypeptide scrw27, seq id 29.

KW Cytostatic; metastasis inhibitor; neuropilin binder; NPB; scFv;

KW single chain antibody; neuropilin-1; Np-1; angiogenesis; tumour; cancer.
 XX OS Mus sp.
 OS Synthetic.

FT Region 87.-103
 FT /note= "complementary determining region claimed under
 FT claim 5"
 PN WO2004056874-A2.

XX PD 08-JUL-2004.

XX 22-DEC-2003; 2003WO-EP014756.

XX 20-JEC-2002; 2002US-043893P.

PR 15-JAN-2003; 2003EP-00000615.

PA (XERI-) XERION PHARM AG.
 PA (TUFT) UNIV TUFTS.

XX Unger CM, Beste G, Zehetmeier C, Lain B, Torella C, Niewohner J;

PI Jay DG, Bustace BK, Knauer R, Jensen KH;

DR DR N-PSDB; ADR28116.

XX Novel neuropilin binder which is scFv, antibody fragment or bioconjugate, that
 PT modulates neuropilin-1 function or inhibits NP-1 dependent
 PT angiogenesis of endothelial cells and/or invasion of tumor cells useful
 for treating cancer.

XX Claim 3; SEQ ID NO 29; 120pp; English.

Query Match 78.3%; Score 47; DB 8; Length 244;
 Best Local Similarity 77.8%; Pred. No. 7.7; Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TYYVFGLDV 11
DB 95 TYYVGMDV 103

RESULT 9

AEB45891 ID AEB45891 standard; protein; 468 AA.

AC AEB45891; DT 06-OCT-2005 (first entry)

XX DE Human monoclonal anti-MAdCAM antibody #27.

XX Monoclonal antibody; mucosal addressin cell adhesion molecule; MAdCAM;
 KW inflammation; inflammatory bowel disease; Crohn disease;
 KW ulcerative colitis; diverticular disease; gastritis; liver disease;
 KW primary biliary cirrhosis; primary sclerosing cholangitis;
 KW insulin dependent diabetes; graft versus host disease; antiinflammatory;
 KW gastrointestinal gen.; antiulcer; hepatotropic; antidiabetic;
 KW immunosuppressive; antibody.
 OS Homo sapiens.
 XX PN WO200507620-A2.
 XX PD 28-JUL-2005.

XX 07-JAN-2005; 2005WO-US000370.

XX PR 09-JAN-2004; 2004US-053549P.

XX PA (PFIZ) PFIZER INC.

PA (ABGENIX INC.

PA (PFIZ) PFIZER LTD.

XX Pullen N, Molloy E, Kellermann S, Green LL, Haak-Frendscho M;

XX WPI; 2004-507700/48.

DR WPI; 2005-554958/56.
 DR N-PSDB; AEB45890.
 XX
 PT New antibody to Mucosal Adressin Cell Adhesion Molecule, useful for
 PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel
 PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or
 PT graft versus host disease.

XX
 PS Claim 8; SEQ ID NO 56; 167pp; English.

CC The invention relates to a human monoclonal antibody or its antigen-binding portion that specifically binds to mucosal addressin cell adhesion molecule (MadCAM). The invention also relates to a hybridoma cell line that produces the human monoclonal antibody, a pharmaceutical composition comprising an amount of the monoclonal antibody or its antigen-binding portion and a pharmaceutical carrier, a method of treating inflammatory disease in a subject, an isolated cell line that produces the monoclonal antibody or its antigen-binding portion or the heavy chain or light chain of the antibody or of its portion, an isolated nucleic acid molecule comprising a nucleotide sequence encoding the heavy chain or its antigen-binding portion or the light chain or its antigen-binding portion of an antibody described above, a vector comprising the nucleic acid molecule, where the vector optionally comprises an expression control sequence operably linked to the nucleic acid molecule, a host cell comprising the vector or the nucleic acid molecule above, a method of producing a human monoclonal antibody or its antigen-binding portion that specifically binds MadCAM, a method of isolating an antibody or its antigen-binding portion that specifically binds to MadCAM, a method of treating a subject in need of a human antibody or its antigen-binding portion that specifically binds to MadCAM and inhibits binding to alpha4beta7, a method of inhibiting alpha4beta7 binding to cells expressing human MadCAM, a method of inhibiting MadCAM-mediated leukocyte -endothelial cell adhesion, migration and infiltration into tissues, a method of inhibiting alpha4beta7/MadCAM-dependent recruitment of lymphocytes to gastrointestinal lymphoid tissue, a method of diagnosing a disorder characterized by circulating soluble human MadCAM and detecting inflammation in a subject. The antibody, composition and methods are useful for diagnosing and treating inflammatory disease, e.g. inflammatory bowel disease, Crohn's disease, ulcerative colitis, diverticular disease, gastritis, liver disease, primary biliary cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and graft versus host disease. This sequence represents a human monoclonal anti-MADCM antibody of the invention.

CC Sequence 468 AA;

Query Match 78.3%; Score 47; DB 9; Length 468;
 Best Local Similarity 77.8%; Pred. No. 15; Mismatches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TYYYGFLDV 11
 ||||:|||:
 Db 123 TYYYGMDV 131

RESULT 10
 AEB45853
 ID AEB45853 standard; protein; 469 AA.
 XX
 AC AEB45853;
 DT 06-OCT-2005 (first entry)
 DB Human monoclonal anti-MADCM antibody #9.
 XX
 Monoclonal antibody; mucosal addressin cell adhesion molecule; MadCAM; inflammation; inflammatory bowel disease; Crohn's disease; ulcerative colitis; diverticular disease; gastritis; liver disease; insulin dependent diabetes; graft versus host disease; antiangiogenesis; antidiabetic; immunosuppressive; antibody.

XX
 HOMO sapiens.
 OS
 XX
 PN WO200507620-A2.
 XX
 PD 28-JUL-2005.
 XX
 PR 07-JAN-2005; 2005WO-US000370.
 XX
 PR 09-JAN-2004; 2004US-0535490P.
 XX
 PA (PFIZ) PFIZER INC.
 PA (ABCE-) ABGENIX INC.
 PA (PFIZ) PFIZER LTD.
 PI Pullen N, Molloy E, Kellermann S, Green LL, Haak-Frendscho M;
 DR DR
 DR N-PSDB; AEB45852.
 XX
 PT New antibody to Mucosal Adressin Cell Adhesion Molecule, useful for
 PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel
 PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or
 PT graft versus host disease.

XX
 PS Claim 8; SEQ ID NO 18; 167pp; English.

CC The invention relates to a human monoclonal antibody or its antigen-binding portion that specifically binds to mucosal addressin cell adhesion molecule (MadCAM). The invention also relates to a hybridoma cell line that produces the human monoclonal antibody, a pharmaceutical composition comprising an amount of the monoclonal antibody or its antigen-binding portion and a pharmaceutical carrier, a method of treating inflammatory disease in a subject, an isolated cell line that produces the monoclonal antibody or its antigen-binding portion or the heavy chain or light chain of the antibody or of its portion, an isolated nucleic acid molecule comprising a nucleotide sequence encoding the heavy chain or its antigen-binding portion or the light chain or its antigen-binding portion of an antibody described above, a vector comprising the nucleic acid molecule, where the vector optionally comprises an expression control sequence operably linked to the nucleic acid molecule, a host cell comprising the vector or the nucleic acid molecule above, a method of producing a human monoclonal antibody or its antigen-binding portion that specifically binds MadCAM, a method of isolating an antibody or its antigen-binding portion that specifically binds to MADCM, a method of treating a subject in need of a human antibody or its antigen-binding portion that specifically binds to MadCAM and inhibits binding to alpha4beta7, a method of inhibiting alpha4beta7 binding to cells expressing human MadCAM, a method of inhibiting MadCAM-mediated leukocyte -endothelial cell adhesion, migration and infiltration into tissues, a method of inhibiting alpha4beta7/MadCAM-dependent recruitment of lymphocytes to gastrointestinal lymphoid tissue, a method of diagnosing a disorder characterized by circulating soluble human MADCM and detecting inflammation in a subject. The antibody, composition and methods are useful for diagnosing and treating inflammatory disease, e.g. inflammatory bowel disease, Crohn's disease, ulcerative colitis, diverticular disease, gastritis, liver disease, primary biliary cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and graft versus host disease. This sequence represents a human monoclonal anti-MADCM antibody of the invention.

XX
 Sequence 469 AA;

Query Match 78.3%; Score 47; DB 9; Length 469;
 Best Local Similarity 77.8%; Pred. No. 15; Mismatches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TYYYGFLDV 11
 ||||:|||:
 Db 123 TYYYGMDV 131

RESULT 11

ADR38712

ID ADR38712 standard; peptide; 13 AA.

XX

AC ADR38712;

DT 02-DEC-2004 (first entry)

DE Mouse heavy chain variable region CDR3 seqid 114.

XX

Db 4 ANYYYGMDV 13

RESULT 12

ID ADW04816

DE ADW04816 standard; peptide; 21 AA.

AC ADW04816;

XX

DT 07-APR-2005 (first entry)

XX

PAPP-A immunoglobulin variable domain AB b03 heavy chain CDR3 SEQ ID 141.

XX

KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody; toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain variable region; complementarity determining region; CDR3.

XX

Mus sp.

OS

PN US2004175385-A1.

XX

PD 09-SEP-2004.

XX

PP 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

XX

PR 01-AUG-2002; 2002US-0400721P.

XX

PA (RESC) UNIV CALIFORNIA.

XX

PJ Marks JD, Amersdorfer P;

XX

DR WPI; 2004-652009/63.

XX

PT New isolated antibody that neutralizes botulinum neurotoxin type A' useful for diagnosing botulism or for treating pathologies associated with botulinum neurotoxin poisoning.

XX

PS Example 3; SEQ ID NO 114; 110pp; English.

CC The invention describes an isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a specific clone where (I) binds to and neutralises botulinum neurotoxin type A' (BONT/A). An isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone S25, C25, C39, IC6, 1C6, 3D12, B4, 1F3, hUC5, A4L, Ar2, WR1(V), WR1(T), 3-1, 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum neurotoxin type A' (BONT/A). Also described are: a polypeptide (II) comprising BONT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I) producing (I); and a composition (III) comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralization than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising (I); and a kit comprising (I). (I) is useful for neutralising BONT/A antibody and for neutralising a botulinum neurotoxin which involves contacting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. (I) is useful for diagnosing the botulism or for treating pathologies associated with botulinum neurotoxin poisoning. (I) exhibits specificity and affinity towards BONT/A. (I) enables rapid detection or diagnosis of botulism. This is the amino acid sequence 113 AA:

Query Match 76.7%; Score 46; DB 9; Length 21;

Best Local Similarity 63.6%; Pred. No. 0.83; Mismatches 2; Indels 0; Gaps 0;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY LATYYFEGDV 11

DB 11 LGNYYYYGMDV 21

SQ Sequence 21 AA:

RESULT 13

ID AD241994

DE AD241994 standard; peptide; 126 AA.

XX

AC AD241994;

XX

DT 30-JUN-2005 (first entry)

XX

IG H chain variable region, B-CLL set II peptide #4.

XX

KW Antibody; antibody engineering; antibody therapy; light chain variable region; heavy chain variable region;

QY 2 ATYYYFGLDV 11

SQ |||||:|||

KW chronic lymphocytic leukemia; cytotoxic: Hodgkin disease; lymphoma;
 KW Burkitt's lymphoma; multiple myeloma; systemic lupus erythematosus;
 KW antiinflammatory; dermatological; immunosuppressive; myasthenia gravis;
 KW muscular-gen; neuroprotective; Graves disease; antithyroid;
 KW insulin dependent diabetes; diabetes mellitus; antidiabetic;
 KW autoimmune hemolytic anemia; antiamic.
 XX OS Homo sapiens.
 XX PN WO2005034733-A2.
 XX PD 21-APR-2005.
 XX PF 08-OCT-2004; 2004WO-US033176.
 XX PR 08-OCT-2003; 2003US-0509473P.
 XX DR (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RBS.
 XX PA Messmer BT, Chiorazzi N, Albesiano E;
 XX WPI; 2005-306220/31.
 XX PS Disclosure: Fig 2; 58pp; English.
 XX
 CC The new invention relates to combinations of light chain antibody genes
 CC and heavy chain antibody genes, useful for treating B cell chronic
 CC lymphocytic leukemia (B-CLL). B-CLL is a disease of slowly proliferating
 CC CD5+ B lymphocytes. These cells express low levels of surface membrane IgG
 CC that serves as the receptor for antigen (BCR). Analysis of V region gene
 CC cassette usage has shown that distribution of variable region gene
 CC cassettes used by B-CLL clones differs from that in normal cells, with an
 CC increased frequency of VH3-07, VH4-34, and VH1-69 genes. This implies
 CC that the structure of the antibody molecule, and antigen specificity,
 CC play a role in the leukemic transformation of particular B cells. The
 CC present invention discloses that a significant proportion of B-CLL
 CC patients with aggressive disease share the same classes of VH, JH, VL
 CC and JL antibody genes, forming sets of patients with highly homologous B
 CC cell receptors. Alternatively, the patients have a disorder selected from
 CC Hodgkin's disease, non-Hodgkin's lymphoma, Burkitt's lymphoma, myeloma or
 CC systemic lupus erythematosus, myasthenia gravis, Grave's disease, type I
 CC diabetes mellitus, autoimmune peripheral neuropathy, and autoimmune
 CC hemolytic anemia. The new members of the antibody genes are: VH4-39/D6-
 CC 13/JH5/vlkappa012/2/Jlkappa1/kappa2 (Set I); VH4-34/D5-
 CC 5/JH6/vlkappa017/Jlkappa1/kappa2 (Set II); VH3-
 CC 21/JH6/vlkappa012/Jlkappa1/kappa2 (Set III); VH1-69/D3-
 CC 16/JH3/vlkappa27/Jlkappa1/kappa4 (Set IV); VH1-69/D3-
 CC 10/JH6/vlkappa012/Jlkappa1/kappa1 (Set V); VH1-02/D6-
 CC 19/JH4/vlkappa012/2/Jlkappa1/kappa2 (Set VI); VH1-03/D6-
 CC 19/JH4/vlkappa012/2/Jlkappa1 (Set VII); VH1-45/D6-19/JH4 (Set VIII); VH5-
 CC 51/D6-19/JH4/vlkappa012/2/Jlkappa2 (Set IX); VH1-69/D3-
 CC 3/JH4/vlkappa012/Jlkappa1 (Set VII); and VH1-69/D2-
 CC 2/JH6/vlkappa012/Jlkappa3 (Set VIII). Treating a patient having B-CLL
 CC with the above genes comprises administering an agent that binds to the
 CC antigen-binding region of an antibody encoded by the antibody genes. The
 CC agent is an anti-idiotypic antibody, a peptide antigen, or an aptamer. The
 CC present sequence is an Ig H chain variable region, B-CLL set II peptide.
 XX Sequence 126 AA;

RESULT 14

| | |
|---|----------------------------|
| ID ADW04810 | standard; protein; 140 AA. |
| XX | |
| AC ADW04810; | |
| XX | |
| DT 07-APR-2005 | (first entry) |
| XX | |
| DE PAPP-A immunoglobulin variable domain AB b03 heavy chain SEQ ID 135. | |
| XX | |
| KW Cytotoxic; Vasotropic; heavy chain variable domain; proliferative disorder; restenosis; glioblastoma; osteosarcoma. | |
| XX | |
| OS Unidentified. | |
| XX | |
| PN US2005009136-A1. | |
| XX | |
| PD 13-JAN-2005. | |
| XX | |
| PP 19-FEB-2004; 2004US-0078311. | |
| XX | |
| PR 19-FEB-2003; 2003US-0448515P. | |
| XX | |
| PA (DYAX-) DYAX CORP. | |
| XX | |
| PI Nixon A, Hogan S; | |
| XX | |
| DR WPI; 2005-080519/09. | |
| XX | |
| PT New pregnancy-associated plasma protein-A (PAPP-A) binding proteins | |
| PT comprising immunoglobulin variable domain sequences, useful for | |
| PT diagnosing, preventing or treating diseases such as cancer. | |
| XX | |
| PS Example; SBQ ID NO 135; 168PP; English. | |
| XX | |
| CC The present invention relates to novel proteins (I) that bind to | |
| CC pregnancy-associated plasma protein A (PAPP-A ADW04676). (I) comprises a | |
| CC first and second immunoglobulin variable domain sequence which binds to | |
| CC PAPP-A. Also claimed are proteins (II) which comprise light chain (LC) | |
| CC and heavy chain immunoglobulin variable domain sequences which binds to | |
| CC PAPP-A. The proteins are useful for diagnosing, preventing or treating | |
| CC proliferative diseases such as glioblastoma, osteosarcoma and overgrowth | |
| CC of vascular smooth muscle cells following e.g., balloon angioplasty | |
| CC (which may cause restenosis). The protein are especially useful for | |
| CC useful for treating diseases involving IGF regulated growth. The present | |
| CC sequence is one such immunoglobulin variable domain sequence. | |
| XX | |
| SQ Sequence 140 AA, | |
| Query Match 76.7%; Score 46; DB 9; Length 140; | |
| Best Local Similarity 63.6%; Pred. No. 6.3; | |
| Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0; | |
| Oy 1 LATVYFGLDV 11 | |
| Db 109 LGNYYYGMDV 119 | |
| RESULT 15 | |
| ADW04952 | |
| ID ADW04952 standard; peptide; 16 AA. | |
| XX | |
| AC ADW04952; | |
| XX | |
| DT 07-APR-2005 (first entry) | |
| XX | |
| DE PAPP-A immunoglobulin variable domain AB f03 heavy chain CDR3 SBQ ID 277. | |
| XX | |
| KW Cytostatic; Vasotropic; heavy chain variable domain; proliferative disorder; restenosis; glioblastoma; osteosarcoma. | |
| XX | |

OS Unidentified.
XX
PN US2005009136-A1.
XX
PD 13-JAN-2005.
XX
PP 19-FEB-2004; 2004US-00783311.
XX
PR 19-FEB-2003; 2003US-0448515P.
XX
PA (DYAX-) DYAX CORP.
XX
PI Nixon A, Hogan S;
XX
DR WPI; 2005-080519/09.
XX
PT New pregnancy-associated plasma protein-A (PAPP-A) binding proteins
PT comprising immunoglobulin variable domain sequences, useful for
PT diagnosing, preventing or treating diseases such as cancer.
XX
PS Example; SEQ ID NO 277; 168pp; English.
XX
CC The present invention relates to novel proteins (I) that bind to
CC pregnancy-associated plasma protein A (PAPP-A) ADW04676). (I) comprises a
CC first and second immunoglobulin variable domain sequence which binds to
CC PAPP-A. Also claimed are proteins (II) which comprise light chain (LC)
CC and heavy chain immunoglobulin variable domain sequences which binds to
CC PAPP-A. The proteins are useful for diagnosing, preventing or treating
CC proliferative diseases such as glioblastoma, osteosarcoma and overgrowth
CC of vascular smooth muscle cells following e.g., balloon angioplasty
CC (which may cause restenosis). The proteins are especially useful for
CC useful for treating diseases involving IGF regulated growth. The present
CC sequence is one such immunoglobulin variable domain sequence.
XX
SQ Sequence 16 AA:

Query Match 75.0%; Score 45; DB 9; Length 16;
Best Local Similarity 63.6%; Preq. No. 0.92;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11
DB ;|:|:|:|:
6 WAGVYYGMDV 16

Search completed: December 4, 2005, 04:44:54
Job time : 98.5625 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:45 ; Search time 15.5833 Seconds
(without alignments)
Sequence: 1 LATYYYFGLDV 11
Scoring table: BLOSUM62
Gapext 10.0 , Gapext: 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80;*
1: Pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 43 | 71.7 | 19 | 2 | PHI1307 |
| 2 | 43 | 71.7 | 23 | 2 | PHI1361 |
| 3 | 43 | 71.7 | 29 | 2 | PHI1328 |
| 4 | 43 | 71.7 | 160 | 2 | D70189 |
| 5 | 43 | 71.7 | 160 | 2 | S05271 |
| 6 | 43 | 71.7 | 408 | 2 | E70380 |
| 7 | 42 | 70.0 | 19 | 2 | PHI1304 |
| 8 | 42 | 70.0 | 19 | 2 | S43960 |
| 9 | 42 | 70.0 | 23 | 2 | PHI1364 |
| 10 | 42 | 70.0 | 24 | 2 | PT0258 |
| 11 | 42 | 70.0 | 27 | 2 | PHI1371 |
| 12 | 42 | 70.0 | 27 | 2 | PHI1355 |
| 13 | 42 | 70.0 | 74 | 2 | S26793 |
| 14 | 42 | 70.0 | 118 | 2 | PHI1666 |
| 15 | 42 | 70.0 | 119 | 2 | PHI0961 |
| 16 | 42 | 70.0 | 120 | 2 | PHI1650 |
| 17 | 42 | 70.0 | 125 | 2 | S24686 |
| 18 | 42 | 70.0 | 128 | 2 | S48797 |
| 19 | 42 | 70.0 | 132 | 2 | PHI0954 |
| 20 | 42 | 70.0 | 133 | 2 | C33548 |
| 21 | 42 | 70.0 | 136 | 2 | A49047 |
| 22 | 42 | 70.0 | 147 | 2 | I37780 |
| 23 | 42 | 70.0 | 627 | 2 | S14683 |
| 24 | 40 | 66.7 | 22 | 2 | PHI1325 |
| 25 | 39.5 | 65.8 | 581 | 2 | PHI3729 |
| 26 | 39 | 65.0 | 126 | 2 | S44107 |
| 27 | 39 | 65.0 | 375 | 2 | A83788 |
| 28 | 38 | 63.3 | 22 | 2 | PHI1359 |
| 29 | 38 | 63.3 | 63.3 | 2 | PHI0094 |

| | | | | | | |
|----|----|------|------|----|---------|----------------------|
| 30 | 38 | 63.3 | 287 | 2 | T27056 | hypothetical prote |
| 31 | 38 | 63.3 | 473 | 2 | H86240 | hypothetical prote |
| 32 | 38 | 63.3 | 979 | 2 | A39792 | transcription acti |
| 33 | 37 | 61.7 | 14 | 2 | PHI1601 | ig H chain V-D-J |
| 34 | 37 | 61.7 | 126 | 1 | MHHUOU | ig heavy chain V-I |
| 35 | 37 | 61.7 | 276 | 2 | S16892 | probable transposa |
| 36 | 37 | 61.7 | 447 | 2 | T09809 | NAB2 dehydrogenase |
| 37 | 37 | 61.7 | 448 | 2 | T12006 | NAB2 dehydrogenase |
| 38 | 37 | 61.7 | 572 | 2 | C70130 | glycerol-3-phosphate |
| 39 | 37 | 61.7 | 571 | 2 | A42138 | conditioned medium |
| 40 | 37 | 61.7 | 571 | 2 | S24482 | conditioned medium |
| 41 | 42 | 36.5 | 61.7 | 2 | T22223 | SE-1 protein - Ca |
| 42 | 42 | 36.5 | 60.8 | 2 | B4950 | IG heavy chain V |
| 43 | 43 | 36.5 | 60.8 | 2 | C75205 | hypothetical prote |
| 44 | 43 | 36.5 | 60.0 | 18 | PH1368 | IG heavy chain DJ |
| 45 | 36 | 60.0 | 145 | 2 | H97707 | 30S ribosomal prot |

ALIGNMENTS

RESULT 1
PHI107
IG heavy chain DJ region (clone C96-119) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PHI107
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J; Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A;Reference number: PHI1302; MUID:93094761; PMID:146419
A;Accession: PHI1307
A;Molecule type: DNA
A;Residues: 1-11 <WAS>
A;Cross-references: UNIPARC:UPI0000176935
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: Ig heavy chain DJ region (clone C178-122B) - human (fragment)

Query Match 71.7%; Score 43; DB 2; Length 19;
Best Local Similarity 65.7%; Pred. No. 0.23; Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 3 TYYFGLDV 11
:|||:||:||:
6 SYYYGMDV 14

RESULT 2
PHI361
IG heavy chain DJ region (clone C178-122B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PHI1361
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J; Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A;Reference number: PHI1302; MUID:93094761; PMID:146419
A;Accession: PHI1361
A;Molecule type: DNA
A;Residues: 1-23 <WAS>
A;Cross-references: UNIPARC:UPI0000176948
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 71.7%; Score 43; DB 2; Length 23;
Best Local Similarity 63.6%; Pred. No. 0.28; Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1 LATYYFGLDV 11
:|||:||:||:
8 LFPYYGMDV 18

RESULT 3
 PH1328
 Ig heavy chain DJ region (clone C113-148) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C;Accession: PH1328
 R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph
 A;Reference number: PH1302; MUID:93094761; PMID:1460419
 A;Accession: PH1328
 A;Molecule type: DNA
 A;Residues: 1-29 <WAS>
 A;Cross-references: UNIPARC:UPI000176939
 C;Superfamily: Immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 Query Match 71.7%; Score 43; DB 2; Length 29;
 Best Local Similarity 66.7%; Pred. No. 0.36;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 TYYFGGLDV 11
 Db 16 SYYYGMGV 24

RESULT 4
 D70189
 conserved hypothetical integral membrane protein BB0717 - Lyme disease spirochete
 C;Species: *Borrelia burgdorferi* (Lyme disease spirochete)
 C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
 C;Accession: D70189
 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, S.; Peterson, J.; Karlaage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, B.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.; Nature 390, 580-586, 1997
 A;Authors: Smith, H.O.; Venter, J.C.
 A;Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.
 A;Reference number: A70100; MUID:9065943; PMID:9403685
 A;Accession: D70189
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-60 <KUE>
 A;Cross-references: UNIPROT:051659; UNIPARC:UPI0000575B2; GB:AE001171; GB:AE000783; NID: A;Experimental source: strain B31

Query Match 71.7%; Score 43; DB 2; Length 160;
 Best Local Similarity 60.0%; Pred. No. 2;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATYYFGGLDV 11
 Db 23 ATYFVFSNDI 32

RESULT 5
 805271
 Ig heavy chain precursor - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
 C;Accession: S05271; S04602
 R;Kishimoto, T.; submitted to the EMBL Data Library, March 1989
 A;Reference number: S05270
 A;Accession: S05271
 A;Molecule type: mRNA
 A;Residues: 1-160 <KSI>
 A;Cross-references: UNIPROT:Q96B99; UNIPARC:UPI000176950; EMBL:X14584
 R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
 Nucleic Acids Res. 17, 4305, 1989
 A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
 A;Reference number: S04601; MUID:89296497; PMID:2500644
 A;Accession: S04602

RESULT 6
 ET70380
 Na+/H+-exchanging protein - *Aquifex aeolicus*
 N;Alternate names: Na+/H+ antiporter
 C;Species: *Aquifex aeolicus*
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
 C;Accession: ET70380
 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ovre
 V.; Nature 392, 353-358, 1998
 A;Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
 A;Reference number: A70300; MUID:98196666; PMID:9537320
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-408 <AQF>
 A;Cross-references: UNIPROT:067072; UNIPARC:UPI0000564AB; GB:AE000714; NID:92983446; PIU:
 A;Experimental source: strain VFS
 C;Genetics:
 A;Gene: napA2
 C;Superfamily: *Aquifex aeolicus* Na+/H+-exchanging protein napA
 Query Match 71.7%; Score 43; DB 2; Length 408;
 Best Local Similarity 54.5%; Pred. No. 5.2; Mismatches 1; Indels 0; Gaps 0;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LATYYFGGLDV 11
 Db 116 IVSYVFFGGLD 126

RESULT 7
 PH1304
 Ig heavy chain DJ region (clone C439-111) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C;Accession: PH1304
 R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph
 A;Reference number: PH1302; MUID:93094761; PMID:1460419
 A;Accession: PH1304
 A;Molecule type: DNA
 A;Residues: 1-19 <WAS>
 A;Cross-references: UNIPARC:UPI000176934
 C;Superfamily: Immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 Query Match 70.0%; Score 42; DB 2; Length 19;
 Best Local Similarity 75.0%; Pred. No. 0.35;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YYFGGLDV 11
 Db 7 YYYYGMGV 14

RESULT 8

Ig mu chain V region (clone 18) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999

C;Accession: S43960

R;Wasserman, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.

A;Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.

A;Reference number: S43960

A;Molecule type: DNA

A;Residues: 1-19 <WAG>

A;Cross-references: UNIPARC:UPI000017690D

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

Query Match Best Local Similarity 70.0%; Score 42; DB 2; Length 19;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGGLDV 11

Db 10 YYYGMDV 17

RESULT 9

Ig heavy chain DJ region (clone C178-136A) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PH1364

R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J;Exp. Med. 176, 1577-1581, 1992

A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphocytes

A;Reference number: PH1302; MUID:93094761; PMID:1460419

A;Accession: PH1364

A;Molecule type: DNA

A;Residues: 1-23 <WAS>

A;Cross-references: UNIPARC:UPI0000176949

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match Best Local Similarity 75.0%; Score 42; DB 2; Length 19;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGGLDV 11

Db 10 YYYGMDV 17

RESULT 10

Ig heavy chain CDR3 region (clone 2-118B) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-May-1997

C;Accession: PT0258

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J;Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J

A;Reference number: PT0222; MUID:9108337; PMID:1899102

A;Accession: PT0258

A;Molecule type: DNA

A;Residues: 1-24 <YAM>

A;Cross-references: UNIPARC:UPI0000176940

A;Experimental source: B Lymphocyte

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match Best Local Similarity 70.0%; Score 42; DB 2; Length 24;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGGLDV 11

Db 10 YYYGMDV 18

RESULT 11

Ig heavy chain DJ region (clone C111-145) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PH1371

R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J;Exp. Med. 176, 1577-1581, 1992

A;Title: Predominance of fetal type DH joining in young children with B precursor lymphocytes

A;Reference number: PH1302; MUID:93094761; PMID:1460419

A;Accession: PH1371

A;Molecule type: DNA

A;Residues: 1-27 <WAS>

A;Cross-references: UNIPARC:UPI000017694B

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match Best Local Similarity 75.0%; Score 42; DB 2; Length 27;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGGLDV 11

Db 15 YYYGMDV 22

RESULT 12

Ig heavy chain DJ region (clone C100-136) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PH1355

R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J;Exp. Med. 176, 1577-1581, 1992

A;Title: Predominance of fetal type DH joining in young children with B precursor lymphocytes

A;Reference number: PH1302; MUID:93094761; PMID:1460419

A;Accession: PH1355

A;Molecule type: DNA

A;Residues: 1-27 <WAS>

A;Cross-references: UNIPARC:UPI0000176945

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match Best Local Similarity 75.0%; Score 42; DB 2; Length 27;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGGLDV 11

Db 15 YYYGMDV 22

RESULT 13

Ig heavy chain V region - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C;Accession: S26793

R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.

Eur. J. Immunol. 22, 241-245, 1992

A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family

A;Reference number: S26786; MUID:92111632; PMID:1730251

A;Accession: S26793

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-74 <NOR>
 A;Cross-references: UNIPARC:UPI0000115FCB; EMBL:X61019; NID:932787; PIDN:CAA43353.1; PIR

C;Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 74;

Best Local Similarity 75.0%; Pred. No. 1.4;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YYYFGHDV 11
 Db 56 YYYGMDV 63

RESULT 14
 PH1666

Ig heavy chain V region (clone 6C9) - human (fragment)

C;Species: Homo sapiens (man)

C;Accession: PH1666

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C;Cross-references: UNIPARC:UPI0000115FCB

R;Hilison, J.L.; Karr, N.S.; Oppiger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-335, 1993

A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo-

A;Reference number: PH1662; MUID:93301610; PMID:815386

A;Accession: PH1666

A;Molecule type: mRNA

A;Residues: 1-118 <HLI>

A;Cross-references: UNIPARC:UPI00001176BE7

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

C;7-90/Domain: immunoglobulin homology <IMM>

Query Match 70.0%; Score 42; DB 2; Length 118;
 Best Local Similarity 75.0%; Pred. No. 2.2;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YYYFGHDV 11
 Db 100 YYYGMDV 107

RESULT 15

PH0951 Ig heavy chain V region (G6+ T-L33) - human (fragment)

C;Species: Homo sapiens (man)

C;Accession: PH0951

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996

R;Martin, T.; Buttry, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 933-931, 1992

A;Title: Evidence for somatic Selection of natural autoantibodies.

A;Reference number: PH0952; MUID:92202880; PMID:1552291

A;Accession: PH0951

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-119 <WAR>

A;Cross references: UNIPARC:UPI0000176CES

C;Superfamily: Immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

C;1-30/Region: Framework 1

F;15-98/Region: Immunoglobulin homology <IMM>

F;31-35/Region: complementarity-determining 1

F;36-50/Region: framework 2

F;51-67/Region: complementarity-determining 2

F;68-98/Region: framework 3

F;99-107/Region: complementarity-determining 3

Query Match 70.0%; Score 42; DB 2; Length 119;
 Best Local Similarity 75.0%; Pred. No. 2.2;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YYYFGHDV 11
 Db 101 YYYGMDV 108

Search completed: December 4, 2005, 04:53:32
 Job time : 17.583 SECs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 4, 2005, 04:31:36 ; Search time 100.375 seconds

Perfect score: US-10-632-706-127
Sequence: 1 LATYYYFFGLDV 11

Title: US-10-632-706-127

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : UniProt-05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match length DB ID Description

| Result No. | Score | Query | Match length | DB | ID | Description |
|------------|-------|-------|--------------|----|---------------|--------------------------|
| 1 | 44 | 73.3 | 1348 | 2 | Q4N9V2_THEPA | Q4n9v2 theileria p |
| 2 | 44 | 73.3 | 2262 | 2 | Q4UFV8_THEPA | Q4ufv8 theileria a |
| 3 | 43 | 71.7 | 160 | 2 | Q51595_BOREU | 051595_boreeu bu |
| 4 | 43 | 71.7 | 160 | 2 | Q660F6_BORGA | 0660f6_borga ga |
| 5 | 43 | 71.7 | 408 | 2 | Q67072_AQUPE | 067072 aquifex aeo |
| 6 | 42 | 70.0 | 364 | 2 | Q7VY71_BORDE | 07vy71_bordetella |
| 7 | 42 | 70.0 | 364 | 2 | Q7W926_BORPA | 07w926_boripa |
| 8 | 42 | 70.0 | 364 | 2 | Q7WKH1_BORBR | 07wkhl bordetella |
| 9 | 42 | 70.0 | 378 | 2 | Q4QAL0_LEIMA | 04qal0_leima |
| 10 | 42 | 70.0 | 382 | 2 | Q89NT2_BRAU4 | 089nt2_brau4 |
| 11 | 42 | 70.0 | 594 | 2 | Q74N07_NANPO | 074n07_nanpo |
| 12 | 42 | 70.0 | 606 | 2 | Q6GMZ5_HUMAN | 06gmz5_human |
| 13 | 42 | 70.0 | 1062 | 2 | Q96X9J_SULFOB | 096x9j_sulfoob |
| 14 | 42 | 70.0 | 3212 | 2 | Q4FWX4_LEIMA | 04fwx4_leima |
| 15 | 41 | 68.3 | 716 | 2 | Q6A0Z1_DESIS | 06a0z1_desis |
| 16 | 40 | 66.7 | 288 | 2 | Q6FF66_ACIDAB | 06ff66_acidab |
| 17 | 40 | 66.7 | 291 | 2 | Q4ZUB1_PSESY | 04zub1_psey |
| 18 | 40 | 66.7 | 293 | 2 | Q6D0Z3_ERMKD | 06d0z3_ermkd |
| 19 | 40 | 66.7 | 447 | 2 | Q8BN7G_OCEPH | 08bn7g_oceph |
| 20 | 40 | 66.7 | 702 | 2 | Q8C3XB_MOUSE | 08c3xb_mus_musculus |
| 21 | 40 | 66.7 | 978 | 2 | Q5AAV6_CANBAL | 05aaav6_candida_alb |
| 22 | 40 | 65.7 | 1113 | 2 | Q6WEQ5_ARALY | 06weq5_arabidopsis |
| 23 | 40 | 66.7 | 3964 | 2 | Q4Q8V4_LEIMA | 04q8v4_leima |
| 24 | 39 | 65.8 | 581 | 1 | Y61243_BACHD | erwinia car |
| 25 | 39 | 65.0 | 188 | 2 | Q52G51_MAGSR | 052g51_magso |
| 26 | 39 | 65.0 | 215 | 2 | Q5YXQ2_NOFCFA | 05yxq2_noctiluciferase |
| 27 | 39 | 65.0 | 317 | 2 | Q97BK3_THEWCO | 097bk3_thermoplasmatales |
| 28 | 39 | 65.0 | 375 | 2 | Q9KDV6_BACHD | 09kd6_bacillus |
| 29 | 39 | 65.0 | 419 | 2 | Q82700_MEDTR | 082700_medicago_tr |
| 30 | 39 | 65.0 | 423 | 2 | Q9STA5_MEDTR | 09sta5_medicago_tr |
| 31 | 39 | 65.0 | 434 | 2 | Q6ZBX7_ORYSA | 06zbx7_orzsa_sativ |

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : UniProt-05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match length DB ID Description

| Result No. | Score | Query | Match length | DB | ID | Description |
|------------|-------|-------|--------------|-----|----|---------------|
| 1 | 32 | 39 | 65.0 | 451 | 2 | Q6ZBX6_ORYSA |
| 2 | 33 | 39 | 65.0 | 478 | 2 | Q6P181_HUMAN |
| 3 | 34 | 39 | 65.0 | 662 | 2 | Q88T57_LACPL |
| 4 | 35 | 39 | 65.0 | 701 | 1 | LSP2_DRONE |
| 5 | 36 | 39 | 65.0 | 779 | 2 | Q65Z21_MANSM |
| 6 | 37 | 39 | 65.0 | 780 | 2 | Q7V0H6_CNBPF |
| 7 | 38 | 38 | 63.3 | 116 | 2 | Q72AY6_HUMAN |
| 8 | 39 | 38 | 63.3 | 148 | 2 | Q5TMX6_ANOXA |
| 9 | 40 | 38 | 63.3 | 159 | 2 | Q96GS0_HUMAN |
| 10 | 41 | 38 | 63.3 | 239 | 2 | Q5XQG3_LEGQL |
| 11 | 42 | 38 | 63.3 | 243 | 2 | Q5Z2R4_IKGPH |
| 12 | 43 | 38 | 63.3 | 307 | 2 | Q6NSD3_RHOPOA |
| 13 | 44 | 38 | 63.3 | 350 | 2 | Q8WTM5_MNTKA |
| 14 | 45 | 38 | 63.3 | 356 | 2 | Q9XTM1_CABEL |

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : UniProt-05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match length DB ID Description

| Result No. | Score | Query | Match length | DB | ID | Description |
|------------|-------|-------|--------------|-----|----|---------------|
| 1 | 32 | 39 | 65.0 | 451 | 2 | Q6ZBX6_ORYSA |
| 2 | 33 | 39 | 65.0 | 478 | 2 | Q6P181_HUMAN |
| 3 | 34 | 39 | 65.0 | 662 | 2 | Q88T57_LACPL |
| 4 | 35 | 39 | 65.0 | 701 | 1 | LSP2_DRONE |
| 5 | 36 | 39 | 65.0 | 779 | 2 | Q65Z21_MANSM |
| 6 | 37 | 39 | 65.0 | 780 | 2 | Q7V0H6_CNBPF |
| 7 | 38 | 38 | 63.3 | 116 | 2 | Q72AY6_HUMAN |
| 8 | 39 | 38 | 63.3 | 148 | 2 | Q5TMX6_ANOXA |
| 9 | 40 | 38 | 63.3 | 159 | 2 | Q96GS0_HUMAN |
| 10 | 41 | 38 | 63.3 | 239 | 2 | Q5XQG3_LEGQL |
| 11 | 42 | 38 | 63.3 | 243 | 2 | Q5Z2R4_IKGPH |
| 12 | 43 | 38 | 63.3 | 307 | 2 | Q6NSD3_RHOPOA |
| 13 | 44 | 38 | 63.3 | 350 | 2 | Q8WTM5_MNTKA |
| 14 | 45 | 38 | 63.3 | 356 | 2 | Q9XTM1_CABEL |

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : UniProt-05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match length DB ID Description

| Result No. | Score | Query | Match length | DB | ID | Description |
|------------|-------|-------|--------------|-----|----|---------------|
| 1 | 32 | 39 | 65.0 | 451 | 2 | Q6ZBX6_ORYSA |
| 2 | 33 | 39 | 65.0 | 478 | 2 | Q6P181_HUMAN |
| 3 | 34 | 39 | 65.0 | 662 | 2 | Q88T57_LACPL |
| 4 | 35 | 39 | 65.0 | 701 | 1 | LSP2_DRONE |
| 5 | 36 | 39 | 65.0 | 779 | 2 | Q65Z21_MANSM |
| 6 | 37 | 39 | 65.0 | 780 | 2 | Q7V0H6_CNBPF |
| 7 | 38 | 38 | 63.3 | 116 | 2 | Q72AY6_HUMAN |
| 8 | 39 | 38 | 63.3 | 148 | 2 | Q5TMX6_ANOXA |
| 9 | 40 | 38 | 63.3 | 159 | 2 | Q96GS0_HUMAN |
| 10 | 41 | 38 | 63.3 | 239 | 2 | Q5XQG3_LEGQL |
| 11 | 42 | 38 | 63.3 | 243 | 2 | Q5Z2R4_IKGPH |
| 12 | 43 | 38 | 63.3 | 307 | 2 | Q6NSD3_RHOPOA |
| 13 | 44 | 38 | 63.3 | 350 | 2 | Q8WTM5_MNTKA |
| 14 | 45 | 38 | 63.3 | 356 | 2 | Q9XTM1_CABEL |

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : UniProt-05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match length DB ID Description

| Result No. | Score | Query | Match length | DB | ID | Description |
|------------|-------|-------|--------------|-----|----|---------------|
| 1 | 32 | 39 | 65.0 | 451 | 2 | Q6ZBX6_ORYSA |
| 2 | 33 | 39 | 65.0 | 478 | 2 | Q6P181_HUMAN |
| 3 | 34 | 39 | 65.0 | 662 | 2 | Q88T57_LACPL |
| 4 | 35 | 39 | 65.0 | 701 | 1 | LSP2_DRONE |
| 5 | 36 | 39 | 65.0 | 779 | 2 | Q65Z21_MANSM |
| 6 | 37 | 39 | 65.0 | 780 | 2 | Q7V0H6_CNBPF |
| 7 | 38 | 38 | 63.3 | 116 | 2 | Q72AY6_HUMAN |
| 8 | 39 | 38 | 63.3 | 148 | 2 | Q5TMX6_ANOXA |
| 9 | 40 | 38 | 63.3 | 159 | 2 | Q96GS0_HUMAN |
| 10 | 41 | 38 | 63.3 | 239 | 2 | Q5XQG3_LEGQL |
| 11 | 42 | 38 | 63.3 | 243 | 2 | Q5Z2R4_IKGPH |
| 12 | 43 | 38 | 63.3 | 307 | 2 | Q6NSD3_RHOPOA |
| 13 | 44 | 38 | 63.3 | 350 | 2 | Q8WTM5_MNTKA |
| 14 | 45 | 38 | 63.3 | 356 | 2 | Q9XTM1_CABEL |

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : UniProt-05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match length DB ID Description

| Result No. | Score | Query | Match length | DB | ID | Description |
|------------|-------|-------|--------------|-----|----|--------------|
| 1 | 32 | 39 | 65.0 | 451 | 2 | Q6ZBX6_ORYSA |
| 2 | 33 | 39 | 65.0 | 478 | 2 | Q6P181_HUMAN |
| 3 | 34 | 39 | 65.0 | 662 | 2 | Q88T57_LACPL |
| 4 | 35 | 39 | 65.0 | 701 | 1 | LSP2_DRONE |
| 5 | 36 | 39 | 65.0 | 779 | 2 | Q65Z21_MANSM |
| 6 | 37 | 39 | 65.0 | 780 | 2 | Q7V0H6_CNBPF |
| 7 | 38 | 38 | 63.3 | 116 | 2 | Q72AY6_HUMAN |
| 8 | 39 | 38 | 63.3 | 148 | 2 | Q5TMX6_ANOXA |
| 9 | 40 | 38 | 63.3 | 159 | 2 | Q96GS0_HUMAN |
| 10 | 41 | 38 | 63.3 | 239 | 2 | Q5XQG3_LEGQL |
| 11 | 42 | 38 | 63.3 | 243 | 2 | Q5Z2R4_IKGPH |
| 12 | 43 | 38 | 63.3 | | | |

| | | Db | 23 ATYFVFSID 32 |
|---|------|----------|-----------------|
| RESULT 2 | | | : : : |
| Q4UFV8_ THEAN | | | |
| ID Q4UFV8_ THEAN PRELIMINARY; | PRT; | 2262 AA. | |
| AC | | | |
| DT 13-SEP-2005 (TREMBLrel. 31, last sequence update) | | | |
| DR 13-SEP-2005 (TREMBLrel. 31, last annotation update) | | | |
| DE Hypothetical protein. | | | |
| GN ORFNAMES=TA19710; | | | |
| OS Theileria annulata. | | | |
| OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae; Theileria; Theileria. | | | |
| OC NCBI_TaxID=5874; | | | |
| RN [1] | | | |
| RP NUCLEOTIDE SEQUENCE. | | | |
| RC STRAIN=Ankara isolate clone C9; | | | |
| RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Berriman M., Hall N., Barrell B.G.; | | | |
| RT "The chromosome 1 sequence of <i>Theileria annulata</i> ." | | | |
| RL Submitted (AFR-2005) to the EMBL/GenBank/DBJ databases. | | | |
| DR EMBL: CR90347; CAI4001.1; -, Genomic_DNA. | | | |
| KW Hypothetical protein. | | | |
| SO SEQUENCE 2262 AA; 262668 MW; FD9E8915243BPF512 CRC64; | | | |
| DR OrderdLocusNames=BG0739; | | | |
| OS Borrelia garinii | | | |
| OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia; Borrelia burgdorferi group. | | | |
| OX NCBI_TaxID=29519; | | | |
| RN [1] | | | |
| RP NUCLEOTIDE SEQUENCE. | | | |
| RC STRAIN=PRI; | | | |
| RA Gloeckner G., Lehmann R., Romualdi A., Pradella S., Schnittel-Spechtel U., Wilcke B., Suenhaj J., Platzter M.; | | | |
| RA RT "Comparative analysis of the <i>Borrelia garinii</i> genome"; | | | |
| RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases. | | | |
| DR EMBL: CP000013; AAU0765.1; -, Genomic_DNA. | | | |
| KW Complete proteome; Hypothetical protein. | | | |
| SO SEQUENCE 160 AA; 19293 MW; B65B15C5197BFB89 CRC64; | | | |
| Query Match 73.3%; Score 44; DB 2; Length 2262; Best Local Similarity 87.5%; Pred. No. 1e+02; Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0; | | | |
| Qy Db 1244 SYYYFGID 1251 | | | |
| RESULT 3 | | | |
| 051659_BORBU | | | |
| ID 051659_BORBU PRELIMINARY; | PRT; | 160 AA. | |
| AC 051659; | | | |
| DT 01-JUN-1998 (TREMBLrel. 06, Created) | | | |
| DT 01-JUN-1998 (TREMBLrel. 06, last sequence update) | | | |
| DR Conserved hypothetical integral membrane protein. | | | |
| GN OrderdLocusNames=BO0717; | | | |
| OS Borrelia burgdorferi (Lyme disease spirochete). | | | |
| OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia; Borrelia burgdorferi group. | | | |
| OC NCBI_TaxID=139; | | | |
| RN [1] | | | |
| RP NUCLEOTIDE SEQUENCE. | | | |
| RC STRAIN=ATCC 35210 / B31; | | | |
| RX MEDLINE=9805943; PubMed=9403685; DOI=10.1038/37551; | | | |
| RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White K.A., Dodson R.J., Hickey E.K., Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D., Richardson D.L., Peterson J.D., Kerlavage A.R., Gackenbush J., Salzberg S.L., Hansen M., van Vugt R., Palmer N., Adams M.D., Weidman J.P., Utterback T.R., Watthey L., McDonald L.A., Artlach P., Bowman C., Garland S.A., Fujii C., Cottont N.D., Horst K., Roberts K.M., Hatch B., Smith H.O., Venter J.C.; RT "Genomic sequence of a Lyme disease spirochete, <i>Borrelia burgdorferi</i> ."; RL Nature 390:580-586(1997). | | | |
| DR EMBL: A00111; AAC67057.1; -; Genomic_DNA. | | | |
| DR PIR: D70189; D70189. | | | |
| DR TIGR: BB017; -; | | | |
| KW Complete proteome; Hypothetical protein. | | | |
| SO SEQUENCE 160 AA; 19300 MW; 9DE20A49/C0F5737 CRC64; | | | |
| Query Match 71.7%; Score 43; DB 2; Length 160; Best Local Similarity 60.0%; Pred. No. 11; Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0; | | | |
| Qy Db 2 ATYYFGID 11 | | | |
| RESULT 4 | | | |
| 0660P6_BORG_A | | | |
| ID 0660P6_BORG_A PRELIMINARY; | PRT; | 160 AA. | |
| AC 0660P6; | | | |
| DT 25-OCT-2004 (TREMBLrel. 28, Created) | | | |
| DT 25-OCT-2004 (TREMBLrel. 28, last sequence update) | | | |
| DR 25-OCT-2004 (TREMBLrel. 28, last annotation update) | | | |
| DE Conserved hypothetical integral membrane protein. | | | |
| DR OrderdLocusNames=BG0739; | | | |
| OS Borrelia garinii | | | |
| OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia; Borrelia burgdorferi group. | | | |
| OX NCBI_TaxID=29519; | | | |
| RN [1] | | | |
| RP NUCLEOTIDE SEQUENCE. | | | |
| RC STRAIN=PRI; | | | |
| RA Gloeckner G., Lehmann R., Romualdi A., Pradella S., Schnittel-Spechtel U., Wilcke B., Suenhaj J., Platzter M.; | | | |
| RA RT "Comparative analysis of the <i>Borrelia garinii</i> genome"; | | | |
| RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases. | | | |
| DR EMBL: CP000013; AAU0765.1; -, Genomic_DNA. | | | |
| KW Complete proteome; Hypothetical protein. | | | |
| SO SEQUENCE 160 AA; 19293 MW; B65B15C5197BFB89 CRC64; | | | |
| Query Match 71.7%; Score 43; DB 2; Length 160; Best Local Similarity 54.5%; Pred. No. 28; Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0; | | | |
| Qy Db 2 ATYYFGID 11 | | | |

QY 1 ATTYYVFGLDV 11
 ; :||:|||||:
 Db 116 IFSVYVFFGLDI 126

RESULT 6
 Q7VY11_BORPE
 ID Q7VY11_BORPE PRELIMINARY; PRT; 364 AA.
 AC
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Putative periplasmic solute-binding protein.
 GN Name=somM; Order=locusNames=BBP1487;
 OS Bordetella pertussis.
 OC Alcaligenaceae; Bordetella; Betaproteobacteria; Burkholderiales;
 OX NCBI_TaxID=520;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Tchamla_I / ATCC BAA-589 / NCTC 13251'
 RX MEDLINE=22827954; PubMed=129010271; DOI=10.1038/ng1227;
 RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
 Harris D.B., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
 Achtman M., Atkin R., Baker S., Basham D., Bason N., Chevrevach I.,
 Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 Fellwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
 Leather S., Moulé S., Norberczak H., O'Neill S., Ormond D., Price C.,
 Rabbinowitsch E., Rutter S., Sanders D., Seeger K.,
 Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,
 Bordetella parapertussis and Bordetella bronchiseptica.";
 RL Nat. Genet. 35:32-40(2003);
 DR EMBL; BX640428; CAB37248.1; -; Genomic_DNA.
 DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . . ; IEA).
 DR InterPro; IPR006311; Tat.
 DR InterPro; IPR004682; TRAP_transprtDctP.
 DR Pfam; PF03480; SBP_bac_7; 1.
 DR TIGRFAMS; TIGR01405; TRT_signal_seq; 1.
 DR KW Complete proteome.
 SQ SEQUENCE 364 AA;
 Query Match 70.0%; Score 42; DB 2; Length 364;
 Best Local Similarity 77.8%; Pred. 38; Mismatches 1; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ATYYVFGLD 10
 Db 98 ASYYVFGKD 106

RESULT 8
 Q7WKL1_BORBR
 ID Q7WKL1_BORBR PRELIMINARY; PRT; 364 AA.
 AC
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Putative periplasmic solute-binding protein.
 GN Name=somM; Order=locusNames=BB1236;
 OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
 OC Alcaligenaceae; Betaproteobacteria; Burkholderiales;
 OX NCBI_TaxID=518;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RBS50 / ATCC BAA-588';
 RX MEDLINE=22827954; PubMed=129010271; DOI=10.1038/ng1227;
 RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
 Harris D.B., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
 Achtman M., Atkin R., Baker S., Basham D., Bason N., Chevrevach I.,
 Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 Fellwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
 Leather S., Moulé S., Norberczak H., O'Neill S., Ormond D., Price C.,
 Rabbinowitsch E., Rutter S., Sanders D., Seeger K.,
 Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,
 Bordetella parapertussis and Bordetella bronchiseptica.";
 RL Nat. Genet. 35:32-40(2003);
 DR EMBL; BX640433; CAB32621.1; -; Genomic_DNA.
 DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . . ; IEA).
 DR InterPro; IPR006311; Tat.
 DR InterPro; IPR004682; TRAP_transprtDctP.
 DR Pfam; PF03480; SBP_bac_7; 1.
 DR TIGRFAMS; TIGR01405; TRT_signal_seq; 1.
 DR KW Complete proteome.
 SQ SEQUENCE 364 AA;
 Query Match 70.0%; Score 42; DB 2; Length 364;
 Best Local Similarity 77.8%; Pred. No. 38;

RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;
 RA Rabus R., Ruepp A., Frickey T., Rettig T., Partmann B., Stark M.,
 RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Geilner K.,
 RA Teseling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
 RA Klank H.-P.,
 RT "The genome of *Desulfotalea psychrophila*, a sulfate-reducing bacterium
 from permanently cold Arctic sediments";
 RL Environ. Microbiol. 6:897-902(2004).
 DR EMBL; CRS22870; CAGG5233.1; -; Genomic_DNA.
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
 DR GO; GO:0050660; F:FAD binding; IEA.
 DR GO; GO:0061118; P:electron transport; IEA.
 DR InterPro; IPR001327; FAD_Pyr_redox.
 DR InterPro; IPR000815; Hg_reductase.
 DR InterPro; IPR006162; Ppantne_S.
 DR InterPro; IPR001100; Pyr_redox.
 DR InterPro; IPR004099; Pyr_redox_dim.
 DR Pfam; PF00070; Pyr_redox; 2.
 DR Pfam; PRO2852; Pyr_redox_dim; 1.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00945; HGMDTASE.
 DR Problem; PR000139; FAD_Pyr_redox; 1.
 DR PROSITE; PS00012; PHOSPHOPANTHENINE; UNKNOWN_1.
 DR PROSITE; PS00075; PYRIDINE_REDUX_1; 1.
 KW Complete proteome.
 SQ SEQUENCE 716 AA; 78725 MW; 68ERFC0600DDE44094 CRC64;

Query Match 68.3%; Score 41; DB 2; Length 716;
 Best Local Similarity 60.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 LATYYFFGLD 10
 Db 14 VSAYIFFGLD 23

Search completed: December 4, 2005, 04:52:20
 Job time : 104.375 secs

OM protein - protein search, using bw model
 Run on: December 4, 2005, 03:59:51 ; Search time 23.6042 Seconds
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GenCore version 5.1.6

Title: US-10-632-706-127
 Perfect score: 60
 Sequence: 1 LATYYVYGLDV 11
 Scoring table: BLOSUM62
 Gapext 10.0 , Gapext 0.5
 Searched: 57260 seqs, 82675679 residues
 Total number of hits satisfying chosen parameters: 57260
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgpn2_6/podata/1/iaa/5-COMB_pep:
 2: /cgpn2_6/podata/1/iaa/6-COMB_pep:
 3: /cgpn2_6/podata/1/iaa/H_COMB_pep:
 4: /cgpn2_6/podata/1/iaa/pCITUS_COMB_pep:
 5: /cgpn2_6/podata/1/iaa/RE_COMB_pep:
 6: /cgpn2_6/podata/1/iaa/backfiles1.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------------------|--------------------|
| 1 | 43 | 71.7 | 33 | 1 US-08-053-131-78 | Sequence 78, AppI |
| 2 | 43 | 71.7 | 33 | 1 US-08-645-641-78 | Sequence 78, AppI |
| 3 | 43 | 71.7 | 33 | 1 US-07-853-408B-78 | Sequence 78, AppI |
| 4 | 43 | 71.7 | 33 | 1 US-08-096-162-78 | Sequence 78, AppI |
| 5 | 43 | 71.7 | 33 | 2 US-09-042-353-275 | Sequence 78, AppI |
| 6 | 43 | 71.7 | 33 | 2 US-08-758-417A-123 | Sequence 78, AppI |
| 7 | 43 | 71.7 | 33 | 4 PCT-US2-10983-78 | Sequence 78, AppI |
| 8 | 43 | 71.7 | 125 | 2 US-09-840-459-84 | Sequence 84, AppI |
| 9 | 43 | 71.7 | 125 | 2 US-09-97-225A-84 | Sequence 84, AppI |
| 10 | 42 | 70.0 | 29 | 1 US-08-53-131-73 | Sequence 73, AppI |
| 11 | 42 | 70.0 | 29 | 1 US-08-645-641-73 | Sequence 73, AppI |
| 12 | 42 | 70.0 | 29 | 1 US-07-853-108B-73 | Sequence 73, AppI |
| 13 | 42 | 70.0 | 29 | 1 US-08-45-641-83 | Sequence 73, AppI |
| 14 | 42 | 70.0 | 29 | 1 US-08-045-641-83 | Sequence 73, AppI |
| 15 | 42 | 70.0 | 29 | 1 US-08-308-865-73 | Sequence 73, AppI |
| 16 | 42 | 70.0 | 29 | 2 US-09-042-353-270 | Sequence 77, AppI |
| 17 | 42 | 70.0 | 29 | 2 US-08-758-417A-118 | Sequence 77, AppI |
| 18 | 42 | 70.0 | 29 | 4 PCT-US2-10983-73 | Sequence 73, AppI |
| 19 | 42 | 70.0 | 31 | 1 US-08-053-131-83 | Sequence 83, AppI |
| 20 | 42 | 70.0 | 31 | 1 US-08-45-641-83 | Sequence 83, AppI |
| 21 | 42 | 70.0 | 31 | 1 US-07-853-408B-83 | Sequence 83, AppI |
| 22 | 42 | 70.0 | 31 | 1 US-08-096-162-83 | Sequence 83, AppI |
| 23 | 42 | 70.0 | 31 | 1 US-08-308-106-83 | Sequence 83, AppI |
| 24 | 42 | 70.0 | 31 | 2 US-09-042-353-280 | Sequence 83, AppI |
| 25 | 42 | 70.0 | 31 | 2 US-08-558-417A-128 | Sequence 128, AppI |
| 26 | 42 | 70.0 | 31 | 1 PCT-US2-10983-83 | Sequence 83, AppI |
| 27 | 42 | 70.0 | 36 | 1 US-08-053-131-84 | Sequence 84, AppI |

RESULT 1
US-08-053-131-78 Application US/08053131
Sequence 78, Application US/08053131
; Patent No. 5661016

GENERAL INFORMATION:
APPLICANT: Lohberg, Niels
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEES: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 200
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #11.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APR-1993
CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-3

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-053-131-78

ALIGNMENTS

28 42 42 70 0 36 1 US-08-645-641-84 Sequence
29 42 42 70 0 36 1 US-08-095-40B-94 Sequence
30 42 70 0 36 1 US-08-096-62-84 Sequence
31 42 70 0 36 1 US-08-308-865-84 Sequence
32 42 70 0 36 2 US-08-042-353-201 Sequence
33 42 70 0 36 2 US-08-758-17A-129 Sequence
34 42 70 0 36 4 PCT-US92-10983-4 Sequence
35 42 70 0 119 2 US-09-840-459-88 Sequence
36 42 70 0 119 2 US-09-497-625A-88 Sequence
37 42 70 0 128 2 US-09-840-459-77 Sequence
38 42 70 0 128 2 US-09-840-459-79 Sequence
39 42 70 0 128 2 US-09-497-625A-77 Sequence
40 42 70 0 128 2 US-09-497-625A-79 Sequence
41 42 70 0 157 2 US-09-472-087-80 Sequence
42 42 70 0 236 2 US-09-456-090A-64 Sequence
43 42 70 0 236 2 US-09-456-090A-104 Sequence
44 42 70 0 236 2 US-09-453-234-64 Sequence
45 42 70 0 236 2 US-09-453-234-104 Sequence

Query Match 71.7%; Score 43; DB 1; Length 33;
 Best Local Similarity 66.7%; Pred. No. 1.6;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TYYYGGLDV 11
 Db 10 SYYYGMDV 18

RESULT 2
 US-08-645-641-78
 Sequence 78, Application US/08645641
 Patent No. 571902
 GENERAL INFORMATION:
 APPLICANT: Lomberg, Nils
 TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
 TITLE OF INVENTION: Producing Heterologous Antibodies
 NUMBER OF SEQUENCES: 150
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: William M. Smith
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/853,408B
 FILING DATE: 19920318
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 14643-9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 78:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-07-853-408B-78

Query Match 71.7%; Score 43; DB 1; Length 33;
 Best Local Similarity 66.7%; Pred. No. 1.6;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TYYYGGLDV 11
 Db 10 SYYYGMDV 18

RESULT 3
 US-07-853-408B-78
 Sequence 78, Application US/07853408B
 Patent No. 5719050
 GENERAL INFORMATION:
 APPLICANT: Lomberg, Nils
 TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
 TITLE OF INVENTION: Producing Heterologous Antibodies
 APPLICATION NUMBER: US 07/990,860
 FILING DATE: 26-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/990,860

NUMBER OF SEQUENCES: 150
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: William M. Smith
 STREET: One Market Plaza, Steuart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 ZIP: 94105
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/096,762
 FILING DATE: 22-JUL-1993
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/053,131
 FILING DATE: 26-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/990,860

FILING DATE: 16-DEC-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/904,068
 FILING DATE: 23-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/853,408
 FILING DATE: 18-MAR-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/810,279
 FILING DATE: 17-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 14643-9-4
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 78:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-036-762-78
 Query Match 71.7%; Score 43; DB 1; Length 33;
 Best Local Similarity 66.7%; Pred. No. 1.6;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 QY 3 TYYVFGLDV 11
 Db :|||:||:|| 18
 10 SYYYGMDV 18
 RESULT 5
 US-08-308-865-78
 Sequence 78, Application US/08308865
 Patent No. 5877937
 GENERAL INFORMATION:
 APPLICANT: Lonberg, Nilg
 APPLICANT: Kay, Robert M.
 TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for Producing Heterologous Antibodies
 NUMBER OF SEQUENCES: 150
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: William M. Smith
 STREET: One Market Plaza, Stewart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/042,353
 FILING DATE: 13-MAR-1998
 CLASSIFICATION: 800
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/810,279
 FILING DATE: 17-DEC-1991
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/853,408
 FILING DATE: 18-MAR-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/904,068
 FILING DATE: 23-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/096,762
 FILING DATE: 16-DEC-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/053,131
 FILING DATE: 26-APR-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/161,739
 FILING DATE: 03-DEC-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/155,301
 FILING DATE: 18-NOV-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/096,762
 FILING DATE: 16-DEC-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/165,699
 FILING DATE: 10-DEC-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/209,741

RESULT 6
 US-09-042-333-785
 Sequence 275, Application US/09042353
 Patent No. 6255458
 GENERAL INFORMATION:
 APPLICANT: Lonberg, Nilg
 APPLICANT: Kay, Robert M.
 TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for Producing Heterologous Antibodies
 NUMBER OF SEQUENCES: 421
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 78:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US92-10983-78

Query Match :|||:|||
 Best Local Similarity 71.7%; Score 43; DB 4; Length 33;
 Matches 6; Conservative 66.7%; Pred. No. 1.6;
 Mismatches 3; N mismatches 0; Indels 0; Gaps 0;

RESULT 9
 US-09-840-459-84
 Patent No. 6696550
 GENERAL INFORMATION:
 Sequence 84; Application US/09840459
 ; Sequence 84, Application US/09840459
 ; APPLICANT: LaRosa, Gregory J.
 ; APPLICANT: Horvath, Christopher
 ; APPLICANT: Newman, Walter
 ; APPLICANT: Jones, S. Tarran
 ; APPLICANT: O'Keefe, Siobhan H.
 ; APPLICANT: O'Keefe, Theresa
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
 FILE REFERENCE: 1855-1-052-012
 CURRENT APPLICATION NUMBER: US/09/840, 459
 CURRENT FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: PCT/US01/03537
 PRIOR FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: 09/497, 625
 PRIOR FILING DATE: 2000-02-03
 PRIOR APPLICATION NUMBER: 09/359, 193
 PRIOR FILING DATE: 1999-07-22
 PRIOR APPLICATION NUMBER: 09/121, 781
 PRIOR FILING DATE: 1998-07-23
 NUMBER OF SEQ ID NOS: 107
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO: 84
 LENGTH: 125
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-840-459-84

Query Match :|||:|||
 Best Local Similarity 71.7%; Score 43; DB 2; Length 125;
 Matches 6; Conservative 66.7%; Pred. No. 6.4;
 Mismatches 3; N mismatches 0; Indels 0; Gaps 0;

RESULT 11
 US-08-053-131-73
 Sequence 73; Application US/08053131
 ; Sequence 73, Application US/08053131
 ; Patent No. 5661016
 GENERAL INFORMATION:
 APPLICANT: Lönberg, Nils
 APPLICANT: Kay, Robert M.
 TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
 TITLE OF INVENTION: Producing Heterologous Antibodies
 NUMBER OF SEQUENCES: 197
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: One Market Plaza, Steuart Tower, Suite 200
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 07/990, 860
 FILING DATE: 26-APR-1993
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/853, 408
 FILING DATE: 18-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/810, 279
 FILING DATE: 17-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/853, 408
 FILING DATE: 18-MAR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30-223
 REFERENCE/DOCKET NUMBER: 14643-9-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 73:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 RESULT 10
 US-09-497-625A-84
 Sequence 84; Application US/09497625A
 ; Sequence 84, Application US/09497625A
 ; Patent No. 6727349
 GENERAL INFORMATION:
 APPLICANT: LaRosa, Gregory J.
 APPLICANT: Horvath, Christopher
 APPLICANT: Newman, Walter
 APPLICANT: Jones, S. Tarran
 APPLICANT: O'Brien, Siobhan H.
 APPLICANT: O'Keefe, Theresa

RESULT 12
US-06-645-641-73
; Sequence 73, Application US/08645641
; Patent No. 5719032
; GENERAL INFORMATION:
; APPLICANT: Lomberg, Nils
; TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/853,408B
; FILING DATE: 15920318
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2422
; TELEX/FAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-853-408B-73
Query Match 70.0%; Score 42; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 2.1; Mismatches 0;
Matches 6; Conservative 2; Indels 0; Gaps 0;
; MOLCULE TYPE: peptide
; US-08-645-641-73
Query Match 70.0%; Score 42; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 2.1; Mismatches 0;
Matches 6; Conservative 2; Indels 0; Gaps 0;
; MOLCULE TYPE: peptide
; US-08-645-641-73
RESULT 13
US-07-853-408B-73
; Sequence 73, Application US/07853408B
; Patent No. 5719032
; GENERAL INFORMATION:
; APPLICANT: Lomberg, Nils
; TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,762
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131

FILING DATE: 26-APR-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/990,860
 FILING DATE: 16-DEC-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/904,068
 FILING DATE: 23-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/853,408
 FILING DATE: 18-MAR-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/810,279
 FILING DATE: 17-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 14643-9-4

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 FAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 73:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide

US-08-308-865-73
 Query Match 70.0%; Score 42; DB 1; Length 29;
 Best Local Similarity 75.0%; Pred. No. 2.1;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YYVFGLDV 11
 Db 7 YYYGMDV 14
 Search completed: December 4, 2005, 04:09:43
 Job time : 24.6042 secs

Query Match 70.0%; Score 42; DB 1; Length 29;

Best Local Similarity 75.0%; Pred. No. 2.1;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YYVFGLDV 11
 Db 7 YYYGMDV 14

RESULT 15
 US-08-308-865-73
 ; Sequence 73, Application US/08308865
 ; Patient No. 5877397
 GENERAL INFORMATION:
 APPLICANT: Lonberg, Nilg
 APPLICANT: Kay, Robert M.
 TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for
 TITLE OF INVENTION: Producing Heterologous Antibodies
 NUMBER OF SEQUENCES: 150
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: William M. Smith
 STREET: One Market Plaza, Steuart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/308,865
 FILING DATE:
 CLASSIFICATION: 800
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/145,707
 FILING DATE:
 APPLICATION NUMBER: US 07/904,068
 FILING DATE: 23-JUN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 14643-9-1-1

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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:07:28 ; Search time 78.8333 Seconds

Sequence: 58.302 Million cell updates/sec

Title: US-10-632-706-127

Perfect score: 60

Sequence: 1 LATYYFFGLDV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:
1: /cgpn2_6/pctodata/1/pubpaas/US07_PUBCOMB.pep:
2: /cgpn2_6/pctodata/1/pubpaas/US08_PUBCOMB.pep:
3: /cgpn2_6/pctodata/1/pubpaas/US09_PUBCOMB.pep:
4: /cgpn2_6/pctodata/1/pubpaas/US10_PUBCOMB.pep:
5: /cgpn2_6/pctodata/1/pubpaas/US11_PUBCOMB.pep:
6: /cgpn2_6/pctodata/1/pubpaas/US12_PUBCOMB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|--------------------|
| 1 | 60 | 100.0 | 11 4 | US-10-632-706-126 |
| 2 | 60 | 100.0 | 11 4 | US-10-632-706-127 |
| 3 | 48 | 80.0 | 122 6 | US-11-031-485-116 |
| 4 | 47 | 78.3 | 129 4 | US-10-364-743-01 |
| 5 | 47 | 78.3 | 129 5 | US-10-452-593-101 |
| 6 | 47 | 78.3 | 134 4 | US-10-364-743-15 |
| 7 | 47 | 78.3 | 134 5 | US-10-452-593-15 |
| 8 | 47 | 78.3 | 468 6 | US-11-031-485-55 |
| 9 | 47 | 78.3 | 469 6 | US-11-031-485-18 |
| 10 | 46 | 76.7 | 13 4 | US-10-632-706-114 |
| 11 | 46 | 76.7 | 21 5 | US-10-783-311-141 |
| 12 | 46 | 76.7 | 140 5 | US-10-783-311-135 |
| 13 | 45 | 75.0 | 16 5 | US-10-783-311-277 |
| 14 | 45 | 75.0 | 21 3 | US-09-880-3068 |
| 15 | 45 | 75.0 | 21 4 | US-10-293-418-3068 |
| 16 | 45 | 75.0 | 117 6 | US-11-009-731-47 |
| 17 | 45 | 75.0 | 135 5 | US-10-783-311-271 |
| 18 | 45 | 75.0 | 256 3 | US-09-880-748-1600 |
| 19 | 45 | 75.0 | 256 4 | US-10-293-418-1600 |
| 20 | 44 | 73.3 | 16 3 | US-09-880-748-2129 |
| 21 | 44 | 73.3 | 16 4 | US-10-293-418-2129 |
| 22 | 44 | 73.3 | 17 3 | US-09-880-748-2876 |
| 23 | 44 | 73.3 | 17 4 | US-10-293-418-2876 |
| 24 | 44 | 73.3 | 18 5 | US-10-984-660A-8 |
| 25 | 44 | 73.3 | 117 4 | US-10-041-860-206 |
| 26 | 44 | 73.3 | 123 4 | US-10-309-762-18 |
| 27 | 44 | 73.3 | 123 4 | US-10-309-762-19 |

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|-------------------|
| 1 | 60 | 100.0 | 11 4 | US-10-293-088-106 |
| 2 | 29 | 44 | 73.3 | 127 4 |
| 3 | 30 | 44 | 73.3 | US-10-041-860-311 |
| 31 | 44 | 73.3 | 127 4 | US-10-041-860-325 |
| 32 | 44 | 73.3 | 127 4 | US-10-663-383-42 |
| 33 | 44 | 73.3 | 127 4 | US-10-466-243-53 |
| 34 | 44 | 73.3 | 127 5 | US-10-984-960A-2 |
| 35 | 44 | 73.3 | 129 4 | US-10-293-088-10 |
| 36 | 44 | 73.3 | 134 4 | US-10-364-743-16 |
| 37 | 44 | 73.3 | 134 4 | US-10-364-743-109 |
| 38 | 44 | 73.3 | 134 4 | US-10-364-743-110 |
| 39 | 44 | 73.3 | 134 5 | US-10-452-593-16 |
| 40 | 44 | 73.3 | 134 5 | US-10-452-593-109 |
| 41 | 44 | 73.3 | 134 5 | US-10-452-593-110 |
| 42 | 44 | 73.3 | 145 4 | US-10-644-277-146 |
| 43 | 44 | 73.3 | 157 5 | US-10-473-287-34 |
| 44 | 44 | 73.3 | 157 5 | US-10-473-287-63 |
| 45 | 44 | 73.3 | 249 5 | US-10-935-290-61 |

ALIGNMENTS

RESULT 1

US-10-632-706-126
; Sequence 116, Application US/0632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOClonal ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS
; FILE REFERENCE: 4077-895120US
; CURRENT APPLICATION NUMBER: US/10/632-706

CURRENT APPLICATION NUMBER: US/10/632-706
CURRENT FILING DATE: 2003-08-01
PRIORITY FILING DATE: 2002-08-01
PRIORITY APPLICATION NUMBER: US 09/144,806
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2

SEQ ID NO: 126
LENGTH: 11

TYPE: PRT
ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: single chain antibody fragment

US-10-632-706-126

Query Match Score: 100.0%; Length: 11;

Best Local Similarity: 100.0%; Pred. No.: 0.0027%; Mismatches: 0; Indels: 0; Gaps: 0;

Matches: 11; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

SEQUENCE:

D**b** 1 LATYYFFGLDV 11

QY

1 LATYYFFGLDV 11

;

GENERAL INFORMATION:

APPLICANT: MARKS, JAMES D.

APPLICANT: AMERSDORFER, PETER

TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM

TITLE OF INVENTION: NEUROTOXINS

FILE REFERENCE: 4077-895120US

CURRENT APPLICATION NUMBER: US/10/632-706

CURRENT FILING DATE: 2003-08-01

PRIORITY FILING DATE: 2002-08-01

PRIORITY APPLICATION NUMBER: US 09/144,806

;

PRIOR FILING DATE: 1998-08-31
 NUMBER OF SEQ ID NOS: 278
 SOFTWARE: Patentin version 3.2
 SEQ ID NO: 127
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: single chain antibody fragment
 US-10-632-706-127

| Query Match | Score | DB | Length |
|-----------------------|------------------|----|--------|
| Best Local Similarity | 100.0% | 4 | 11 |
| Matches | 11 | 0 | 0 |
| Qy | 1 DATYYFFGLDV 11 | | |
| Db | 1 DATYYFFGLDV 11 | | |

RESULT 3
 US-11-031-485-116
 Sequence 116 Application US/11031485
 Publication No. US2005232917A1
 GENERAL INFORMATION:
 APPLICANT: PUTLEN, NICHOLAS
 APPLICANT: MOLLOY, ELIZABETH
 APPLICANT: KELLERMANN, STRID-AMEE
 APPLICANT: GREEN, LARRY L.
 APPLICANT: HAAK-FREUNDSCO, MARY
 TITLE OF INVENTION: ANTIBODIES TO MADCAM
 FILE REFERENCE: ABX-P66
 CURRENT APPLICATION NUMBER: US/11/031,485
 CURRENT FILING DATE: 2005-01-07
 PRIOR APPLICATION NUMBER: 60/525,490
 PRIOR FILING DATE: 2004-01-09
 NUMBER OF SEQ ID NOS: 147
 SOFTWARE: Patentin Ver. 3.3
 SEQ ID NO: 116
 LENGTH: 122
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-031-485-116

Query Match 80.0% Score 48 DB 6 Length 122;
 Best Local Similarity 63.6%; Pred. No. 2.8;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 DATYYFFGLDV 11
 Db 100 VVTYYYYGMDV 110

RESULT 4
 US-10-364-743-101
 Sequence 101 Application US/10364743
 Publication No. US2004009178A1
 GENERAL INFORMATION:
 APPLICANT: Bowdish, Katherine S.
 APPLICANT: Frederickson, Shana
 APPLICANT: Wild, Martha A.
 APPLICANT: Maruyama, Toshiaki
 APPLICANT: No. US2004009178A1, Mary Jean
 TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
 FILE REFERENCE: B4 (1087-73)
 CURRENT APPLICATION NUMBER: US/10/364,743
 CURRENT FILING DATE: 2003-02-11
 PRIOR APPLICATION NUMBER: US 60/428,807
 CURRENT FILING DATE: 2003-02-11
 PRIOR FILING DATE: 2002-11-25
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: Patentin version 3.2
 SEQ ID NO: 101
 LENGTH: 129

RESULT 5
 US-10-452-593-101
 Sequence 101 Application US/0452593
 Publication No. US2004025699A1
 GENERAL INFORMATION:
 APPLICANT: Bowdish, Katherine S.
 APPLICANT: Frederickson, Shana
 APPLICANT: Wild, Martha A.
 APPLICANT: Maruyama, Toshiaki
 APPLICANT: Nolan, Mary Jean
 TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
 FILE REFERENCE: 98 CIP (1087-73 CIP)
 CURRENT APPLICATION NUMBER: US/10/452,593
 CURRENT FILING DATE: 2003-06-02
 PRIOR APPLICATION NUMBER: US 10/364,743
 PRIOR FILING DATE: 2003-02-11
 PRIOR APPLICATION NUMBER: US 60/356,086
 PRIOR FILING DATE: 2002-07-11
 PRIOR APPLICATION NUMBER: US 60/376,408
 PRIOR FILING DATE: 2002-04-29
 PRIOR APPLICATION NUMBER: US 60/428,807
 PRIOR FILING DATE: 2002-11-25
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: Patentin version 3.2
 SEQ ID NO: 101
 LENGTH: 129
 TYPE: PRT
 ORGANISM: human
 US-10-452-593-101

RESULT 6
 US-10-364-743-15
 Sequence 15 Application US/10364743
 Publication No. US2004009178A1
 GENERAL INFORMATION:
 APPLICANT: Bowdish, Katherine S.
 APPLICANT: Frederickson, Shana
 APPLICANT: Wild, Martha A.
 APPLICANT: Maruyama, Toshiaki
 APPLICANT: No. US2004009178A1, Mary Jean
 TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
 FILE REFERENCE: B4 (1087-73)
 CURRENT APPLICATION NUMBER: US/10/364,743
 CURRENT FILING DATE: 2003-02-11
 PRIOR APPLICATION NUMBER: US 60/428,807
 CURRENT FILING DATE: 2003-02-11
 PRIOR FILING DATE: 2002-11-25
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: Patentin version 3.2
 SEQ ID NO: 15
 LENGTH: 134
 TYPE: PRT

; ORGANISM: human
US-10-364-743-15

US-11-031-485-56

Y Query Match 78.3%; Score 47; DB 4; Length 144;
 Best Local Similarity 77.8%; Pred. No. 4.5;
 Matches 7; Conservative 2; Mismatches 0; Indels 0
 3 TYYFGLDV 11

RESULT /
US-10-452-593-15
; Sequence 15, Application US/10452593
Publication No. US20040258699A1

US-11-031-485-18
; Sequence 18, Application US/11031485
; Publication No. US20050232917A1
; GENERAL INFORMATION:

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APPLICANT: Bowdish, Katherine S.
APPLICANT: Fredrickson, Shana
APPLICANT: Wild, Martha A.
APPLICANT: Maruyama, Toshiaki
APPLICANT: Nolan, Mary Jean
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 98 CIP (1087-73 CIP)
CURRENT APPLICATION NUMBER: US/10/452,593
CURRENT FILING DATE: 2003-06-02
PRIORITY APPLICATION NUMBER: US 10/364,743
PRIORITY FILING DATE: 2003-02-11
PRIORITY APPLICATION NUMBER: US 60/356,086
PRIORITY FILING DATE: 2002-02-11
PRIORITY APPLICATION NUMBER: US 60/376,408
PRIORITY FILING DATE: 2002-04-29
PRIORITY APPLICATION NUMBER: US 60/428,807
PRIORITY FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.2
SEQ ID NO 15
LENGTH: 134
TYPE: PRT
ORGANISM: human
;US-10-452-593-15

Query Match          78.3%; Score 47; DB 5; Length 134;
Best Local Similarity 77.8%; Pred. No. 4; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Ov      3 TTYYFGLDV 11
Db      110 TTYYFGMDV 118

RESULT 8
US-11-0311-485-56
Sequence 56, Application US/11031485
Publication No. US20050232917A1
GENERAL INFORMATION:
APPLICANT: PULLEN, NICHOLAS
APPLICANT: MOLLOY, ELIZABETH
APPLICANT: KEILERMANN, SIRID-AIMEE
APPLICANT: GREEN, LARRY L.
APPLICANT: HAKK-FRENDSCHO, MARY
TITLE OF INVENTION: ANTIbODIES TO MADCAM
FILE REFERENCE: ABK-PF6
CURRENT APPLICATION NUMBER: US/11/031,485
CURRENT FILING DATE: 2005-01-07
PRIORITY APPLICATION NUMBER: 60/535,490
PRIORITY FILING DATE: 2004-01-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 56
LENGTH: 468
TYPE: PRT
ORGANISM: Homo sapiens
;US-11-0311-485-18

Query Match          78.3%; Score 47; DB 5; Length 134;
Best Local Similarity 77.8%; Pred. No. 15; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Ov      3 TTYYFGLDV 11
Db      123 TTYYGYMDV 131

RESULT 10
US-10-632-706-114
Sequence 114, Application US/10632706
Publication No. US2004017538A1
GENERAL INFORMATION:
APPLICANT: MARKS, JAMES D.
APPLICANT: AMERSDORFER, PETER
APPLICANT: KELLERMAN, SIRID-AIMEE
APPLICANT: HAKK-FRENDSCHO, MARY
TITLE OF INVENTION: THERAPEUTIC MONOClonAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
FILE REFERENCE: 407T-855120US
CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT FILING DATE: 2003-08-01
PRIORITY APPLICATION NUMBER: US 60/400,721
PRIORITY FILING DATE: 2002-08-01
PRIORITY APPLICATION NUMBER: US 09/144,806
PRIORITY FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 114
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial
FEATURE: OTHER INFORMATION: single chain antibody fragment
;US-10-632-706-114

Query Match          76.7%; Score 46; DB 4; Length 13;
Best Local Similarity 70.0%; Pred. No. 0; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy      2 ATYYFFGLDV 11
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Db      4 ANYYYGMDV 13
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; NUMBER OF SEQ ID NOS: 394
; SEQ ID NO: 277
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy Chain amino acid sequence
; US-10-783-311-141

Query Match    76.7%; Score 46; DB 5; Length 21;
Best Local Similarity 63.6%; Pred. No. 1;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy      1 LATYYFFGLDV 11
      ||||:|:|
Db      11 LGNYYYGMDV 21
; GENERAL INFORMATION:
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; NUMBER OF SEQ ID NOS: 394
; SEQ ID NO: 141
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Heavy Chain amino acid sequence
; US-10-783-311-141

Query Match    76.7%; Score 46; DB 5; Length 21;
Best Local Similarity 63.6%; Pred. No. 1;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy      1 LATYYFFGLDV 11
      ||||:|:|
Db      11 LGNYYYGMDV 21
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; NUMBER OF SEQ ID NOS: 394
; SEQ ID NO: 141
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Heavy Chain amino acid sequence
; US-10-783-311-141

RESULT 12
US-10-783-311-135
; Sequence 135; Application US/10783311
; Publication No. US2005009136A1
; GENERAL INFORMATION:
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; NUMBER OF SEQ ID NOS: 394
; SEQ ID NO: 141
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Heavy Chain amino acid sequence
; US-10-783-311-135

Query Match    75.0%; Score 45; DB 5; length 16;
Best Local Similarity 63.6%; Pred. No. 1.2;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy      1 LATYYFFGLDV 11
      :|:||:|:|
Db      6 VAGYYYYGMDV 16
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 3068
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-3068

Query Match    75.0%; Score 45; DB 3; length 21;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy      2 ATYYFFGLDV 11
      ||||:|:|
Db      12 APYYYGMDV 21
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; US-10-293-418-3068
; Sequence 3068; Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; US-10-783-311-277
; Sequence 277; Application US/10783311
; RESULT 13
; US-10-783-311-277
; Sequence 277; Application US/10783311

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; FILE REFERENCE: PP523F2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3068
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-418-3068
```

Query Match 75.0%; Score 45; DB 4; Length 21;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

| QY | 2 ATYYFGLDV | 11 |
|----|--------------|----|
| | : : | |
| Db | 12 APYYYGMDV | 21 |

Search completed: December 4, 2005, 04:37:28
Job time : 80.8333 sec

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 4, 2005, 04:08:08 ; Search time 3.20833 Seconds
Sequence: 1 LATYYFGLDV 11

Title: US-10-632-706-127
Perfect score: 60

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0
Maximum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep:
2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:
3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:
4: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:
5: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep:
6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep:
7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep:
8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|--------------------|
| 1 | 45 | 75.0 | 21 | US-11-054-515-3068 |
| 2 | 45 | 75.0 | 256 | US-11-054-515-1600 |
| 3 | 44 | 73.3 | 16 | US-11-054-515-2129 |
| 4 | 44 | 73.3 | 17 | US-11-054-515-2876 |
| 5 | 44 | 73.3 | 252 | US-11-054-515-1431 |
| 6 | 44 | 73.3 | 254 | US-11-054-515-3 |
| 7 | 44 | 73.3 | 254 | US-11-054-515-838 |
| 8 | 44 | 73.3 | 254 | US-11-054-515-870 |
| 9 | 44 | 73.3 | 254 | US-11-054-515-1287 |
| 10 | 44 | 73.3 | 254 | US-11-054-515-1288 |
| 11 | 43 | 71.7 | 306 | US-11-017-550-47 |
| 12 | 42 | 70.0 | 13 | US-11-054-515-3091 |
| 13 | 42 | 70.0 | 17 | US-11-054-515-2817 |
| 14 | 42 | 70.0 | 19 | US-11-054-515-2735 |
| 15 | 42 | 70.0 | 19 | US-11-054-515-2899 |
| 16 | 42 | 70.0 | 19 | US-11-054-515-2928 |
| 17 | 42 | 70.0 | 19 | US-11-054-515-2935 |
| 18 | 42 | 70.0 | 19 | US-11-054-515-3038 |
| 19 | 42 | 70.0 | 19 | US-11-054-515-3052 |
| 20 | 42 | 70.0 | 19 | US-11-054-515-3067 |
| 21 | 42 | 70.0 | 19 | US-11-054-515-3087 |
| 22 | 42 | 70.0 | 19 | US-11-054-515-3145 |
| 23 | 42 | 70.0 | 20 | US-11-040-159-4 |
| 24 | 42 | 70.0 | 20 | US-11-054-515-2767 |
| 25 | 42 | 70.0 | 7 | US-11-054-515-3039 |

ALIGNMENTS

RESULT 1
US-11-054-515-3068
; Sequence 3068, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS
; FILE REFERENCE: PEP23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; REMAINING PRIOR APPLICATION DATA REMOVED - SEE FILE WRAPPER OR PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3068
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-3068

Sequence 2926, AP
Sequence 8, AP
Sequence 16, AP
Sequence 4, AP
Sequence 1965, AP
Sequence 1974, AP
Sequence 1315, AP
Sequence 1440, AP
Sequence 1921, AP
Sequence 1731, AP
Sequence 934, AP
Sequence 1001, AP
Sequence 1259, AP
Sequence 1334, AP
Sequence 1701, AP
Sequence 1735, AP
Sequence 1739, AP
Sequence 1271, AP
Sequence 1284, AP
Sequence 1209, AP

QY 2 ATTYFGLDV 11

Db 12 APYYYGKDV 21

RESULT 2

US-11-054-515-1600
; Sequence 1600, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2003-05-25
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1600
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-1600
; Query Match 75.0%; Score 45; DB 7; Length 256;
; Best Local Similarity 70.0%; Pred. No. 0.19; 1; Mismatches 2; Indels 0; Gaps 0;
; Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
; QY 2 ATYYYFGDV 11
; Db 110 APVYYGMDV 119
; RESULT 3
; Sequence 2129, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-10
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2076
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-2876
; Query Match 73.3%; Score 44; DB 7; Length 17;
; Best Local Similarity 63.6%; Pred. No. 0.021; 2; Mismatches 2; Indels 0; Gaps 0;
; Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
; QY 1 LATYYYFGDV 11
; Db 7 LTGYYYGMDV 17
; RESULT 5
; Sequence 1431, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.

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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PFS53P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO: 1431
LENGTH: 252
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1431

RESULT 6
US-11-054-515-3
Query Match 73.3%; Score 44; DB 7; Length 252;
Best Local Similarity 63.6%; Pred. No. 0.28; Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
GAP: | :|:||:|:|
Db 105 LTGYYYFGMDV 115

RESULT 6
US-11-054-515-3
Query Match 73.3%; Score 44; DB 7; Length 252;
Best Local Similarity 63.6%; Pred. No. 0.28; Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
GAP: | :|:||:|:|
Db 107 LTGYYYFGMDV 117

RESULT 7
US-11-054-515-838
Query Match 73.3%; Score 44; DB 7; Length 254;
Best Local Similarity 63.6%; Pred. No. 0.28; Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
GAP: | :|:||:|:|
Db 107 LTGYYYFGMDV 117

RESULT 7
US-11-054-515-838
Query Match 73.3%; Score 44; DB 7; Length 254;
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PFS53P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO: 838
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-838

RESULT 8
US-11-054-515-870
Query Match 73.3%; Score 44; DB 7; Length 254;
Best Local Similarity 63.6%; Pred. No. 0.28; Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
GAP: | :|:||:|:|
Db 107 LTGYYYFGMDV 117

RESULT 8
US-11-054-515-870
Query Match 73.3%; Score 44; DB 7; Length 254;
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PFS53P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247

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PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580,347
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 10/293,418
 PRIOR FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/340,817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/880,748
 PRIOR FILING DATE: 2001-05-15
 PRIOR APPLICATION NUMBER: 60/293,499
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/277,379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/276,248
 PRIOR FILING DATE: 2000-10-17
 SEQ ID NO: 3247
 LENGTH: 254
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: Site
 LOCATION: (42)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: Site
 LOCATION: (45)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: Site
 LOCATION: (51)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: Site
 LOCATION: (57)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: Site
 LOCATION: (51)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: Site
 LOCATION: (65)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: Site
 LOCATION: (67)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: Site
 LOCATION: (70)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: Site
 LOCATION: (170)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: Site
 LOCATION: (176)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: Site
 LOCATION: (235)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: Site
 LOCATION: (239)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

Remaining Prior Application data removed - See File Wrapper or PALM.

Query Match 73.3%; Score 44; DB 7; Length 254;
 Best Local Similarity 63.6%; Pred. No. 0.28; 2; Indels 0; Gaps 0;

| Qy | 1 LATYYFGLDV 11 |
|----|--------------------|
| Db | 107 LTGYYYGMDV 117 |

RESULT 9
 US-11-054-515-1287
 ; Sequence 1287, Application US/11054515
 ; Publication No. US2005025532A1
 GENERAL INFORMATION:
 ; APPLICANT: Rubin et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 FILE REFERENCE: PF523P3
 CURRENT APPLICATION NUMBER: US/11/054,515
 CURRENT FILING DATE: 2005-02-10
 PRIOR APPLICATION NUMBER: 60/543,296
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580,347
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 10/293,418
 PRIOR FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/277,379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/276,248
 PRIOR FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/293,499
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 09/880,748
 PRIOR FILING DATE: 2000-10-17
 Remaining Prior Application data removed - See File Wrapper or PALM.

SEQ ID NO: 1287
 LENGTH: 254
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-054-515-1287

Query Match 73.3%; Score 44; DB 7; Length 254;
 Best Local Similarity 63.6%; Pred. No. 0.28; 2; Indels 0; Gaps 0;

| Qy | 1 LATYYFGLDV 11 |
|----|--------------------|
| Db | 107 LTGYYYGMDV 117 |

RESULT 10
 US-11-054-515-1288
 ; Sequence 1288, Application US/11054515
 ; Publication No. US2005025532A1
 GENERAL INFORMATION:
 ; APPLICANT: Rubin et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 FILE REFERENCE: PF523P3
 CURRENT APPLICATION NUMBER: US/11/054,515
 CURRENT FILING DATE: 2005-02-10
 PRIOR APPLICATION NUMBER: 60/543,296

PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580,347
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 10/233,418
 PRIOR FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/340,817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/880,748
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/293,499
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/277,379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/276,248
 PRIOR FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/240,816
 PRIOR FILING DATE: 2000-10-17
 Remaining Prior Application data removed - See File Wrapper or PALM.
 SEQ ID NO: 1288
 LENGTH: 254
 TYPE: PRT
 ORGANISM: Homo sapiens
; US-11-054-515-1288

RESULT 11
US-11-017-550-47
Query Match 73.3%; Score 44; DB 7; length 254;
Best Local Similarity 63.6%; Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2;
Indels 0; Gaps 0;
QY 1 LATYYFGLDV 11
Db 107 LTGIVTYGMDV 117

GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
APPLICANT: Schultz, Peter G
APPLICANT: Wang, Lei
APPLICANT: Anderson, John C
APPLICANT: Chin, Jason
APPLICANT: Liu, David R
APPLICANT: Magliery, Thomas
APPLICANT: Meggers, Eric L
APPLICANT: Mehl, Ryan A
APPLICANT: Pasternak, Miro
APPLICANT: Santoro, Stephen W
APPLICANT: Zhang, Zhilwen
TITLE OF INVENTION: In Vivo Incorporation of Unnatural Amino Acids
FILE REFERENCE: 54-000120S
CURRENT APPLICATION NUMBER: US/11/017,550
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: US/10/126,927
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,030
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 60/355,514
PRIOR FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 47
LENGTH: 306
TYPE: PRT
ORGANISM: Methanococcus jannaschii
; US-11-017-550-47

Query Match 71.7%; Score 43; DB 7; length 306;
Best Local Similarity 77.8%; Pred. No. 0.5;

RESULT 12
US-11-054-515-3091
Sequence 3091, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS
FILE REFERENCE: PFF23P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/293,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO: 3091
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
; US-11-054-515-3091

RESULT 13
US-11-054-515-2817
Sequence 2817, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS
FILE REFERENCE: PFF52P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/293,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO: 2817
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
S 11-05-515-2817

Remaining Prior Application data removed - See file Wrapper or PAML.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2817
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2817

US-11-054515-2899
Sequence 2899, Application US/11054515
Publication No. US20050255512A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immune
FILE REFERENCE: PFP52P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14

ospecifically Bind Blys

Query Match: Best Local Similarity: 75.0%; Score: 42; DB: 7; Length: 17; Matches: 6; Conservative: 2; Mismatches: 0; Index: 0; Gaps: 0

| | |
|----|--|
| Qy | 4 YYFGGLDV 11 : : 10 YYYGMDV 17 |
| Db | |

US-11-054515-2735
Sequence 2735, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Rubin et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BIVs

```
CURRENT APPLICATION NUMBER: US/11/054,515  
CURRENT FILING DATE: 2005-02-10  
PRIOR APPLICATION NUMBER: 60/543,296  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
Remaining Prior Application data removed -  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 2735  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-054-515-2735
```

Query Match 70.0%; Score 42; DB 7; Length 19;
 Best Local Similarity 75.0%; Pred. No. 0.051; Matches 6;
 Conservative 2; Mismatches 0; Indels 0;

DB

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model
Run on: December 4, 2005, 04:09:54 ; Search time 95.5625 seconds
(without alignments)
50.576 Million cell updates/sec

Title: US-10-632-706-128
Perfect score: 66
Sequence: 1 GPWELVGYFDS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_21:*

1: geneseq1980s:*

2: geneseq21990s:*

3: geneseq2000s:*

4: geneseq2001s:*

5: geneseq2002s:*

6: geneseq2003s:*

7: geneseq2003s:*

8: geneseq2004s:*

9: geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description | ALIGNMENTS |
|------------|-------|--------------------|-----------------|--|---|
| 1 | 66 | 100.0 | 11 8 ADR38726 | RESULT 1 ID ADR38726 standard; peptide; 11 AA. XX | aag38801 Arabidops Aag69053 Amino aci Abg30761 Arabidops Aag38800 Arabidops Aag05439 Arabidops Aag05438 Arabidops Aag38799 Arabidops Abg32172 Herbicide Abn95054 M. xanthu Aag3760 Arabidops Aag30759 Arabidops Agt60469 Plant pol Abu1890 Protein e Abg20404 Novel hum Aau48754 Propionib Abm6594 Propionib Adm45273 Propionib Aag36913 Arabidops Aag36912 Arabidops Aag36911 Arabidops Aan95055 Human rep |
| 2 | 44 | 100.0 | 6 ABU47042 | ID ADR38726; XX DT 02-DEC-2004 (first entry) | |
| 3 | 44 | 66.7 | 367 6 ABU47042 | DE Mouse heavy chain variable region CDR3 seqid 128. XX | |
| 4 | 44 | 66.7 | 367 6 ABU47877 | DE Mouse heavy chain variable region CDR3 seqid 128. XX | |
| 5 | 43 | 65.2 | 207 8 ADH12894 | DE Mouse heavy chain variable region CDR3 seqid 128. XX | |
| 6 | 42 | 63.6 | 415 7 ABM89126 | DE antibacterial; antibody; botulinum neurotoxin type A; Bont/A; KW Bont/A neutralising epitope; anti-botulinum neurotoxin antibody; KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; KW heavy chain variable region; complementarity determining region; CDR3. XX | |
| 7 | 41 | 62.1 | 114 4 ARQ0873 | OS Mus sp. XX | |
| 8 | 41 | 62.1 | 121 2 AAR89504 | OS Mus sp. XX | |
| 9 | 41 | 62.1 | 475 6 ABU20453 | OS US2004175385-A1. XX | |
| 10 | 41 | 62.1 | 792 7 ADC01986 | PD 09-SEP-2004. XX | |
| 11 | 41 | 62.1 | 1352 4 ABB67542 | PF 01-AUG-2003; 2003US-00632706. XX | |
| 12 | 40 | 60.6 | 146 6 ABP56556 | PR 31-AUG-1998; 98US-00144866. PR 01-AUG-2002; 2002US-0400721P. | |
| 13 | 40 | 60.6 | 283 6 ABM70292 | PR (REGC) UNIV CALIFORNIA. XX | |
| 14 | 40 | 60.6 | 477 8 ADY22314 | PI Marks JD, Amerstorfer P; XX | |
| 15 | 40 | 60.6 | 885 3 ANG32050 | PI Marks JD, Amerstorfer P; XX | |
| 16 | 40 | 60.6 | 931 3 ANG32049 | PT New isolated antibody that neutralizes botulinum neurotoxin type A, PT useful for diagnosing botulism or for treating pathologies associated with botulinum neurotoxin poisoning. XX | |
| 17 | 40 | 60.6 | 956 3 ARG3048 | PS Example 3; SEQ ID NO 128; 110pp; English. | |
| 18 | 39.5 | 59.8 | 511 8 ADX8944 | CC The invention describes an isolated antibody (I) that specifically binds CC to an epitope specifically bound by an antibody expressed by a specific CC clone where (I) binds to and neutralises botulinum neurotoxin type A (Bont/A). An isolated antibody (I) that specifically binds to an epitope CC specifically bound by an antibody expressed by a clone chosen from clone CC S25, C25, C39, IC5, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1, CC 3-10 and ING31, where (I) binds to and neutralizes botulinum CC neurotoxin type A (Bont/A). Also described are a polypeptide (II) CC comprising Bont/A neutralizing epitope having an epitope that is | |
| 19 | 39 | 59.1 | 79 3 ARG13553 | | |
| 20 | 39 | 59.1 | 103 3 ARG13552 | | |
| 21 | 39 | 59.1 | 112 3 ARG13551 | | |
| 22 | 39 | 59.1 | 166 4 ARW06660 | | |
| 23 | 39 | 59.1 | 211 8 ADM50765 | | |
| 24 | 39 | 59.1 | 233 3 ANG05440 | | |

CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulinum
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain variable region complementarity determining
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.
 XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 66; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 11; Conservatve 0; Indels 0; Gaps 0;

QY 1 GPWELVGYFDS 11
 DB 1 GPWELVGYFDS 11

RESULT 2

ABU45531 ABU45531 standard; protein; 306 AA.

AC ABU45531; DT 19-JUN-2003 (first entry)

DR Protein encoded by prokaryotic essential gene #31058.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design..
 OS Salmonella paratyphi.

PN WO200277183-A2.
 PD 03-OCT-2002.
 PR 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342223P.
 PR 08-FEB-2002; 2002US-0072851.
 PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

PI Wang L, Zamudio C, Malone C, Hesselbeck R, Ohlsen KL, Zywicki JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-02926/02.

XX PT New antisense nucleic acids, useful for identifying proteins or screening
 PT isolate candidate molecules for rational drug discovery programs.
 XX PS Claim 25; SEQ ID NO 73455; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolat candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than S. aureus, S. typhimurium,
 CC K. pneumoniae or P. aeruginosa. The sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 306 AA;

RESULT 3

ABU47042 ABU47042 standard; protein; 367 AA.

AC ABU47042; DT 19-JUN-2003 (first entry)

DR Protein encoded by Prokaryotic essential gene #22569.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design..
 OS Salmonella typhimurium.

PN WO200277183-A2.
 PD 03-OCT-2002.
 PR 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342223P.
 PR 08-FEB-2002; 2002US-0072851.
 PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

PI Wang L, Zamudio C, Malone C, Hesselbeck R, Ohlsen KL, Zywicki JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-02926/02.

XX PT New antisense nucleic acids, useful for identifying proteins or screening
 PT isolate candidate molecules for rational drug discovery programs.
 XX PS Claim 25; SEQ ID NO 73455; 1766pp; English.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 74966; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX Sequence 367 AA;

Query Match 66.7%; Score 44; DB 6; Length 367;
 Best local Similarity 69.2%; Pred. No. 48;
 Matches 9; Conservative 0; Mismatches 0;
 QY 1 GPWELV---GYF 9
 DB 127 GPWELVLGPPGYF 139

RESULT 4
 ABU47877
 ID ABU47877 standard; protein; 367 AA.
 AC ABU47877;
 XX DT 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #33404.
 XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX OS *Salmonella typhi*.

XX WO200277183-A2.
 XX PD 03-OCT-2002.
 XX PF 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0162695P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW; Wall D, Trwick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-039926/02.
 N-PSDB; ACA51747.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 75801; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX Sequence 367 AA;

Query Match 66.7%; Score 44; DB 6; Length 367;
 Best Local Similarity 69.2%; Pred. No. 48;
 Matches 9; Conservative 0; Mismatches 0;
 QY 1 GPWELV---GYF 9
 DB 127 GPWELVLGPPGYF 139

RESULT 5
 ADH12894
 ID ADH12894 Standard; protein; 207 AA.
 XX AC ADH12894;
 XX DT 25-MAR-2004 (first entry)
 XX DE *Francisella tularensis* immunogenic protein 75, SEQ ID NO:75.
 XX KW Immunogenic protein; protective immune response; vaccine;
 KW genetic vaccine; antibacterial.
 XX OS *Francisella tularensis*.

XX WO2004003009-A2.
 PN XX Moughamer T, Provart N, Ricke D, Zhu T;
 XX DR WPI; 2003-248011/24.
 PD XX
 XX 08-JAN-2004.
 XX PR XX
 XX 26-JUN-2003; 2003WO-GB002718.
 XX PT
 XX New stress-responsive nucleic acid, useful for altering the
 XX responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
 XX stress, salt stress or osmotic stress.
 XX PS
 XX Claim 1; SEQ ID NO 7372; 89pp; English.
 XX XQ
 XX Tithall RW, Mayers CN, Duffield ML, Miller J, Rowe SC;
 XX DR XX
 XX (MINA) UK SEC FOR DEFENCE.
 XX PR XX
 XX New protein, useful as a vaccine for producing a protective immune
 XX response in a mammal against infection by *Francisella tularensis*, or
 XX preventing or treating *Francisella tularensis* infection in a mammal.
 XX PS
 XX Claim 1; SEQ ID NO 75; 21pp; English.
 XX
 CC The invention relates to 100 potentially immunogenic proteins from
 CC *Francisella tularensis* (ADH12920-ADH13019) which may be used in vaccines. The nucleic acids
 CC may be contained within a vaccine, bacterial or plasmid vector. The invention also relates to a pharmaceutical composition comprising the
 CC protein or the nucleic acid in combination with a pharmaceutical carrier
 CC or excipient. The proteins and nucleic acids are useful in vaccine
 CC compositions for producing a protective immune response against
 CC *Francisella tularensis* infection in a mammal, or for preventing or
 CC treating *Francisella tularensis* infection in a mammal. The present
 CC sequence represents a *Francisella tularensis* protein of the invention.
 XX SQ Sequence 207 AA;
 Query Match 65.2%; Score 43; DB 8; Length 207;
 Best Local Similarity 100.0%; Pred. No. 39; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC Qy 1 GPWELVGC 7
 Db 120 GPWELVGC 126
 XX
 RESULT 6
 ABM89126 ABM89126 standard; protein; 415 AA.
 ID XX
 AC XX
 AC ABM89126;
 XX DT 02-JUN-2005 (first entry)
 XX DE Rice abiotic stress responsive polypeptide SEQ ID NO:7372.
 XX KW abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
 XX OS Oryza sativa.
 XX PN WO2003008540-A2.
 XX DD 30-JAN-2003.
 XX PR 21-JUN-2002; 2002WO-US019668.
 XX PR 22-JUN-2001; 2001US-0300112P.
 XX PR 24-AUG-2001; 2001US-031462P.
 XX PR 26-SEP-2001; 2001US-032577P.
 XX PR 21-NOV-2001; 2001US-0332132P.
 XX PA (SYGN) SINGENTA PARTICIPATIONS AG.
 XX PI Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;

XX WO2004003009-A2.
 PN XX Moughamer T, Provart N, Ricke D, Zhu T;
 XX DR WPI; 2003-248011/24.
 XX
 XX New stress-responsive nucleic acid, useful for altering the
 XX responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
 XX stress, salt stress or osmotic stress.
 XX PS
 XX Claim 1; SEQ ID NO 7372; 89pp; English.
 XX XQ
 XX The invention relates to novel abiotic stress responsive polynucleotides
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host
 CC cells, and plants containing such polynucleotides. Also disclosed are
 CC methods for using the polynucleotides and polypeptides to alter the
 CC responsiveness of a plant to abiotic stress. The invention is useful in
 CC agriculture. The nucleic acid is useful for determining whether a test
 CC plant has been exposed to an abiotic stress condition. It is also useful
 CC for selecting an agent that alters abiotic stress regulated
 CC polynucleotide expression in a plant cell, and to identify a homolog or
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
 CC molecule and the polypeptide encoded by it are useful in altering the
 CC stress responsiveness of a plant to an abiotic stress, such as cold stress, salt
 CC stress, osmotic stress or any of their combinations. The present sequence
 CC is used in the exemplification of the invention
 XX SQ Sequence 415 AA;
 Query Match 63.6%; Score 42; DB 7; Length 415;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 CC Qy 1 GPWELVGY 8
 Db 176 GPWELVGF 183
 XX
 RESULT 7
 AAC0873 AAC0873 standard; protein; 114 AA.
 ID XX
 AC AAC0873;
 AC AAC0873;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human polypeptide SEQ ID NO 22665.
 XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haemopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX OS Homo sapiens.
 XX PN WO200164835-A2.
 XX DD 07-SEP-2001.
 XX PR 26-FEB-2001; 2001WO-US004927.
 XX PR 28-FEB-2000; 2000US-00515126.
 PR 18-MAY-2000; 2000US-00577409.
 XX PA (HYSE-) HYSEQ INC.
 XX
 Tang YT, Liu C, Drmanac RT;
 XX PR WPI; 2001-514838/56.
 DR N-PSDB; AAI88704.
 XX
 XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 XX
 XX Claim 20; SEQ ID NO 22665; 1399pp + Sequence Listing; English.

xx
 cc The invention relates to human polynucleotides (AKR79941-AN193841) and
 cc the encoded proteins (AK00010-AK013910) that exhibit activity elating to
 cc cytokine, cell proliferation or cell differentiation or which may induce
 cc production of other cytokines in other cell populations. The
 cc polynucleotides and polypeptides are useful in gene therapy, vaccines or
 cc peptide therapy. The polypeptides have various cytokine-like activities,
 e.g. stem cell growth factor activity, haematopoiesis regulating
 cc activity, tissue growth factor activity, immunomodulatory activity and
 cc activin/inhibin activity and may be useful in the diagnosis and/or
 treatment of cancer. Note: The sequence data for this patent did not form part
 of the printed specification, but was obtained in electronic format
 directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

SQ Sequence 114 AA;

Query Match 62.1%; Score 41; DB 4; Length 114;
 Best Local Similarity 55.6%; Pred. No. 46;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPWELVGYP 9
 Db 76 GPWKERGF 84

RESULT 8

AAR8504
 ID AAR8504 Standard; protein; 121 AA.

XX
 AC AAR8504;
 XX
 DT 31-JUL-1996 (first entry)

DE VHmu for antibody BR34/A5.

XX
 KW Antibody; variable heavy chain; VHmu; human; monoclonal; Mab; BT34/A5;
 KW BT32/A6; cell cycle independent; tumour specific; glioma; therapy;
 KW detection; complementarity determining region; CUR.
 XX
 OS Homo sapiens.

FH Location/Qualifiers

PT Region 31. .35 /note= "complementarity determining region (specifically
 claimed)"

PT Region 50. .66 /note= "complementarity determining region (specifically
 claimed)"

PT Region 99. .110 /note= "complementarity determining region (specifically
 claimed)"

PT Region WO9535374-A1.

XX
 PD 28-DEC-1995.

PP 16-JUN-1995; 95WO-CA000361.

PR 21-JUN-1994; 94US-00264093.
 (DANM/) DAN M D.

PI Dan MD;

XX
 DR WPI: 1996-058411/06.
 DR N-PSDB; AAC10938.

PT Novel monoclonal antibodies, BT34/A5 and BT32/A6 - used to characterise
 PT glioma specific cell surface antigens, and in the treatment of glioma.
 XX
 PS Claim 8; Page 33; 53pp; English.

cc AAR8504-R88510 represent regions of the human monoclonal antibodies
 cc (MAb's) BT34/A5 and BT32/A6. This sequence represents the variable region
 cc of the heavy chain subgroup mu, (VHmu) of BT34/A5. The complementarity
 cc determining regions (CDR's) of this sequence are specifically claimed.
 cc This sequence preferably has an N-terminal extension comprising the
 cc signal sequence represented in AAR8505. The BT34/A5 and BT32/A6 MAb's
 cc recognise a cell cycle independent tumour specific antigen. They also
 cc bind equally well to tumour cells in vitro regardless of their culture
 cc viability, growth characteristics, or culture density. The antibodies
 cc effectively label the tumour cells by binding to the antigen present on
 cc the cell surface. The Mab's are useful in the detection and the treatment
 cc of glioma. These Mab's are specific for glioma and show none of the cross
 cc -reactivity seen with previous antibodies
 XX
 SQ Sequence 121 AA;

Query Match 62.1%; Score 41; DB 2; Length 121;
 Best Local Similarity 60.0%; Pred. No. 49;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPWELVGYFD 10
 Db 100 GWWDLNYFD 109

RESULT 9

ABU0453
 ID ABU20453 Standard; protein; 475 AA.

XX
 AC ABU0453;
 XX
 DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #5980.

XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX
 OS Bacteroides fragilis.

XX
 PN WO200277183-A2.

XX
 PD 03-OCT-2002.

XX
 PF 21-MAR-2002; 2002WO-US009107.

XX
 PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-0048993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX
 PA (ELIT-) BLITRA PHARM INC.

XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Travick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX
 WPI: 2003-028926/02.

DR N-PSDB; AAC24323.

XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 isolate candidate molecules for rational drug discovery programs.

XX
 PS Claim 25; SEQ ID NO 48377; 176pp; English.

XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polyPeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences
 XX SQ Sequence 475 AA:
 Query Match 62.1%; Score 41; DB 6; Length 475;
 Best Local Similarity 54.5%; Pred. No. 2.1e-02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 CC Qv 1 GPWMEVGDYPS 11
 CC Db 404 GDWKLUVYVDS 414
 XX RESULT 10
 ADC07986
 ID ADC07986 Standard; protein; 792 AA.
 XX
 AC ADC07986;
 XX DT 18-DEC-2003 (first entry)
 XX DE Rice protein sequence Seq ID252 related to grain filling.
 XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 KW carbohydrate degradation; carbohydrate; plant; grain; grain filling; corn;
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal; grain;
 KW gene; ds; plant.
 OS *Oryza sativa*.
 XX PN WO200300905-H2.
 XX PD 03-JAN-2003.
 XX PF 21-JUN-2002; 2002WO-1B002450.
 XX PR 22-JUN-2001; 2001US-0300112P.
 PR 26-SEP-2001; 2001US-032277P.
 PR 20-DEC-2001; 2001US-0342327P.
 XX PA (SGCN) SYNGENTA PARTICIPATIONS AG.
 XX PI Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 PI Glazebrook J, Katgirri P, Krebs J, Provart N, Rieke D;
 XX DR N-PSSDB; ADC07985.
 PT WPI; 2003-229341/22.
 PT New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates
 PT N-PSSDB; DR

CC This invention, in the area of plant biotechnology, relates to novel
 CC polynucleotides comprising a nucleotide sequence encoding a protein which
 CC is involved in or associated with the synthesis, metabolism or
 CC degradation of carbohydrates in the plant grain and the expression of
 CC which is up-regulated during grain filling. The plant is selected from
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 CC sugarbeet, wheat, and rice. The invention may be useful for the
 CC improvement of protein, oil, starch, fibre and moisture content of the
 CC cereal grains. In addition, carbohydrate levels may be modified to a more
 CC desirable level using the present invention. The present sequence is the
 CC amino acid sequence of a rice protein of the invention. Note: The
 CC sequence data for this protein did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at http://www.wipo.int/pub/publishedpc_t-sequences.

XX Sequence 792 AA;

| Query Match | Score | DB | % Identity | Length | AA |
|-----------------------|-------|----|------------|---------|----|
| Best Local Similarity | 62.1% | 7 | 66.7% | 792 | |
| Matches | 6 | | Pred. No. | 3.66+02 | |
| | | | Mismatches | 1 | |
| QY | 2 | | Indels | 0 | |
| | | | Gaps | 0 | |
| Db | 245 | | | | |
| | | | | | |
| | | | | | |

XX SQ

RESULT 11

| ID | Accession | Score | DB | % Identity | Length | AA |
|---------------------|--|----------|--------|------------|--------|----|
| ABB67542 | ABB67542 standard; protein; 1352 AA. | | | | | |
| XX | | | | | | |
| AC | ABB67542; | | | | | |
| XX | | | | | | |
| DT | 26-MAR-2002 (first entry) | | | | | |
| XX | Drosophila melanogaster polypeptide | SQ ID NO | 29418. | | | |
| KW | Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical. | | | | | |
| OS | Drosophila melanogaster. | | | | | |
| XX | | | | | | |
| PN | WO200171042-A2. | | | | | |
| XX | | | | | | |
| PD | 27-SEP-2001. | | | | | |
| XX | | | | | | |
| PP | 23-MAR-2001; 2001WO-US009231. | | | | | |
| XX | | | | | | |
| PR | 23-MAR-2000; 2000US-0191637P. | | | | | |
| PR | 11-JUL-2000; 2000US-00614150. | | | | | |
| XX | | | | | | |
| (PERE) PE CORP NY. | | | | | | |
| PA | | | | | | |
| XX | | | | | | |
| PI | Venter JC, Adams M, Li PMD, Myers EW; | | | | | |
| XX | | | | | | |
| DR | WPI; 2001-656660/75. | | | | | |
| DR | N-PADB; ABL11645. | | | | | |
| XX | | | | | | |
| PT | New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions. | | | | | |
| XX | | | | | | |
| PS | Disclosure; SEQ ID NO 29418; 21pp + Sequence Listing; English. | | | | | |

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC

CC discloses genomic DNA sequences (ABL16176-ABL3051), expressed DNA
 CC sequences (ABL01840-ABL6175) and the encoded proteins (ABP5773)-
 CC ABB2072). The sequence information for this patient did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/pub/published_pct_sequences

SQ Sequence 1352 AA;

| | | | | | | | |
|-----------------------|-------|--------------|---------|------------|---|--------|------|
| Query Match | 62.1% | Score | 41 | DB | 4 | Length | 1352 |
| Best Local Similarity | 77.8% | Pred. No. | 6.3e+02 | Indels | 0 | Gaps | 0 |
| Matches | 7 | Conservative | 0 | Mismatches | 2 | | |
| Db | 161 | WRNNGYFDS | 169 | | | | |

RESULT 12

| | | |
|---|--|--------------------------------------|
| ID | ABP56656 | ABPS56656 standard; protein; 146 AA. |
| AC | ABP56656; | |
| XX | | |
| DT | 25-MAR-2003 | (first entry) |
| DE | Chimpanzee C68 adenovirus E3 16 kDa protein SEQ ID NO:21. | |
| XX | | |
| KW | Chimpanzee; C68; adenovirus; rapid screening; bacterial transformant; simian adenovirus; cytosatic; antipsoriatic; antimicrobial; vaccine; adenovirin; capsid protein; hexon; penton; fibre protein; cancer; hyperproliferative condition; psoriasis; infection. | |
| KW | Mastadenovirus. | |
| OS | | |
| XX | | |
| FH | Key | Location/Qualifiers |
| FT | Mis-difference | 62 |
| FT | /note= "any amino acid" | |
| XX | | |
| PN | WO200300851-A2. | |
| XX | | |
| PD | 03-JAN-2003. | |
| PP | 20-JUN-2002; 2002WO-US019735. | |
| XX | | |
| PR | 22-JUN-2001; 2001US-0300501P. | |
| PR | 04-JUN-2002; 2002US-0385632P. | |
| XX | | |
| PA | (UFR-) UNIV PENNSYLVANIA. | |
| PA | XX | |
| PI | Gao G, Wilson JM; | |
| XX | | |
| DR | WPI; 2003-184043/18. | |
| DR | N-P5DB; ABB22473. | |
| XX | | |
| PT | New C68 chimpanzee adenoviral capsid protein, useful for preparing a composition for treating hyperproliferative conditions e.g., cancer or psoriasis and as a vaccine against bacterial, fungal, viral or parasitic infection. | |
| PT | Disclosure: Page 88; 124pp; English. | |
| XX | | |
| The present invention describes a chimpanzee C68 adenoviral capsid protein, which is substantially free of other viral proteins with which it is naturally associated, comprising: (a) a hexon protein comprising 513-amino acid sequence (see ABP56647); (b) a penton protein comprising 534-amino acid sequence (see ABP56647); (c) a fibre protein comprising 425-amino acid sequence (see ABP5662); or (d) a unique fragment of any of (A)-(C) comprising 8-amino acid residues in length. Also described: (1) a novel adenovirus serotype comprising a unique fragment of the C68 hexon protein fused to a heterologous adenovirus hexon peptide; (2) a recombinant or pseudotyped adenovirus comprising a capsid of the novel adenovirus serotype encapsidating a molecule for delivery to a target cell; (3) an adenoviral capsid; (4) a pharmaceutical composition; (5) | | |

RESULT 13

| | | |
|---|--|-------------------------------------|
| ID | ABM70292 | ABM70292 standard; protein; 283 AA. |
| AC | ABM70292; | |
| XX | | |
| DT | 20-NOV-2003 | (first entry) |
| DE | Photorhabdus luminescens protein sequence #3389. | |
| XX | | |
| KW | Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague; whooping cough. | |
| KW | | |
| OS | Photorhabdus luminescens. | |
| XX | | |
| PN | WO200294867-A2. | |
| XX | | |
| PD | 28-NOV-2002. | |
| XX | | |
| PF | 07-FEB-2002; 2002WO-IB003040. | |
| XX | | |
| PR | 07-FEB-2001; 2001FR-00001659. | |
| XX | | |
| PA | (INSP) INST PASTEUR. | |
| PA | (CNRS) CNRS CENT NAT RECH SCI. | |
| XX | | |
| PI | Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A; | |
| PI | Buchrieser C; | |
| XX | | |
| DR | WPI; 2003-148459/14. | |
| XX | | |
| PT | Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides. | |
| PT | Claim 2; SEQ ID NO 3389; 1205pp; French. | |
| XX | | |
| The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of <i>P. luminescens</i> and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of <i>P. luminescens</i> , e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than <i>P. luminescens</i> and are able to alter responses or sensitivity to toxins and antibiotics produced by <i>P. luminescens</i> . Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibiotics useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful | | |

CC therapeutically (to treat microbial infection by bacteria or fungi that
 CC are sensitive to *P. luminescens* encoded toxins or antibiotics) and as
 CC biopesticides. Other uses of the genes and the proteins are as virulence
 CC factors and for identifying targets of human diseases for which *P.
 CC luminescens* is a model (particularly plague and whooping cough). This
 CC sequence represents one of the isolated *P. luminescens* proteins
 XX SQ Sequence 283 AA;

Query Match 60.6%; Score 40; DB 6; Length 283;
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WELVGYFDS 11
 Db 238 WLIVGVYFDA 246

RESULT 14

ID ADV22314 Standard; protein; 477 AA.
 XX
 AC ADV22314;
 XX

DT 21-APR-2005 (first entry)

XX DB Plant full length insert polypeptide seqid 70098.
 XX KW plant protectant; plant growth regulator; gene therapy; plant;
 recombinant DNA construct; physical array; plant breeding marker;
 cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 extreme osmotic condition; pathogen tolerance; pest tolerance;
 growth rate; cell cycle pathway; disease resistance;
 galactomannan production; lignin production; plant growth regulator;
 protein content; plant growth; plant development; seed oil; protein yield;
 protein content.

XX OS Unidentified.

XX PN US2004034888-A1.
 XX PD 19-FEB-2004.

XX PR 28-APR-2003; 2003US-00425114.

XX PR 06-MAY-1999; 99US-00304517.

XX PR 05-NOV-2001; 2001US-00985678.

XX PA (LIUJ/) LIU J.
 PA (ZHOJ/) ZHOU Y.

PA (KOVAJ/) KOVALIC D K.
 PA (SCREB/) SCREEN S E.

PA (TABAJ/) TABASKA J E.
 PA (CAOY/) CAO Y.

XX PI Liu J, Zhou Y, Kovacic DK, Screen SE, Tabaska JE, Cao Y;
 XX DR WPI; 2004-180133/17.

XX PT New recombinant DNA construct, useful for improving plant tolerance to
 cold, heat, drought, herbicide, extreme osmotic conditions, pathogens or
 pests, for conferring increased resistance to plant disease, or for
 improving yield.

XX PS Claim 1; SEQ ID NO 70098; 15pp; English.

XX CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp://seqdata.uspto.gov/Sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 improving plant tolerance to cold, heat, drought, herbicides, extreme

CC osmotic conditions. Pathogens or pests for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.

SQ Sequence 477 AA;

Query Match 60.6%; Score 40; DB 8; Length 477;
 Best Local Similarity 60.0%; Pred. No. 3.1e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPWELVGYFD 10
 Db 307 GPWEMMREFD 316

RESULT 15

ID AAG32050 Standard; protein; 885 AA.
 XX
 AC AAG32050;
 XX DT 17-OCT-2000 (first entry)

XX DB Arabidopsis thaliana protein fragment SEQ ID NO: 38593.
 XX KW Protein identification; Signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX OS Arabidopsis thaliana.
 XX FN EP1033405-A2.
 XX PD 06-SEP-2000.
 XX PR 25-FEB-2000; 2000EP-00301439.
 XX PR 25-FEB-1999; 99US-0121825P.
 PR 05-MAR-1999; 99US-0123180P.
 PR 09-MAR-1999; 99US-0123548P.
 PR 23-MAR-1999; 99US-0123788P.
 PR 25-MAR-1999; 99US-0126264P.
 PR 29-MAR-1999; 99US-0126785P.
 PR 01-APR-1999; 99US-0127462P.
 PR 06-APR-1999; 99US-0128234P.
 PR 08-APR-1999; 99US-0128714P.
 PR 16-APR-1999; 99US-0128845P.
 PR 19-APR-1999; 99US-0129077P.
 PR 21-APR-1999; 99US-0134449P.
 PR 23-APR-1999; 99US-0130510P.
 PR 28-APR-1999; 99US-0131449P.
 PR 30-APR-1999; 99US-0132048P.
 PR 04-MAY-1999; 99US-0132484P.
 PR 05-MAY-1999; 99US-0132485P.
 PR 06-MAY-1999; 99US-0132486P.
 PR 07-MAY-1999; 99US-013263P.
 PR 11-MAY-1999; 99US-013256P.
 PR 14-MAY-1999; 99US-0134218P.
 PR 14-MAY-1999; 99US-0134219P.
 PR 14-MAY-1999; 99US-0134221P.
 PR 14-MAY-1999; 99US-0134370P.
 PR 18-MAY-1999; 99US-0134768P.

| | | | | | |
|----|--------------|----------------|----|--------------|----------------|
| PR | 19-MAY-1999; | 99US-0134941P. | PR | 28-JUL-1999; | 99US-0145951P. |
| PR | 20-MAY-1999; | 99US-0135124P. | PR | 02-AUG-1999; | 99US-0146386P. |
| PR | 21-MAY-1999; | 99US-0135353P. | PR | 03-AUG-1999; | 99US-0146383P. |
| PR | 22-MAY-1999; | 99US-013562P. | PR | 02-AUG-1999; | 99US-0147031P. |
| PR | 25-MAY-1999; | 99US-0136021P. | PR | 03-AUG-1999; | 99US-0147204P. |
| PR | 27-MAY-1999; | 99US-0136392P. | PR | 04-AUG-1999; | 99US-0147302P. |
| PR | 28-MAY-1999; | 99US-0136782P. | PR | 04-AUG-1999; | 99US-014793P. |
| PR | 01-JUN-1999; | 99US-0137222P. | PR | 05-AUG-1999; | 99US-0147192P. |
| PR | 03-JUN-1999; | 99US-0137528P. | PR | 06-AUG-1999; | 99US-0147260P. |
| PR | 04-JUN-1999; | 99US-013752P. | PR | 06-AUG-1999; | 99US-0147303P. |
| PR | 07-JUN-1999; | 99US-0137724P. | PR | 06-AUG-1999; | 99US-0147416P. |
| PR | 08-JUN-1999; | 99US-0138094P. | PR | 07-AUG-1999; | 99US-0147493P. |
| PR | 10-JUN-1999; | 99US-0138540P. | PR | 09-AUG-1999; | 99US-014793P. |
| PR | 10-JUN-1999; | 99US-0138847P. | PR | 10-AUG-1999; | 99US-0148171P. |
| PR | 14-JUN-1999; | 99US-0139119P. | PR | 11-AUG-1999; | 99US-0148311P. |
| PR | 16-JUN-1999; | 99US-0139452P. | PR | 12-AUG-1999; | 99US-014941P. |
| PR | 16-JUN-1999; | 99US-0139453P. | PR | 13-AUG-1999; | 99US-0149456P. |
| PR | 17-JUN-1999; | 99US-0139492P. | PR | 17-AUG-1999; | 99US-0149461P. |
| PR | 18-JUN-1999; | 99US-0139455P. | PR | 18-AUG-1999; | 99US-0139456P. |
| PR | 18-JUN-1999; | 99US-0139462P. | PR | 20-AUG-1999; | 99US-0149722P. |
| PR | 18-JUN-1999; | 99US-0139457P. | PR | 20-AUG-1999; | 99US-0149723P. |
| PR | 18-JUN-1999; | 99US-0139458P. | PR | 20-AUG-1999; | 99US-0149929P. |
| PR | 18-JUN-1999; | 99US-0139459P. | PR | 23-AUG-1999; | 99US-0149460P. |
| PR | 18-JUN-1999; | 99US-0139817P. | PR | 23-AUG-1999; | 99US-0149902P. |
| PR | 22-JUN-1999; | 99US-0139899P. | PR | 23-AUG-1999; | 99US-0149175P. |
| PR | 23-JUN-1999; | 99US-0140353P. | PR | 25-AUG-1999; | 99US-0149425P. |
| PR | 23-JUN-1999; | 99US-0140421P. | PR | 26-AUG-1999; | 99US-0150565P. |
| PR | 24-JUN-1999; | 99US-0139750P. | PR | 27-AUG-1999; | 99US-0150884P. |
| PR | 24-JUN-1999; | 99US-0139763P. | PR | 27-AUG-1999; | 99US-0151065P. |
| PR | 24-JUN-1999; | 99US-0139817P. | PR | 27-AUG-1999; | 99US-0151080P. |
| PR | 30-JUN-1999; | 99US-0142287P. | PR | 30-AUG-1999; | 99US-0151303P. |
| PR | 31-JUL-1999; | 99US-0142977P. | PR | 31-AUG-1999; | 99US-0151438P. |
| PR | 01-JUL-1999; | 99US-014215P. | PR | 01-SEP-1999; | 99US-0151930P. |
| PR | 02-JUL-1999; | 99US-0140695P. | PR | 02-SEP-1999; | 99US-0152363P. |
| PR | 28-JUN-1999; | 99US-0140823P. | PR | 10-SEP-1999; | 99US-0153070P. |
| PR | 29-JUN-1999; | 99US-0140991P. | PR | 13-SEP-1999; | 99US-0153758P. |
| PR | 30-JUN-1999; | 99US-0142920P. | PR | 16-SEP-1999; | 99US-0154018P. |
| PR | 12-JUL-1999; | 99US-0142977P. | PR | 20-SEP-1999; | 99US-0154779P. |
| PR | 13-JUL-1999; | 99US-0143425P. | PR | 22-SEP-1999; | 99US-0155139P. |
| PR | 13-JUL-1999; | 99US-014354P. | PR | 23-SEP-1999; | 99US-0155485P. |
| PR | 14-JUL-1999; | 99US-0143624P. | PR | 13-SEP-1999; | 99US-0155659P. |
| PR | 06-JUL-1999; | 99US-0142390P. | PR | 24-SEP-1999; | 99US-0155659P. |
| PR | 07-JUL-1999; | 99US-0142803P. | PR | 28-SEP-1999; | 99US-0156458P. |
| PR | 09-JUL-1999; | 99US-0142877P. | PR | 16-SEP-1999; | 99US-0156565P. |
| PR | 11-JUL-1999; | 99US-014325P. | PR | 20-SEP-1999; | 99US-015717P. |
| PR | 13-JUL-1999; | 99US-0143425P. | PR | 04-OCT-1999; | 99US-015753P. |
| PR | 14-JUL-1999; | 99US-014354P. | PR | 05-OCT-1999; | 99US-0157753P. |
| PR | 14-JUL-1999; | 99US-0143624P. | PR | 06-OCT-1999; | 99US-0157865P. |
| PR | 15-JUL-1999; | 99US-0144005P. | PR | 07-OCT-1999; | 99US-0158029P. |
| PR | 16-JUL-1999; | 99US-0144085P. | PR | 08-OCT-1999; | 99US-0158232P. |
| PR | 16-JUL-1999; | 99US-0144086P. | PR | 12-OCT-1999; | 99US-0158369P. |
| PR | 17-JUL-1999; | 99US-014431P. | PR | 13-OCT-1999; | 99US-0159293P. |
| PR | 19-JUL-1999; | 99US-0144332P. | PR | 13-OCT-1999; | 99US-0159294P. |
| PR | 19-JUL-1999; | 99US-0144333P. | PR | 14-OCT-1999; | 99US-0159295P. |
| PR | 19-JUL-1999; | 99US-0144334P. | PR | 14-OCT-1999; | 99US-0159330P. |
| PR | 20-JUL-1999; | 99US-0144352P. | PR | 14-OCT-1999; | 99US-0159331P. |
| PR | 20-JUL-1999; | 99US-0144632P. | PR | 14-OCT-1999; | 99US-0159637P. |
| PR | 20-JUL-1999; | 99US-0144884P. | PR | 14-OCT-1999; | 99US-0159638P. |
| PR | 21-JUL-1999; | 99US-0144814P. | PR | 18-OCT-1999; | 99US-0159584P. |
| PR | 21-JUL-1999; | 99US-0145086P. | PR | 21-OCT-1999; | 99US-0160741P. |
| PR | 21-JUL-1999; | 99US-0145335P. | PR | 21-OCT-1999; | 99US-0160767P. |
| PR | 22-JUL-1999; | 99US-0145085P. | PR | 21-OCT-1999; | 99US-0160768P. |
| PR | 22-JUL-1999; | 99US-0145276P. | PR | 25-OCT-1999; | 99US-0161404P. |
| PR | 27-JUL-1999; | 99US-0145913P. | PR | 25-OCT-1999; | 99US-0161405P. |
| PR | 27-JUL-1999; | 99US-0145918P. | PR | 25-OCT-1999; | 99US-0161406P. |
| PR | 27-JUL-1999; | 99US-0145919P. | PR | 26-OCT-1999; | 99US-0161359P. |

Mon Dec 5 10:18:12 2005

us-10-632-706-128.rag

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| | | |
|----|--------------|----------------|
| PR | 26-OCT-1999; | 99US-0161360P |
| PR | 26-OCT-1999; | 99US-0161361P. |
| PR | 28-OCT-1999; | 99US-0161920P. |
| PR | 28-OCT-1999; | 99US-0161992P. |
| PR | 28-OCT-1999; | 99US-0161993P. |
| PR | 29-OCT-1999; | 99US-0162142P. |

Query Match 60.6%; Score 40; DB 3; Length 885;
Best Local Similarity 85.7%; Fred. No. 6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

| | |
|----|-----------------|
| Qy | 1 GPWELVG 7 |
| | : |
| Db | 411 GPWOLVG 417 |

Search completed: December 4, 2005, 04:44:57
Job time : 98.5625 secs.

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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:45 ; Search time 15.5833 Seconds

Post-processing: (without alignments) 67.918 Million cell updates/sec

Title: US-10-632-706-128
Perfect score: 66
Sequence: 1 GFWBLVGSYFDS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80.4*

pir1:*

pir2:*

pir3:*

pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query | Length | DB ID | Description |
|------------|-------|---------|-------|--------|---------------------------|---|
| 1 | 45 | 68.2 | 279 | 2 | T35791 | probable transmembrane sugar transport protein - Streptomyces coelicolor |
| 2 | 44 | 66.7 | 367 | 2 | AD0922 | C;Species: Streptomyces coelicolor |
| 3 | 43 | 65.2 | 1788 | 2 | T29043 | C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004 |
| 4 | 41 | 62.1 | 491 | 2 | 869368 | C;Accession: T35791 |
| 5 | 41 | 62.1 | 550 | 2 | B84900 | R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. |
| 6 | 41 | 62.1 | 619 | 1 | S48729 | submitted to the EMBL data library, July 1998 |
| 7 | 41 | 62.1 | 697 | 2 | G70704 | A;Reference number: Z21570 |
| 8 | 40 | 60.6 | 724 | 2 | B87015 | A;Accession: T35791 |
| 9 | 40 | 60.6 | 726 | 2 | T44905 | A;Status: preliminary; translated from GB/EMBL/DDJB |
| 10 | 40 | 60.6 | 888 | 2 | D84824 | A;Molecule type: DNA |
| 11 | 40 | 60.6 | 931 | 2 | R84637 | A;Residues: 1-273 <SEE> |
| 12 | 39 | 59.1 | 299 | 2 | D71051 | A;Cross-references: UNIPROT:087858; UNIPARC:UPI00000DACA7; EMBL:AL031013; PIDN:CAA19796. |
| 13 | 39 | 59.1 | 320 | 2 | T33303 | C;Gene: SCOEDB:SCB16.24 |
| 14 | 39 | 59.1 | 459 | 2 | S17907 | C;Superfamily: maltose transport protein malG |
| 15 | 39 | 59.1 | 471 | 2 | S28476 | Query Match 68.2%; Score 45; DB 2; Length 279; |
| 16 | 39 | 59.1 | 578 | 2 | B88204 | Best Local Similarity 68.2%; Pred. No. 2.8; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Db 160 WMLIGYFDS 168 |
| 17 | 39 | 59.1 | 949 | 1 | PXMU1 | RESULT 2 |
| 18 | 38 | 57.6 | 173 | 2 | S44403 | Qy 3 WMLIGYFDS 11 |
| 19 | 38 | 57.6 | 2 | C75335 | Db 160 WMLIGYFDS 168 | |
| 20 | 38 | 57.6 | 409 | 2 | S63614 | Probable undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase SIV3637 [imported] |
| 21 | 38 | 57.6 | 432 | 2 | T17829 | Probable undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase SIV3637 [imported] |
| 22 | 38 | 57.6 | 465 | 2 | T26146 | ABC transporter ML |
| 23 | 38 | 57.6 | 496 | 2 | G71693 | ABC-type transport |
| 24 | 38 | 57.6 | 499 | 2 | G37761 | probable DNA-directed |
| 25 | 38 | 57.6 | 532 | 2 | AP3498 | probable plasma membrane protein |
| 26 | 38 | 57.6 | 1091 | 2 | T34247 | probable membrane protein |
| 27 | 38 | 57.6 | 1107 | 2 | T34246 | probable membrane protein |
| 28 | 38 | 57.6 | 2100 | 2 | T03223 | probable membrane protein |
| 29 | 36.1 | 213 | 2 | C64041 | probable membrane protein | |

ALIGNMENTS

frnE protein VCA01
hypothetical prote
spu protein homol
probable 60S acidic
probable ABC trans
ABC transporter m
hypothetical prote
hypothetical prote
probable drug resi
conserved hypothet
choline monooxygen
SHT3 receptor subu
hypothetical prote
hypothetical prote
heat shock protein
acetyl-CoA synthet

| Query Match | Best Local Similarity | Score | DB | Length | Pred. No. | Matches | Conservative | Mismatches | Indels | Gaps | Db | Qy | Description |
|-------------|-----------------------|-------|----|--------|-----------|---------|--------------|------------|--------|------|----|-----|---------------|
| 69.2% | 66.7% | 44 | 2 | 367 | 2 | 3 | WMLIGYFDS 11 | 1 | 1 | 0 | 0 | 160 | WMLIGYFDS 168 |

RESULT 3

T29043 hypothetical protein B0228.2 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T29043
 R;Leimbach, D.
 Submitted to the EML Data Library, March 1995
 A;Description: The sequence of *C. elegans* cosmid B0228.
 A;Reference number: Z18224
 A;Accession: T29043
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1788 <LEI>
 A;Cross-references: UNIPROT:Q8IG61; UNIPARC:UPI00000851C9; EMBL:U23168; PIDN:AAC38806.1;
 A;Experimental source: strain Bristol N2
 C;Genetics:

A;Gene: CBSP:BU228.2
 A;Introns: 1456/2; 1482/3; 1516/2; 1551/3; 1595/3; 1646/1; 1671/1; 1716/2; 1749/3

Query Match 65.2%; Score 43; DB 2; Length 1788;
 Best Local Similarity 60.0%; Pred. No. 44;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPWELVGYFD 10
 Db 1722 GPWNMMGRFD 1731

RESULT 4

B69368 glutamine synthetase (glnA) homolog - *Archaeoglobus fulgidus*
 C;Species: *Archaeoglobus fulgidus*
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C;Accession: B69368
 R;Klein, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketcham, K.A.; Dodson, R.J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 365-370, 1997
 A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.; Smith, H.O.; Weese, C.R.; Venter, J.C.
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon *Archaeoglobus fulgidus*
 A;Reference number: A69250; MUID:9804943; PMID:3389475
 A;Accession: B69368
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-991 <KLE>
 A;Cross-references: UNIPROT:O09313; UNIPARC:UPI0000056F0D; GB:AE001039; GB:AE000782; NCBI Superfamily: glutamate-ammonia ligase
 C;Superfamily: glutamate-ammonia ligase

Query Match 62.1%; Score 41; DB 2; Length 491;
 Best Local Similarity 66.7%; Pred. No. 25;
 Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PHELVGYFD 10
 Db 482 PNEFMKYFD 490

RESULT 5

B84900 hypothetical protein At2g46220 [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C;Accession: B84900
 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Sten, M.; VanAken, S.E.; Mayam, L.; Tallon, L.; Eubiss, D.; Nieman, W.C.; White, O.; Esen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: B84900
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-550 <STO>
 A;Cross-references: UNIPROT:O82347; UNIPARC:UPI000017A71B; GB:AE002093; NID:93702327; P110
 C;Genetics:
 A;Gene: At2g46220
 A;Map position: 2

Query Match 62.1%; Score 41; DB 2; Length 550;
 Best Local Similarity 70.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPWELVGYFD 10
 Db 176 GPWETRGRFD 185

RESULT 6

S48729 glucokinase regulator - African clawed frog
 C;Species: *Xenopus laevis* (African clawed frog)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: S48729; S9339
 R;Veiga-da-Cunha, M.; Dethieux, M.; Watelet, N.; van Schaffingen, E.
 Bur, J. *Biochem.* 225, 43-51, 1994
 A;Title: Cloning and expression of a *Xenopus laevis* cDNA encoding a fructose-phosphate-in
 A;Reference number: S48729; MUID:95010134; PMID:7925465
 A;Accession: S48729
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-619 <VEI>
 A;Cross-references: UNIPROT:O91754; UNIPARC:UPI000012B2E2; EMBL:X80901; NID:9556677; PID: C;Superfamily: glucokinase regulator

Query Match 62.1%; Score 41; DB 1; Length 619;
 Best Local Similarity 63.6%; Pred. No. 32;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPWELVGYFD 11
 Db 17 GKWEGLAGYEE 27

RESULT 7

G70704 hypothetical protein Rv2326c - *Mycobacterium tuberculosis* (strain H37RV)
 C;Species: *Mycobacterium tuberculosis*
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C;Accession: G70704
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentle, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
 A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A;Reference number: A70500; MUID:98295987; PMID:9634230
 A;Accession: G70704
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-697 <COL>
 A;Cross-references: UNIPROT:P71186; UNIPARC:UPI000013BA74; GB:279702; GB:AL123456; NID:9
 A;Experimental source: strain H37RV
 C;Genetics:
 A;Gene: RV2326c
 Query Match 62.1%; Score 41; DB 2; Length 697;
 Best Local Similarity 66.7%; Pred. No. 36;

RESULT 8
Qy 2 PWELVGYFD 10
Db 196 PWVLVGYFN 204

ABC transporter ML0849 [imported] - *Mycobacterium leprae*
 C;Species: *Mycobacterium leprae*
 C;Accession: B87015
 C;Date: 20-Apr-2001 #sequence_revision 20-pr-2001 #text_change 09-Jul-2004
 R.; Cole, S.T.; Eiglemeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
 eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001

A;Authors: Rutten, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; sq
 A;Title: Massive gene decay in the leprosy bacillus.
 A;Reference number: A86909; MUID:2128732; PMID:11234002

A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: UNIPROT:09CCF9; UNIPARC:UPI00000C6D27; GB:AL450380; NID:g13092926; F
 C;Genetics:
 A;Gene: ML0848

Query Match 60.6%; Score 40; DB 2; Length 724;
 Best local Similarity 55.0%; Pred. No. 57;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PWELVGYF 9
Db 224 PWMLLGYF 231

RESULT 9
Qy T44905
Db

ABC-type transporter homolog [imported] - *Mycobacterium leprae*
 C;Species: *Mycobacterium leprae*
 C;Accession: T44905
 C;Date: 21-Jan-2000 #sequence_revision 21-jan-2000 #text_change 09-Jul-2004
 R.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Library, August 1997
 A;Reference number: Z22664
 A;Accession: T44905
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-726 <PAR>
 A;Cross-references: UNIPROT:032971; UNIPARC:UPI00000BED0E; EMBL:Z98741; PIDN:CAB11403.1
 A;Experimental source: cosmid B22
 C;Genetics:
 A;Note: MLCB22.38C

Query Match 60.6%; Score 40; DB 2; Length 726;
 Best Local Similarity 55.0%; Pred. No. 57;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PWELVGYF 9
Db 226 PWMLLGYF 233

RESULT 10
Qy D84824
Db

probable DNA-directed RNA polymerase II subunit [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C;Accession: D84824
 R.; Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Taiton, L.;
 euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Saizberg, S.M.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: PW4637
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-888 <STD>
 A;Cross-references: UNIPROT:004206; UNIPARC:UPI00000A517F; GB:AE002093; NID:g2088656; PI:
 C;Genetics:
 A;Gene: At2g40030
 A;Map position: 2

Query Match 60.6%; Score 40; DB 2; Length 888;
 Best Local Similarity 63.6%; Pred. No. 70;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPWELVGFDS 11
Db 544 GPKETIGFRDS 554

RESULT 11
Qy F84637
Db

probable plasma membrane proton ATPase [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Accession: F84637
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
 R.; Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Taiton, L.;
 euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Saizberg, S.M.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: PW4637
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-931 <STD>
 A;Cross-references: UNIPARC:UPI000016237B; GB:AE002093; NID:g4572678; PIDN:AAD23893.1; G:
 C;Genetics:
 A;Gene: At2g24520
 A;Map position: 2

Query Match 60.6%; Score 40; DB 2; Length 931;
 Best local Similarity 85.7%; Pred. No. 74;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPWELVG 7
Db 457 GPWQLVG 463

RESULT 12
Qy D71051
Db

hypothetical protein PH1107 - *Prochlorococcus horikoshii*
 C;Species: *Prochlorococcus horikoshii*
 C;Accession: D71051
 R.; Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine,
 M.; Ohfuku, Y.; Funakoshi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kuhida, N.; Oguchi,
 DNA Res. 5, 55-76, 1998
 A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A;Accession: D71051
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-299 <KAN>
 A;Cross-references: UNIPROT:058334; UNIPARC:UPI0000062FB7; GB:AP000005; NID:g3236132; PIDN:PH1107
 A;Experimental source: strain OR3
 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C;Genetics:
 A;Gene: PH1107
 C;Superfamily: glycosidase, PH1107 type

Query Match 59.1%; Score 39; DB 2; Length 299;

Best Local Similarity 60.0%; Pred. No. 33; Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PWELVGYFDS 11
Db 247 PWELSGHVDN 256

RESULT 13

T3303 hypothetical protein R01B10.4 - *Ceenorhabditis elegans*
C;Species: *Ceenorhabditis elegans*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

R;Langston, Y.; Beck, C.
Submitted to the EMBL Data Library, May 1998

A;Description: The sequence of *C. elegans* cosmid R01B10.
A;Reference number: 221318

A;Accession: T3303
A;Status: preliminary; translated from GB/EMBL/DDJB

A;Residues: DNA
A;Cross-references: UNIPROT:O61975; UNIPARC:UPI0000080228; EMBL:AF068718; PMID: AAC17768.

A;Experimental source: strain Bristol N2; clone R01B10
C;Genetic: A;Gene: CESP; R01B10.4

A;Map position: 5; Map: 25/2; 73/2; 211/3; 241/2

A;Introns: 25/2; 73/2; 211/3; 241/2
Query Match 59.1%; Score 39; DB 2; Length 320;
Best Local Similarity 55.6%; Pred. No. 36; Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WELVGFPDS 11
Db 65 WDTIGHRDS 73

RESULT 14

S17907 glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Yeast (*Schwanomyces occidentalis* var. *occidentalis*)
C;Species: *Schwanomyces occidentalis* var. *occidentalis*
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Oct-2004

R;de Zoyza, P.A.; Connerton, I.F.; Watson, D.C.; Johnston, J.R.
Curr. Genet. 20, 219-224, 1991

A;Title: Cloning, sequencing and expression of the *Schwanomyces occidentalis* NADP-dep
A;Reference number: S17907; MUID:92035089; PMID:1934128

A;Accession: S17907
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-159 <DBZ>
A;Cross-references: UNIPROT:P23507; UNIPARC:UPI0001292F9
C;Superfamily: glutamate dehydrogenase
C;Keywords: NADP; oxidoreductase

Query Match 59.1%; Score 39; DB 2; Length 459;
Best Local Similarity 66.7%; Pred. No. 52; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PWELVGYFD 10
Db 308 PWAKVGHFD 316

RESULT 15

S28476 rfbL protein VCO249 [similarity] - *Vibrio cholerae* (strain N16961 serogroup O1)

C;Species: *Vibrio cholerae*
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C;Accession: S28476; H82346

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OM protein - protein search, using sw model
Run on: December 4, 2005, 04:31:36 ; Search time 100.375 Seconds
Post-processing: Minimum Match 0% ; Maximum Match 100% ; Listing first 45 summaries

Title: US-10-632-706-128
Perfect score: 66
Sequence: 1 GPWELVGYFDS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% ; Maximum Match 100% ; Listing first 45 summaries

Database : UniProt_05_80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|----------------|-----------------|
| 1 | 45 | 68.2 | 279 | 08758_STRCO |
| 2 | 45 | 68.2 | 290 | 082M5B_STRAW |
| 3 | 45 | 68.2 | 748 | 05NQ32_ZYMMO |
| 4 | 44 | 66.7 | 367 | 1_WECA_SALT |
| 5 | 44 | 66.7 | 367 | 1_WBKA_SALTY |
| 6 | 44 | 66.7 | 367 | 0SPKKL_SALPA |
| 7 | 44 | 66.7 | 449 | 063N53_BURRS |
| 8 | 43 | 65.2 | 231 | 2_04K719_PSEPS |
| 9 | 43 | 65.2 | 1201 | 2_07UYR6_RHOBA |
| 10 | 43 | 65.2 | 1533 | 1_YPT7_CHEEL |
| 11 | 43 | 65.2 | 7548 | 2_Q5WRUJ_CAEEL |
| 12 | 43 | 63.6 | 272 | 2_Q74SB8_GEOSEL |
| 13 | 42 | 63.6 | 381 | 2_06KL15_ORYSA |
| 14 | 42 | 63.6 | 454 | 2_08TUV9_METAC |
| 15 | 42 | 63.6 | 578 | 2_08D959_VIBRY |
| 16 | 42 | 63.6 | 578 | 2_07MLB3_VIBRY |
| 17 | 42 | 63.6 | 1275 | 2_08Q061_METMA |
| 18 | 41 | 62.1 | 211 | 2_08KH7_PSEHK7 |
| 19 | 41 | 62.1 | 241 | 2_08Z347_ARATH |
| 20 | 41 | 62.1 | 273 | 2_07UND8_RHOBA |
| 21 | 41 | 62.1 | 318 | 2_Q4KEFO_PSEPS |
| 22 | 41 | 62.1 | 491 | 1_GINA_ARCFU |
| 23 | 41 | 62.1 | 518 | 2_Q5LH40_BACEN |
| 24 | 41 | 62.1 | 518 | 2_064XZ7_BACER |
| 25 | 41 | 62.1 | 613 | 2_Q6BTU3_DEBRA |
| 26 | 41 | 62.1 | 619 | 1_GCKR_XENLA |
| 27 | 41 | 619 | 619 | 1_O5SKA5_THETB |
| 28 | 41 | 619 | 619 | 2_O6PAX3_XENIA |
| 29 | 41 | 62.1 | 697 | 1_Y2326_WCTU |
| 30 | 41 | 62.1 | 697 | 1_Y2353_MYCBO |
| 31 | 41 | 62.1 | 697 | 1_Y2353_MYCBO |
| 31 | 41 | 63.50 | 2_Q9V5J7_DROMA | |

32 41 62.1 1370 2 Q7KQX6_DROMA
33 41 62.1 2581 2 Q7TT75_91TRU
34 40 122 2 Q8E577_SIBON
35 40 60.6 146 2 Q8UT74_RADEN
36 40 60.6 206 2 Q6QP97_RADEN
37 40 207 2 Q6QD93_RADEN
38 40 60.6 208 2 Q6QG99_RADEN
39 40 60.6 210 2 Q6H1B6_RADEN
40 40 60.6 210 2 Q8BEU6_AB04
41 40 60.6 282 2 Q7N944_PROLL
42 40 60.6 304 2 Q877Q4_PBSM
43 40 60.6 319 2 Q4ZPN4_PBSY
44 40 60.6 323 2 Q4INB2_GCBZE
45 40 60.6 392 2 Q8LRJ7_PETHY

ALIGNMENTS

RESULT 1
ID 08758_STRCO PRELIMINARY; PRT; 279 AA.
AC 08758;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Putative transmembrane sugar transport protein.
GN OrderidicbunName=SC06603; ORFNames=SC8A6_24;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN_A3(2) / ML45;
MEDLINE:219841; PubMed:12000953; DOI:10.1038/417141a;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman S., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howard S.,
Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
Rabbowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wetzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
Hopwood D.A.;
RA "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)." Nature 417:41-47 (2002).
RL Nature 417:41-47 (2002).
CC -!- FUNCTION: Part of a binding-protein-dependent transport system.
CC Probably responsible for the translocation of the substrate across
the membrane (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the binding-protein-dependent transport
system permease family.
DR EMBL: AL939128; CDA19796.1; - ; Genomic_DNA.
DR PIR: T35791; T35791.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0053521; F:sugar porter activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR00515; BPD:transp.
DR InterPro; IPR00515; BPD:transp.
DR PROSITE; PS50928; ABC_TML-1.
DR PROSITE; PS50928; ABC_TML-1.
KW Complete proteome; sugar transport; Transmembrane; Transport.
SQ Sequence 279 AA, 0335 MW, 886063385893BFA CRC64;

Query Match Score 68.2%; DB 2; Length 279;
Best Local Similarity 77.8%; Pred. No. 25; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Q9v5j7 drosophila

| Db | 160 WMLGYFDS 168 |
|---|------------------|
| RESULT 2 | |
| Q82M58 STRAW PRELIMINARY; | PRT; 290 AA. |
| ID Q82M58 STRAW PRELIMINARY; | PRT; 290 AA. |
| AC 082M58; | PRT; 290 AA. |
| DT 01-JUN-2003 (TREMBLrel. 24, Created) | PRT; 290 AA. |
| DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update) | PRT; 290 AA. |
| DT 01-JUN-2003 (TREMBLrel. 26, Last annotation update) | PRT; 290 AA. |
| DR Putative sugar ABC transporter permease protein. | PRT; 290 AA. |
| GN OrderedLocusNames=SV1802; | PRT; 290 AA. |
| OS Streptomyces avermitilis. | PRT; 290 AA. |
| OC Bacteria; Actinobacteria; Actinomycetales; | PRT; 290 AA. |
| OC Streptomycineae; Streptomycetaceae; Streptomyces. | PRT; 290 AA. |
| OX NCBI_TaxID=542; | PRT; 290 AA. |
| RN [1] | PRT; 290 AA. |
| RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]. | PRT; 290 AA. |
| RC STRAIN=ATCC 31821 / ZM4 / C74; | PRT; 290 AA. |
| RX PubMed=15592456; DOI=10.1038/nbt1045; | PRT; 290 AA. |
| RA Seo J.-S., Chong H., Park H.S., Yoon K.-O., Jung C., Kim J.J., | PRT; 290 AA. |
| RA Hong J.H., Kim J.-H., Kil J.-I., Park C.G.J., Oh H.-M., | PRT; 290 AA. |
| RA Lee J.-S., Jin S.-J., Um H.-W., Lee H.-J., Oh S.-J., Kim J.Y., | PRT; 290 AA. |
| RA Kang H.J., Lee S.Y., Lee K.J., Kang H.S., | PRT; 290 AA. |
| RA "The genome sequence of the ethanologenic bacterium <i>Zymomonas mobilis</i> ZM4." | PRT; 290 AA. |
| RT Nat. Biotechnol. 23:63-68 (2005). | PRT; 290 AA. |
| RL EMBL; AE008622; AAW89173.1; -; Genomic_DNA. | PRT; 290 AA. |
| DR GO; GO:000175; F3'-5'-exoribonuclease activity; IEA. | PRT; 290 AA. |
| DR GO; GO:004654; F-polyribonucleotide nucleotidyltransferase a...; IEA. | PRT; 290 AA. |
| DR GO; GO:003733; F-RNA binding; IEA. | PRT; 290 AA. |
| DR GO; GO:001670; F-RNA processing; IEA. | PRT; 290 AA. |
| DR InterPro; IPR01247; 3_ExoRNase. | PRT; 290 AA. |
| DR InterPro; IPR04087; KH. | PRT; 290 AA. |
| DR InterPro; IPR004088; KH type_1. | PRT; 290 AA. |
| DR InterPro; IPR01262; PHFase. | PRT; 290 AA. |
| DR InterPro; IPR03039; SL. | PRT; 290 AA. |
| DR Pfam; PF00013; KH_1; 1. | PRT; 290 AA. |
| DR Pfam; PF03726; PHFase_1. | PRT; 290 AA. |
| DR Pfam; PF01138; RNase_PH_2. | PRT; 290 AA. |
| DR Pfam; PF003725; RNase_PH_C_2. | PRT; 290 AA. |
| DR PIRSF; PIRSP005499; PHFase; 1. | PRT; 290 AA. |
| DR SMART; SM00322; KH; 1. | PRT; 290 AA. |
| DR SMART; SM00316; SL; 1. | PRT; 290 AA. |
| DR PROSITE; PS50084; KH_TYPE_1; 1. | PRT; 290 AA. |
| DR PROSITE; PS50126; SL; 1. | PRT; 290 AA. |
| KW Complete proteome; Nucleotidyltransferase; Transferase. | PRT; 290 AA. |
| SQ SEQUENCE 748 AA; 81949 MN; BB8C43821F885F6DB CRC64; | PRT; 290 AA. |
| Query Match 68.2%; Score 45; DB 2; Length 748; | PRT; 290 AA. |
| Best Local Similarity 80.0%; Pred. No. 67; | PRT; 290 AA. |
| Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0; | PRT; 290 AA. |
| QY 2 PWELGYFDS 11 | PRT; 290 AA. |
| DB 230 PWELVSYDD 239 | PRT; 290 AA. |
| RESULT 3 | |
| WECA_SALTI WECA_SALTI STANDARD; | PRT; 367 AA. |
| AC Q8Z56; | PRT; 367 AA. |
| DT 28-FEB-2003 (Rel. 41, Created) | PRT; 367 AA. |
| DT 28-FEB-2003 (Rel. 41, Last sequence update) | PRT; 367 AA. |
| DT 10-MAY-2005 (Rel. 47, Last annotation update) | PRT; 367 AA. |
| DB Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate | PRT; 367 AA. |
| DB transferase (EC 2.7.8.-) (Ump-GlcNAc:undecaprenyl-phosphate GlcNAc-1- | PRT; 367 AA. |
| DS phosphate transferase). | PRT; 367 AA. |
| Name=weca; Synonyms=rfe; OrderedLocusNames=STY3637, t3379, | PRT; 367 AA. |
| OS <i>Salmonella typhimurium</i> . | PRT; 367 AA. |
| OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobactriales; | PRT; 367 AA. |
| OC Enterobacteriaceae; <i>Salmonella</i> . | PRT; 367 AA. |
| OC NCBI_TaxID=601; | PRT; 367 AA. |
| RN [1] | PRT; 367 AA. |
| RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]. | PRT; 367 AA. |
| RC STRAIN=C74; | PRT; 367 AA. |
| RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607; | PRT; 367 AA. |
| RA Parkhill J., Dougan G., James K.D., Thomson N.R., Richard D., Main J., | PRT; 367 AA. |
| RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahnia M., | PRT; 367 AA. |
| RA Baker S., Basham D., Brook K., Chillingworth T., Connerton P., | PRT; 367 AA. |
| RA Cronin A., Davies R.M., Dowd L., White N., Farrar J., | PRT; 367 AA. |
| RA Fellwell T., Hamlin N., Haque A., Hiley T.T., Holroyd S., Jagels K., | PRT; 367 AA. |
| RA Krogh A., Larrea T.S., Leather S., Moile S., O'Gara P., Parry C., | PRT; 367 AA. |
| RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., | PRT; 367 AA. |
| OY 3 WELVGFD 11 | PRT; 367 AA. |
| QY 3 WELVGFD 11 | PRT; 367 AA. |
| DB 171 WMLGYFDS 179 | PRT; 367 AA. |
| RESULT 4 | |
| WECA_SALTI WECA_SALTI STANDARD; | PRT; 367 AA. |
| AC Q8Z56; | PRT; 367 AA. |
| DT 28-FEB-2003 (Rel. 41, Created) | PRT; 367 AA. |
| DT 28-FEB-2003 (Rel. 41, Last sequence update) | PRT; 367 AA. |
| DT 10-MAY-2005 (Rel. 47, Last annotation update) | PRT; 367 AA. |
| DB Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate | PRT; 367 AA. |
| DS transferase (EC 2.7.8.-) (Ump-GlcNAc:undecaprenyl-phosphate GlcNAc-1- | PRT; 367 AA. |
| DS phosphate transferase). | PRT; 367 AA. |
| GN Name=weca; Synonyms=rfe; OrderedLocusNames=STY3637, t3379, | PRT; 367 AA. |
| OS <i>Salmonella typhimurium</i> . | PRT; 367 AA. |
| OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobactriales; | PRT; 367 AA. |
| OC Enterobacteriaceae; <i>Salmonella</i> . | PRT; 367 AA. |
| OC NCBI_TaxID=601; | PRT; 367 AA. |
| RN [1] | PRT; 367 AA. |
| RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]. | PRT; 367 AA. |
| RC STRAIN=C74; | PRT; 367 AA. |
| RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607; | PRT; 367 AA. |
| RA Parkhill J., Dougan G., James K.D., Thomson N.R., Richard D., Main J., | PRT; 367 AA. |
| RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahnia M., | PRT; 367 AA. |
| RA Baker S., Basham D., Brook K., Chillingworth T., Connerton P., | PRT; 367 AA. |
| RA Cronin A., Davies R.M., Dowd L., White N., Farrar J., | PRT; 367 AA. |
| RA Fellwell T., Hamlin N., Haque A., Hiley T.T., Holroyd S., Jagels K., | PRT; 367 AA. |
| RA Krogh A., Larrea T.S., Leather S., Moile S., O'Gara P., Parry C., | PRT; 367 AA. |
| RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., | PRT; 367 AA. |
| OY 3 WELVGFD 11 | PRT; 367 AA. |
| QY 3 WELVGFD 11 | PRT; 367 AA. |
| DB 171 WMLGYFDS 179 | PRT; 367 AA. |

RA Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi CT18.", *Nature* 413:848-852 (2001). [2]

RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RP STRAIN=Ty2 / ATCC 70931; RX MEDLINE=22531367; PubMed=12644504; RX DOI=10.1128/JB.185.7.2330-2337.2003; RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwarz D.C., Blattner F.R.; *Burkholderia* *enterica* serovar Typhi strains Ty2 and Ctr18 ". J. Bacteriol. 185:2330-2337(2003).

CC -!- FUNCTION: Catalyzes the synthesis of Und-PP-GlcNAc (lipid I), the first lipid-linked intermediate involved in ECA synthesis. This lipid is also an acceptor for the addition of subsequent sugars to complete the biosynthesis of *Salmonella enterica* serovar Typhi strains Ty2 and Ctr18 ".

CC -!- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + undecaprenyl phosphate = UMP + N-acetyl-alpha-D-glucosaminylidiphospho-undecaprenol.

CC -!- CORACTOR: Magnesium and manganese (BY similarity).

CC -!- PATHWAY: Synthesis of enterobacterial common antigen (ECA).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane (BY similarity).

CC -!- SIMILARITY: Belongs to the glycosyltransferase 4 family. WecA subfamily.

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CC EMBL; AU627279; CA09398; 1; -; Genomic DNA.

DR InterPro; IPR012750; ECA_WecA_rel.

DR Pfam; PF00953; Glyco_transf_4; 1.

DR TIGRFAMS; TIGR02380; ECA_wecA; 1.

DR Complete proteome; Glycosyltransferase; Inner membrane; Membrane; Lipopolysaccharide biosynthesis; Magnesium; Manganese; Membrane; Transferease; Transmembrane.

FT TRANSMEM 3 Potential.

FT TRANSMEM 45 Potential.

FT TRANSMEM 69 Potential.

FT TRANSMEM 106 Potential.

FT TRANSMEM 129 Potential.

FT TRANSMEM 158 Potential.

FT TRANSMEM 187 Potential.

FT TRANSMEM 213 Potential.

FT TRANSMEM 242 Potential.

FT TRANSMEM 294 Potential.

FT TRANSMEM 310 Potential.

FT SEQUENCE 367 AA; 41086 MW; 28DAA31CB1AB2D930 CRC64;

Query Match 66.7%; Score 44; DB 1; Length 367; Best Local Similarity 69.2%; Fred. No. 49; Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1; Result 5

QY 1 GPWELV---GYF 9 ID WECA_SALTY STANDARD; PRT; 367 AA.

Db 127 GPWELVLGPGYF 139

DE Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase (EC 2.7.8.-) (Und-PP-GlcNAc:undecaprenyl-phosphate GlcNAc-1-phosphate transferase; OrderedLocusNames=STM918; ORFNames=STM0172; Name=wech; Synonyms=arfe; Order=LocusNames=STM918; ORFNames=STM0172; OS *Salmonella typhimurium*; Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; *Salmonella*. NCBI_TaxID=602; OX NCBI_TaxID=602;

RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]. [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=LM2 / SGSC1412 / ATCC 700720; RX MEDLINE=2154948; PubMed=1677609; DOI=10.1038/35101614; RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguen S., Scott K., Holmes A., Grimaldi N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; RT Complete genome sequence of *Salmonella enterica* serovar Typhimurium LT2.; RX Nature 413:852-856(2001). RN 413:852-856(2001). [2]

RC NUCLEOTIDE SEQUENCE OF 111-367.

RC STRAIN=LM2; RX MEDLINE=98409259; PubMed=9738879; DOI=10.1007/s004380050787; RA Moulim C., Cano D.A., Casadesus J.; CC "The sfix, rie and metn genes of *Salmonella typhimurium* and their RT involvement in the HisC(+) pleiotropic response."; CC Mol. Gen. Genet. 255:46-53(1998).

CC -!- FUNCTION: Catalyzes the synthesis of Und-PP-GlcNAc (lipid I), the first lipid-linked intermediate involved in ECA synthesis. This lipid is also an acceptor for the addition of subsequent sugars to complete the biosynthesis of O-antigen (BY similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane (BY similarity).

CC -!- CORACTOR: Magnesium and manganese (BY similarity).

CC -!- PATHWAY: Synthesis of enterobacterial common antigen (ECA).

CC -!- ENZYME REGULATION: Inhibited by tunicamycin.

CC -!- SIMILARITY: Belongs to the glycosyltransferase 4 family. WecA subfamily.

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CC EMBL; AU23324; AAFF33469; 1; -; Genomic DNA.

DR EMBL; AR00883; AAL2767; 1; -; Genomic DNA.

DR EMBL; AU002215; CA05287; 1; -; Genomic DNA.

DR StvGene; SG????; rfe; DR InterPro; IPR012750; ECA_WecA_rel.

DR InterPro; IPR000715; Glyco_transf_4; 1.

DR TIGRFAMS; TIGR02380; ECA_wecA; 1.

DR Complete proteome; Glycosyltransferase; Inner membrane; Membrane; Lipopolysaccharide biosynthesis; Magnesium; Manganese; Membrane; Transferease; Transmembrane.

FT TRANSMEM 3 Potential.

FT TRANSMEM 45 Potential.

FT TRANSMEM 69 Potential.

FT TRANSMEM 106 Potential.

FT TRANSMEM 129 Potential.

FT TRANSMEM 158 Potential.

FT TRANSMEM 187 Potential.

FT TRANSMEM 213 Potential.

FT TRANSMEM 242 Potential.

FT TRANSMEM 294 Potential.

FT TRANSMEM 318 Potential.

FT CONFLICT 118 120 HLG --> ALU (in Ref. 2).

PT CONFLICT 128 138 PWELVIGPGFY -- ALGYSAMPWHL (in Ref. 2).
 PT CONFLICT 146 148 WAA -- LNG (in Ref. 2).
 PT CONFLICT 220 220 S -> C (in Ref. 2).
 SQ SEQUENCE 367 AA; 41087 MW; 1ED31CBAE2D938 CRC64;
 RN RP
 RESULT 6 Best Local Similarity 69.2%; Score 44; DB 1; Length 367;
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 QY 1 GPWELV---GYF 9
 AC 05PKCL SALPA
 ID 05PKCL_SALPA PRELIMINARY; PRT; 367 AA.
 DT 01-FEB-2005 (TREMBLrel. 29, Created)
 DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
 DE Putative undecaprenyl-phosphate alpha-N-
 DE acetylglucosaminyltransferase.
 DE Name=fe; OrderdLocusNames=SRA3758;
 OS Salmonella paratyphi-a.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TAXID=5488;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 9150;
 RX PubMed=15331882; DOI=10.1038/ng1470;
 RA McClelland M., Sanderson K.E., Clinton S.W., Latreille P.,
 RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McLellan M.,
 RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
 RA Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
 RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,
 RA Spiehler J., Wilson R.K.; Delehaunty K., Fronick C., Magrini V., Khan M., Warren W., Florea L.,
 RA Spieth J., Wilson R.K.; "Comparison of genome degradation in Paratyphi A and Typhi, human-
 RT restricted serovars of *Salmonella enterica* that cause typhoid.";
 RT Nat. Genet. 36(1268-1274 (2004)).
 DR EMBL; CP000026; AAVY9540_1; -; Genomic_DNA.
 DR GO; GO:0019866; C:inner membrane; IEA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016757; F:transferase activity; transferring glycosyl. . .; IEA.
 DR GO; GO:0006629; P:lipid metabolism; IEA.
 DR GO; GO:0019103; P:lipopolysaccharide biosynthesis; IEA.
 DR InterPro; IPR000715; Glyco_trans_4.
 DR InterPro; IPR001865; Ribosomal_S2.
 DR Pfam; PF00953; Glycos_transf_4_1.
 DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
 DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
 KW complete proteome; GlycosylTransferase; Transferase.
 SEQUENCE 367 AA; 41086 MW; 1ED31CBAE2D938 CRC64;
 Query Match 66.7%; Score 44; DB 2; Length 367;
 Best Local Similarity 69.2%; Pred. No. 49;
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 QY 1 GPWELV---GYF 9
 AC 063N53_BURPS
 ID 063N53_BURPS PRELIMINARY; PRT; 449 AA.
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=BPS0443;
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=996243;
 RX PubMed=15377794; DOI=10.1073/pnas.0403302101;
 RA Holden M.T.G., Tibball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
 RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
 RA Bentley S.D., Sebaiha M., Thomson N.R., Bason N., Beacham I.R.,
 RA Brooks K., Brown K.A., Brown N.P., Chilis G.L., Chevrevach I.,
 RA Chillingworth T., Cronin A., Crossett B., Davis P., Deshazer D.,
 RA Feltwell T., Fraser A., Hanse Z., Hauser H., Holroyd S., Jagels K.,
 RA Keith K.E., Maddison M., Sanders M., Simmonds M.,
 RA Songavilai S., Stevens K., Tumapa S., Vesparatchavest M.,
 RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.,
 RA Feltwell T., Fraser A., Hanse Z., Hauser H., Holroyd S., Jagels K.,
 RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
 RA "Genomic plasticity of the causative agent of melioidosis,"
 RT Burkholderia pseudomallei."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).
 DR EMBL; BX71966; CAR37899_1; -; Genomic_DNA.
 KW Complete proteome; Hypothetical protein.
 SQ Sequence 449 AA; 4931 MW; F1618BY466D15240 CRC64;
 Query Match 66.7%; Score 44; DB 2; Length 449;
 Best Local Similarity 75.0%; Pred. No. 60;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GPWELVGY 8
 AC 04K719_PSEF5
 ID 04K719_PSEF5 PRELIMINARY; PRT; 231 AA.
 AC 04K719_PSEF5
 DT 13-SBP-2005 (TREMBLrel. 31, Created)
 DT 13-SBP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SBP-2005 (TREMBLrel. 31, Last annotation update)
 DE Phosphoserine phosphatase, putative.
 DR ORFnames=PFL_4883;
 OS Pseudomonas Fluorescens (strain PF-5).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TAXID=220664;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PF-5;
 RX PubMed=15980861; DOI=10.1038/nbt1110;
 RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
 RA Mavrodili D., Debey R.T., Sesshadri R., Ren Q., Madupu R., Dodson R.J.,
 RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosevitz M.,
 RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
 RA Khouri H.M., Pierson E., Pierson L., III, Thomashow L., Loper J.,
 RT "Complete genome sequence of the plant commensal Pseudomonas
 RT fluorescens PF-5.";
 RT Nat. Biotechnol. 23:873-878 (2005).
 DR EMBL; CP000076; AAV94113_1; -; Genomic_DNA.
 SQ Sequence 231 AA; 25717 MW; A4DBA84C59107CF2 CRC64;
 Query Match 65.2%; Score 43; DB 2; length 231;
 Best Local Similarity 80.0%; Pred. No. 46;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PWBLVGFDS 11
 AC 07UYR6_RHOBA
 ID 07UYR6_RHOBA
 DE OrderedLocusNames=BPS0443;

ID OTUVR6_RHOBIA PRELIMINARY; PRT; 1201 AA.
 AC Q7UVR6;
 DT 01-OCT-2003 (TREMBIrel. 25, Created)
 DR Ensemble; EMBL; B0228.4; Caenorhabditis elegans.
 DT 01-MAR-2004 (TREMBIrel. 26, Last annotation update)
 DR WormBase; WBGene00015051; B0228.4.
 DR Hypothetical protein.
 DR OrderedLocusName=RHOB26;
 DR Rhodopirellula baltica.
 OC Bacteria; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 OC NCBI_TaxID=117;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 RA Schleiner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 strain 1.", Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
 RL GO; GO:000037; F:home binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR012282; Cytochrome_c_R.
 DR InterPro; IPR011444; DUF1549.
 DR InterPro; IPR011429; PSC3.
 DR Pfam; PF0635; PSCY1; 1.
 DR Pfam; PF0583; PSCY2; 1.
 DR Pfam; PF0587; PSD1; 1.
 KW Complete Proteome; Hypothetical protein.
 SEQUENCE 1201 AA; 134482 MW; 7286B27735130D01 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 1201;
 Best Local Similarity 72.7%; Pred. No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GPWELVGFDS 11
 OX 1029 GLWEAVGVTDS 1039

RESULT 10

YP74_CAEEL STANDARD; PRT; 1633 AA.
 AC 00921; Q00908; [1]
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Hypothetical protein B0228.4 in chromosome II.
 GN GNNames=B0228.4/B0228.2;
 OS Caenorhabditis elegans.
 OC Rhabditida; Peiloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;

RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology.", Science 282:2012-2018 (1998).
 RL EMBL; U23168; AAU97832.1; Genomic DNA.
 DR Ensemble; B0228.4; Caenorhabditis elegans.
 DR WormBase; WBGene00015051; B0228.4.
 DR WormPep; B0228.4C; CE7470.
 DR InterPro; IPR010734; Copine.
 DR InterPro; IPR020205; VWF_A.
 DR Pfam; PF07002; Copine; 1.
 DR SMART; SM00327; VWA; 1.
 KW Complete proteome; Hypothetical protein.
 SEQUENCE 7548 AA; 840584 MW; 8BEC3CC03D12C1C8 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 7548;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPWELVGFDS 10
 OX 7482 GPWNMGFDFD 7491

RESULT 12

O748SB_GROS1 PRELIMINARY; PRT; 272 AA.
 AC Q748SB;
 DT 05-JUL-2004 (TREMBIrel. 27, Created)
 DT 05-JUL-2004 (TREMBIrel. 27, Last annotation update)
 DR Glutamate racemase (EC 5.1.1.3).
 GN Name=mur1; OrderedLocusName=GSU2923;

CC -----
 DR EMBL; U23168; AAC38806.2; -; Genomic DNA.
 DR Ensemble; B0228.4; Caenorhabditis elegans.
 DR WormBase; WBGene00015051; B0228.4.
 DR InterPro; IPR010734; Copine.
 DR Pfam; PF07002; Copine; 1.
 DR PRINTS; PR00053; VWF_DOMAIN.
 KW Complete proteome; Hypothetical protein.
 FT COMBIAS 155 165 Cys-rich.
 FT COMBIAS 316 338 Lys-rich.
 FT COMBIAS 892 1019 Glu-rich.

SQ SEQUENCE 1633 AA; 183328 MW; 3B4EB46800B7A44D CRC64;

Query Match 65.2%; Score 43; DB 1; Length 1633;
 Best Local Similarity 60.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPWELVGFDS 10
 OX 1567 GPWNMGFDFD 1576

RESULT 11

QSWRUI_CAEEL STANDARD; PRT; 7548 AA.
 ID QSWRUI CAEEL PRELIMINARY; PRT; 7548 AA.

DR QSWRUI; CAEEL PRELIMINARY; PRT; 7548 AA.
 AC 00921; Q00908; [1]
 DT 25-OCT-2004 (TREMBIrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBIrel. 28, Last annotation update)
 DE Hypothetical Protein B0228.4.
 GN ORFnames=B0228.4;
 OS Caenorhabditis elegans.
 OC Bokaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peiloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;

RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology.", Science 282:2012-2018 (1998).
 RL EMBL; U23168; AAU97832.1; Genomic DNA.
 DR Ensemble; B0228.4; Caenorhabditis elegans.
 DR WormBase; WBGene00015051; B0228.4.
 DR WormPep; B0228.4C; CE7470.
 DR InterPro; IPR010734; Copine.
 DR InterPro; IPR020205; VWF_A.
 DR Pfam; PF07002; Copine; 1.
 DR SMART; SM00327; VWA; 1.
 KW Complete proteome; Hypothetical protein.
 SEQUENCE 7548 AA; 840584 MW; 8BEC3CC03D12C1C8 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 7548;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPWELVGFDS 10
 OX 7482 GPWNMGFDFD 7491

RESULT 10

YP74_CAEEL STANDARD; PRT; 1633 AA.
 AC 00921; Q00908; [1]
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Hypothetical protein B0228.4 in chromosome II.
 GN GNNames=B0228.4/B0228.2;
 OS Caenorhabditis elegans.
 OC Rhabditida; Peiloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;

RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology.", Science 282:2012-2018 (1998).
 RL EMBL; U23168; AAU97832.1; Genomic DNA.
 DR Ensemble; B0228.4; Caenorhabditis elegans.
 DR WormBase; WBGene00015051; B0228.4.
 DR WormPep; B0228.4C; CE7470.
 DR InterPro; IPR010734; Copine.
 DR InterPro; IPR020205; VWF_A.
 DR Pfam; PF07002; Copine; 1.
 DR SMART; SM00327; VWA; 1.
 KW Complete proteome; Hypothetical protein.
 SEQUENCE 7548 AA; 840584 MW; 8BEC3CC03D12C1C8 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 7548;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPWELVGFDS 10
 OX 7482 GPWNMGFDFD 7491

RESULT 12

O748SB_GROS1 PRELIMINARY; PRT; 272 AA.
 AC Q748SB;
 DT 05-JUL-2004 (TREMBIrel. 27, Created)
 DT 05-JUL-2004 (TREMBIrel. 27, Last annotation update)
 DR Glutamate racemase (EC 5.1.1.3).
 GN Name=mur1; OrderedLocusName=GSU2923;

CC -----
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 the European Bioinformatics Institute. There are no restrictions on its
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 removed.

DR EMBL; AE016906; AAO11091.1; -; Genomic_DNA.
DR HSSP; P02542; IQU7.
DR GO; GO:0019866; C:inner membrane; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:007165; P:signal transduction; IEA.
DR InterPro; IPR004089; Chntaxis_transd.
DR InterPro; IPR003660; His_kin_HAMP.
DR Pfam; PF00677; HAMP; 1.
DR PFam; PF00015; MCPsignal; 1.
DR SMART; SMO0304; HAMP; 1.
DR SMART; SMO0283; MA; 1.
DR PROSITE; PS5011; CHEMOTAXIS_TRANSUDC_2; 1.
DR PROSITE; PS50885; HAMP; 1.
KW Complete Proteome.
SQ SEQUENCE 578 AA; 63178 MW; 55004ADC7356DA18 CRC64;

Query Match 63.6%; Score 42; DB 2; Length 578;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WELVGYFD 10
Db 204 WELIGYID 211

Search completed: December 4, 2005, 04:52:22
Job time : 102.375 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: December 4, 2005, 03:59:51 ; Search time 23.6042 Seconds
Sequence: 1 GPWELVGYFDS 11

Title: US-10-632-706-128
Perfect score: 66
Sequence: 1 GPWELVGYFDS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext. 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:
Post-processing: Minimum Match 0%
Maximum DB seq length: 0
Minimum DB seq length: 2000000000

572060

ALIGNMENTS

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 41 | 62.1 | 12 | 1 | US-08-264-093-17 Sequence 17, Appli |
| 2 | 41 | 62.1 | 121 | 1 | US-08-264-093-3 Sequence 3, Appli |
| 3 | 39 | 59.1 | 274 | 2 | US-09-902-540-14253 Sequence 14253, A |
| 4 | 38 | 57.6 | 332 | 2 | US-09-902-540-1763-5 Sequence 5, Appli |
| 5 | 38 | 57.6 | 332 | 2 | US-09-941-367B-5 Sequence 5, Appli |
| 6 | 38 | 57.6 | 493 | 2 | US-09-949-016-10836 Sequence 10836, A |
| 7 | 38 | 57.6 | 1207 | 2 | US-09-976-594-4 Sequence 4, Appli |
| 8 | 37 | 56.1 | 427 | 2 | US-09-902-540-15261 Sequence 15261, A |
| 9 | 37 | 56.1 | 484 | 2 | US-09-943-681A-6615 Sequence 6615, Ap |
| 10 | 36 | 54.5 | 132 | 2 | US-09-311-021-162 Sequence 162, App |
| 11 | 36 | 54.5 | 140 | 2 | US-09-698-341-29 Sequence 29, Appli |
| 12 | 36 | 54.5 | 174 | 2 | US-09-902-540-13916 Sequence 13916, A |
| 13 | 36 | 54.5 | 194 | 1 | US-08-260-202A-15 Sequence 15, Appli |
| 14 | 36 | 54.5 | 194 | 1 | US-08-260-202A-24 Sequence 24, Appli |
| 15 | 36 | 54.5 | 194 | 1 | US-08-017-114-15 Sequence 17, Appli |
| 16 | 36 | 54.5 | 194 | 1 | US-08-017-114-17 Sequence 17, Appli |
| 17 | 36 | 54.5 | 194 | 2 | US-08-505-307-15 Sequence 15, Appli |
| 18 | 36 | 54.5 | 194 | 2 | US-08-505-307-17 Sequence 17, Appli |
| 19 | 36 | 54.5 | 194 | 2 | US-09-609-151A-15 Sequence 15, Appli |
| 20 | 36 | 54.5 | 194 | 2 | US-09-609-151A-17 Sequence 17, Appli |
| 21 | 36 | 54.5 | 194 | 4 | PCT-US94-02034-15 Sequence 15, Appli |
| 22 | 36 | 54.5 | 194 | 4 | PCT-US94-02034-17 Sequence 17, Appli |
| 23 | 36 | 54.5 | 206 | 2 | US-09-902-540-15467 Sequence 16467, A |
| 24 | 36 | 54.5 | 235 | 2 | US-09-252-991A-29814 Sequence 29814, A |
| 25 | 36 | 54.5 | 266 | 2 | US-09-252-991A-21116 Sequence 21116, A |
| 26 | 36 | 54.5 | 321 | 2 | US-09-134-000C-3783 Sequence 3783, Ap |
| 27 | 36 | 54.5 | 500 | 2 | US-09-538-092-831 Sequence 831, Ap |

RESULT 1
Sequence 17, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; NUMBER OF INVENTIONS: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Riddot & Maybee
; STREET: 2300 Richmond-Adeleide Centre
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE:
; CLASSIFICATION: 536
; PRIORITY APPLICATION: NO. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 362-0823
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: not applicable
; TOPOLOGY: linear
; US-08-264-093-17

Query Match 62.1%; Score 41; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. 0.51; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 2;

Qy 1 GPWELVGYFD 10
Db 2 GWDLNLNYFD 11

RESULT 2
US-08-264-093-3
; Sequence 3, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adeelaide Centre
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2T7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264, 093
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: No. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 362-0923
; TELEFAX: (416) 688-1482
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDBEADNESS: not applicable
; TOPOLOGY: linear
; US-08-264-093-3

Query Match 62.1%; Score 41; DB 1; Length 121;
Best Local Similarity 60.0%; Pred. No. 6.7;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GPWELVGYFD 10
Db 100 GWWDDLYNYYFD 109

RESULT 3
US-09-902-540-14253
; Sequence 14253, Application US/09902540
; Patent No. 6533447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-101(15849)B
; CURRENT APPLICATION NUMBER: US/09/902, 540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217, 883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14253
; LENGTH: 274

Query Match 59.1%; Score 39; DB 2;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 3 WELVGYFDS 11
Db 153 WNLKGKFPT 161

RESULT 4
US-09-561-763-5
; Sequence 5, Application US/09561763
; Patent No. 6664373
; GENERAL INFORMATION:
; APPLICANT: Curris, Rory A.J. et al.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNT-074CP2
; CURRENT APPLICATION NUMBER: US/09/561, 763
; CURRENT FILING DATE: 2000-04-29
; PRIOR APPLICATION NUMBER: 09/431, 367
; PRIOR FILING DATE: 01-11-1999
; PRIOR APPLICATION NUMBER: US 09/259, 951
; PRIOR FILING DATE: 01-03-1999
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-561-763-5

Query Match 57.6%; Score 38; DB 2;
Best Local Similarity 77.8%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GPWELVGYF 9
Db 99 GRWELVGSF 107

RESULT 5
US-09-431-367B-5
; Sequence 5, Application US/09431367B
; Patent No. 6670449
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A. J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNT-074CP
; CURRENT APPLICATION NUMBER: US/09/431, 367B
; CURRENT FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/259, 951
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-431-367B-5

Query Match 57.6%; Score 38; DB 2;
Best Local Similarity 77.8%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GPWELVGYF 9
Db 99 GRWELVGSF 107

RESULT 6

US-09-949-016-10836
; Sequence 10836, Application US/09949016
; Patent No. 6812319
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 10836
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10836

Query Match 57.6%; Score 38; DB 2; Length 493;
Best Local Similarity 60.0%; Pred. No. 1.1e+02; Mismatches 3; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PWELVGYFDS 11
Db 69 PWTKVDYFDN 78

RESULT 7
US-09-976-594-4
; Sequence 4, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-00411 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO: 4
; LENGTH: 1207
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1863336CD1
; US-09-976-594-4

Query Match 57.6%; Score 38; DB 2; Length 1207;
Best Local Similarity 77.8%; Pred. No. 3.1e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPWELVGYF 9
Db 389 GPTEAVGYF 397

RESULT 8
US-09-902-540-15261
; Sequence 15261, Application US/09902540
; Patent No. 6833347
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.

Query Match 56.1%; Score 37; DB 2; Length 427;
Best Local Similarity 66.7%; Pred. No. 1.5e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPWELVGYF 9
Db 82 GPFSFVGYF 90

RESULT 9
US-09-543-681A-6615
; Sequence 6615, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRSTON
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2705.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO: 6615
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; US-09-543-681A-6615

Query Match 56.1%; Score 37; DB 2; Length 484;
Best Local Similarity 55.6%; Pred. No. 1.7e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WELVGYFDS 11
Db 155 WALIGYQYS 163

RESULT 10
US-09-311-021-162
; Sequence 162, Application US/09311021
; Patent No. 6706869
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agoetino, Michael J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6300-11A
; CURRENT APPLICATION NUMBER: US/09/311,021
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 162
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-311-021-162

Query Match 54.5%; Score 36; DB 2; Length 132;

Best Local Similarity 55.6%; Pred. No. 59; Mismatches 5;

Matches 2; Indels 0; Gaps 0;

Qy 1 GPWELVGF 9
Db 121 GPWDQLPF 129

RESULT 11

US-09-698-341-29
Sequence 29, Application US/09698341

Patent No. 6946273

GENERAL INFORMATION:

APPLICANT: Sogge, Joseph

APPLICANT: Hurlibut Hognere, Holly

APPLICANT: Connie, Hansen

TITLE OF INVENTION: Compositions and Methods Utilizing DNA Polymerases

FILE REFERENCE: 25426/1560

CURRENT APPLICATION NUMBER: US/09/698,341

PRIORITY FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patentin version 3.0

SEQ ID NO 29

LENGTH: 140

TYPE: PRT

ORGANISM: Thermococcus sp. JDF-3

FEATURE: UNSURE

NAME/KEY: UNSURE

LOCATION: (92); (92)

OTHER INFORMATION: X = Unknown

US-09-698-341-29

Query Match 54.5%; Score 36; DB 2; Length 140;

Best Local Similarity 50.0%; Pred. No. 63; Mismatches 5;

Matches 2; Indels 3; Gaps 0;

Qy 1 GPWELVGF 10
Db 55 GPWDQNLVLD 64

RESULT 12

US-09-902-540-13916

Sequence 13916, Application US/09902540

PATENT NO. 6333447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-101(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

PRIORITY FILING DATE: 2001-07-10

PRIORITY APPLICATION NUMBER: 60/217,883

PRIMER FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 13916

LENGTH: 174

TYPE: PRT

ORGANISM: Myxococcus xanthus

US-09-902-540-13916

Query Match 54.5%; Score 36; DB 2; Length 174;
Best Local Similarity 85.7%; Pred. No. 81; Mismatches 6;
Matches 1; Indels 0; Gaps 0;

Qy 5 LVGYFDS 11

Db 6 LIGIFDS 12

RESULT 13

US-08-260-202A-15

Sequence 24, Application US/08260202A

Patent No. 5573910

GENERAL INFORMATION:

APPLICANT: Derevic, Vojko

TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCOIDY IN PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS: ADDRESS: Arnold, White & Durkee

STREET: P. O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/260,202A

FILING DATE: 12-FEB-1993

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/260,202

FILING DATE: 15-JUN-1994

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/017,114

FILING DATE: 12-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: Hodgins, Daniel S.

REGISTRATION NUMBER: 31,026

REFERENCE/DOCKET NUMBER: UTSK:221:HOD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acidsTYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

US-08-260-202A-15

Query Match 54.5%; Score 36; DB 1; Length 194;

Best Local Similarity 71.4%; Pred. No. 91; Mismatches 5;

Matches 1; Indels 1; Gaps 0;

Qy 1 GPWELVGF 7
Db 81 GPWRMVG 87

RESULT 14

US-08-260-202A-24

Sequence 24, Application US/08260202A

Patent No. 5573910

GENERAL INFORMATION:

APPLICANT: Derevic, Vojko

TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCOIDY IN PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Durkee

STREET: P. O. Box 4433

CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/260,202A
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/260,202

FILING DATE: 15-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/017,114

FILING DATE: 12-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: Hodgins, Daniel S.

REGISTRATION NUMBER: 31,026

REFERENCE/DOCKET NUMBER: UTSK:221\HOD

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/320-7200

TELEFAX: 512/474-7577

TELEX: N/A

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 194 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

Query Match 54.5%; Score 36; DB 1; Length 194;
Best Local Similarity 71.4%; Pred. No. 91; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

| Qy | 1 GPWELVG 7 |
|----|-----------------------|
| Db | : 81 GPWRWVG 87 |

Search completed: December 4, 2005, 04:09:43
Job time : 23.6042 secs

RESULT 15
US-08-017-114-15
; Sequence 15, Application US/08017114
; Patent No. 5591838
; GENERAL INFORMATION:
; APPLICANT: Deretic, Vojo
; APPLICANT: Martin, Daniel W.
; TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCOIDY IN
; TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/017,114
; FILING DATE: 19950212
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSK:205/HOD

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GenCore version 5.1.6

Search time 78.8333 Seconds

OM protein - protein search, using sw model
Run on: December 4, 2005, 04:07:28 ; Search time 78.8333 Seconds
Sequence: 1 GPWELVGYFDS 11

Title: US-10-632-706-128
Perfect score: 66
Sequence: 1 GPWELVGYFDS 11

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Gapop 10.0 , Gapext. 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Post-processing: Minimum Match 0%
Maximum DB seq length: 0
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/pctoda/1/pubpaal/us08_pubcomb.pep: *
3: /cgn2_6/pctoda/1/pubpaal/us09_pubcomb.pep: *
4: /cgn2_6/pctoda/1/pubpaal/us10_pubcomb.pep: *
5: /cgn2_6/pctoda/1/pubpaal/us10_pubcomb.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|----------------------|
| 1 | 66 | 100 | 11 | US-10-632-706-128 |
| 2 | 45 | 68 | 2 | US-10-156-761-9341 |
| 3 | 44 | 66 | 7 | US-10-282-122A-73455 |
| 4 | 44 | 66 | 7 | US-10-282-122A-74966 |
| 5 | 44 | 66 | 7 | US-10-282-122A-75801 |
| 6 | 42 | 63 | 6 | US-10-437-963-19224 |
| 7 | 41 | 62 | 1 | US-10-425-115-233365 |
| 8 | 41 | 62 | 1 | US-10-424-599-186549 |
| 9 | 41 | 62 | 1 | US-10-282-122A-48377 |
| 10 | 41 | 62 | 1 | US-10-437-963-187947 |
| 11 | 41 | 62 | 1 | US-10-481-032A-252 |
| 12 | 41 | 62 | 1 | US-10-097-143-23418 |
| 13 | 40 | 60 | 6 | US-10-424-599-182764 |
| 14 | 40 | 60 | 6 | US-10-425-115-319649 |
| 15 | 40 | 60 | 6 | US-10-477-527-21 |
| 16 | 40 | 60 | 6 | US-10-425-115-33207 |
| 17 | 40 | 60 | 6 | US-10-425-114-0098 |
| 18 | 40 | 60 | 6 | US-10-424-599-29226 |
| 19 | 40 | 60 | 6 | US-10-425-115-229314 |
| 20 | 40 | 60 | 6 | US-10-732-923-22388 |
| 21 | 40 | 60 | 6 | US-10-732-923-22387 |
| 22 | 40 | 60 | 6 | US-10-437-963-110486 |
| 23 | 39 | 59 | 8 | US-10-425-114-55208 |
| 24 | 39 | 59 | 1 | US-10-424-599-197468 |
| 25 | 39 | 59 | 1 | US-10-424-599-163986 |
| 26 | 39 | 59 | 1 | US-10-732-923-22418 |
| 27 | 39 | 59 | 1 | US-10-424-599-224678 |

Sequence 194057,
Sequence 10546, A
Sequence 121136,
Sequence 46814, A
Sequence 50763, A
Sequence 22882, A
Sequence 2283, A
Sequence 20079,
Sequence 121132,
Sequence 11662,
Sequence 37713, AP
Sequence 277808,
Sequence 15254,
Sequence 14911,
Sequence 142846,
Sequence 60011, A
Sequence 230098,
Sequence 53725, A

ALIGNMENTS

RESULT 1
US-10-632-706-128
; Sequence 128, Application US/0632706
; Publication No. US20040175385A1

; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.

; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS

; FILE REFERENCE: 4079-4789-205846
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01

; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01

; PRIOR APPLICATION NUMBER: US 09/144,806
; NUMBER OF SEQ ID NOS: 278

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 128
; LENGTH: 11
; TYPE: PRT

; ORGANISM: Artificial
; FEATURE:

; OTHER INFORMATION: single chain antibody fragment

US-10-632-706-128
Query Match 100.0%; Score 66; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00072; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Sequence 18747, APP
Sequence 253365, APP
Sequence 29418, APP
Sequence 182764, APP
Sequence 319849, APP
Sequence 21, APP
Sequence 333207, APP
Sequence 70058, APP
Sequence 22926, APP
Sequence 229314, APP
Sequence 22388, APP
Sequence 22387, APP
Sequence 9341, APP
Publication No. US2003019018A1

; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAOHI
; APPLICANT: SAKAI, YOSHIOKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2001-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO: 9341
 LENGTH: 290
 TYPE: PRT
 ORGANISM: *Streptomyces avermitilis*
 US-10-156-761-9341

RESULT 3
 Query Match 68.2%; Score 45; DB 4; length 290;
 Best Local Similarity 77.8%; Pred. No. 38;
 Matches 7; Conservative 1; Mismatches 1;
 Qy 3 WELVGFDs 11
 Db 171 WMLIGFDS 179

RESULT 4
 US-10-282-122A-74966
 Sequence 74966, Application US/10282122A
 Publication No. US20040029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Hesselbeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forbryth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA_034A
 CURRENT APPLICATION NUMBER: US10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-15
 Remaining Prior Application data removed - See File Wrapper or PALM.
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 74966
 LENGTH: 367
 TYPE: PRT
 ORGANISM: *Salmonella typhimurium*
 US-10-282-122A-74966

RESULT 5
 Query Match 66.7%; Score 44; DB 4; length 367;
 Best Local Similarity 69.2%; Pred. No. 69;
 Matches 9; Conservative 0; Mismatches 0;
 Indels 4; Gaps 1;
 Qy 1 GPWELVY---GYF 9
 Db 127 GPWELVLGPGFY 139

RESULT 6
 US-10-282-122A-75801
 Sequence 75801, Application US/10282122A
 Publication No. US20040029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos

Query Match 66.7%; Score 44; DB 4; Length 306;
 Best Local Similarity 69.2%; Pred. No. 58;

```

APPLICANT: Malone, Cheryl
APPLICANT: Hasenbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282.122A

PRIORITY FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/205,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/206,848
PRIORITY FILING DATE: 2000-09-06
PRIORITY APPLICATION NUMBER: 60/230,347
PRIORITY FILING DATE: 2000-09-09
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/267,636
PRIORITY FILING DATE: 2001-02-09
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1

; SEQ ID NO: 75801
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Salmonella typhi
; US-10-282-122A-75801

RESULT 6
US-10-437-963-192224
; Publication No. US20040123343A1
; Sequence 192224, Application US/10437963
GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Li, Ping
; APPLICANT: Barbatuk, Brad

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 3B-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO: 192224
LENGTH: 381

; SEQ ID NO: 192224
; LENGTH: 381

Query Match 63.6%; Score 42; DB 4; Length 381;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CQY 1 GYWELVGY 8
Db 176 GYWELVGF 183

RESULT 7
US-10-425-115-233365
; Sequence 25335, Application US/10425115
; Publication No. US2004014272A1
GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Li, Ping
; APPLICANT: Barbatuk, Brad

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 3B-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO: 253365
LENGTH: 125
TYPE: PRT
ORGANISM: Zea mays
FEATURE: OTHER INFORMATION: Clone ID: MRR4577_16264C.1.pep
; US-10-425-115-233365

Query Match 62.1%; Score 41; DB 4; Length 125;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CQY 1 GYWELVGYF 9
Db 75 GYWELLKEF 83

RESULT 8
US-10-424-599-116545
; Sequence 186545, Application US/10424599
; Publication No. US200401072A1
GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovacic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; APPLICANT: Wu Wei
; APPLICANT: Boukharov Andrey A
; APPLICANT: Li Ping
; APPLICANT: Barbatuk Brad

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 3B-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO: 186545
LENGTH: 171
TYPE: PRT
ORGANISM: Glycine max
FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_139463C.1.pep
; US-10-424-599-186545

Query Match 62.1%; Score 41; DB 4; Length 171;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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RESULT 9
US-10-282-122A-48377
; Sequence 48377, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangguo
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forayth, R.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA_034A
; CURRENT APPLICATION NUMBER: US1/0/282,122A
CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR APPLICATION NUMBER: 60/205,848
; PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 48377
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Bacteroides fragilis
US-10-282-122A-48377

Query Match 62.1%; Score 41; DB 4; Length 475;
Best Local Similarity 70.0%; Pred. No. 2.7e+02; Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 11
US-10-481-032A-252
; Sequence 252, Application US/10481032A
; Publication No. US20050177901A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Cheng, Wengqiong
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen A.
; APPLICANT: Moughamer, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katigiri, Fumiaki
; APPLICANT: Krebs, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Riche, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
FILE REFERENCE: 60148USPCT
; CURRENT APPLICATION NUMBER: US1/0/481,032A
CURRENT FILING DATE: 2005-12-16
; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/342,327
; PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: PCT/IB02/02450
; PRIOR FILING DATE: 2002-01-21
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO: 252
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(14)
; OTHER INFORMATION: Xaa = any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(16)

RESULT 10
US-10-437-963-187947
; Sequence 187947, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

OTHER INFORMATION: Xaa = any naturally occurring amino acid
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (399)..(399)
 OTHER INFORMATION: Xaa = any naturally occurring amino acid
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (493)..(493)
 OTHER INFORMATION: Xaa = any naturally occurring amino acid
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (671)..(671)
 OTHER INFORMATION: Xaa = any naturally occurring amino acid
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (673)..(673)
 OTHER INFORMATION: Xaa = any naturally occurring amino acid
 US-10-481-032A-252

Query Match 62.1%; Score 41; DB 5; Length 792;
 Best Local Similarity 66.7%; Pred No. 4.3e+02; 2; Mismatches 1; Indels 0; Gaps 0;
 Matches 6; Conservative 2; Nucleic Acid Molecules and Other Molecules Associated With Plant and Uses Thereof for Plant Improvement

Qy 2 PWELVGYFD 10
 Db 245 PWQQLGGD 253

RESULT 12

US-11-097-143-29418
 Sequence 20418, Application US/11097143
 Publication No. US2005020558A1

GENERAL INFORMATION:

APPLICANT: Venner, J. Craig
 APPLICANT: et al.
 TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID EXPRESSION OF 10,000 OR MORE ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE TITLES OF INVENTION: DROSOPHILA GENES.
 FILE REFERENCE: CL00072B
 CURRENT APPLICATION NUMBER: US/11/097,143
 CURRENT FILING DATE: 2005-04-04
 PRIOR APPLICATION NUMBER: 60/157,832
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: 60/160,191
 PRIOR FILING DATE: 1999-10-19
 PRIOR APPLICATION NUMBER: 60/161,932
 PRIOR FILING DATE: 1999-10-28
 PRIOR APPLICATION NUMBER: 60/164,769
 PRIOR FILING DATE: 1999-11-12
 PRIOR APPLICATION NUMBER: 60/173,383
 PRIOR FILING DATE: 1999-12-28
 PRIOR APPLICATION NUMBER: 60/175,693
 PRIOR FILING DATE: 2000-01-12
 PRIOR APPLICATION NUMBER: 60/184,831
 PRIOR FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: 60/191,637
 PRIOR FILING DATE: 2000-03-23
 NUMBER OF SEQ ID NOS: 43008
 SOFTWARE: FastSBQ for Windows Version 4.0
 SEQ ID NO 29418
 LENGTH: 1352
 TYPE: PRT
 ORGANISM: DROSOPHILA
 US-11-097-143-29418

Query Match 62.1%; Score 41; DB 6; Length 1352;
 Best Local Similarity 77.8%; Pred No. 7.2e+02; 2; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Nucleic Acid Molecules and Other Molecules Associated With Plant and Uses Thereof for Plant Improvement

Qy 1 3 WELVGFPS 11
 Db 161 WRNVGFPS 169

RESULT 13

US-10-424-599-182764
 Sequence 182764, Application US/10424599
 Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J
 APPLICANT: Kovacic David K
 APPLICANT: Zhou Yihua
 APPLICANT: Cao Yongwei
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(5223)B
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 285684
 SEQ ID NO 182764
 LENGTH: 50

TYPE: PRT
 ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT3847_13604C.1.pep

US-10-424-599-182764

Query Match 60.6%; Score 40; DB 4; Length 50;
 Best Local Similarity 66.7%; Pred No. 48; 2; Mismatches 1; Indels 0; Gaps 0;
 Matches 6; Conservative 2; Nucleic Acid Molecules and Other Molecules Associated With Plant and Uses Thereof for Plant Improvement

Qy 1 GPWELVGF 9
 Db 32 GKWKLVGF 40

RESULT 14

US-10-425-115-319649
 Sequence 319649, Application US/10425115
 Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovacic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(5322)B
 CURRENT APPLICATION NUMBER: US/10/425,115
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 369326
 SEQ ID NO 319649
 LENGTH: 78

TYPE: PRT
 ORGANISM: Zea mays
 FEATURE:
 OTHER INFORMATION: Clone ID: MRT4577_54590C.1.pep

US-10-425-115-319649

Query Match 60.6%; Score 40; DB 4; Length 78;
 Best Local Similarity 66.7%; Pred No. 73; 2; Mismatches 2; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Nucleic Acid Molecules and Other Molecules Associated With Plant and Uses Thereof for Plant Improvement

Qy 1 GPWELVGF 9
 Db 21 GPWVLAGWF 29

RESULT 15

US-10-477-527-21
 Sequence 21, Application US/10477527
 Publication No. US20040171807A1

US-11-097-143-29418

; GENERAL INFORMATION:
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Gao, Guangping
; APPLICANT: Wilson, James M.
; TITLE OF INVENTION: Method for Rapid Screening of Bacterial Transformants and Novel S
; FILE REFERENCE: UPN-N2630PCT
; CURRENT APPLICATION NUMBER: US/10/477,527
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/300,501
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/385,632
; PRIOR FILING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 21
; LENGTH: 146
; TYPE: PRT
; ORGANISM: chimpanzee C68 adenovirus protein
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (62)..(62)
; OTHER INFORMATION: Xaa can be any amino acid
US-10-477-527-21

Query Match 60.6%; Score 40; DB 4; Length 146;
Best Local Similarity 85.7%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPWELVVG 7
Db ||||:|||
Db 101 GPWEVVG 107

Search completed: December 4, 2005, 04:37:29
Job time : 79.8333 secs

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Om protein - protein search, using BW model

Run on: December 4, 2005, 04:08:08 ; Search time 3.20033 Seconds

(without alignments)
16.417 Million cell updates/sec

Title: US-10-632-706-128

Perfect score: 66 Sequence: 1 GPWELVGYFDS 11

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

1: /cgn2_6/pctodata/1/pubpaa/us09_NEW_PUB.pep:*

2: /cgn2_6/pctodata/1/pubpaa/us05_NEW_PUB.pep:*

3: /cgn2_6/pctodata/1/pubpaa/us07_NEW_PUB.pep:*

4: /cgn2_6/pctodata/1/pubpaa/us08_NEW_PUB.pep:*

5: /cgn2_6/pctodata/1/pubpaa/PCT_NEW_PUB.pep:*

6: /cgn2_6/pctodata/1/pubpaa/us10_NEW_PUB.pep:*

7: /cgn2_6/pctodata/1/pubpaa/us11_NEW_PUB.pep:*

8: /cgn2_6/pctodata/1/pubpaa/us60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

| RESULT 1 | | | | | | | | | |
|--|--|--|--|--|--|--|--|--|--|
| US-10-467-657-6026 | | | | | | | | | |
| ; Sequence 6026, Application US/10467657 | | | | | | | | | |
| ; Publication No. US20050260581A1 | | | | | | | | | |
| ; GENERAL INFORMATION: | | | | | | | | | |
| ; APPLICANT: CHIRON SpA | | | | | | | | | |
| ; APPLICANT: FONTANA Maria Rita | | | | | | | | | |
| ; APPLICANT: PIZZA Mariagrazia | | | | | | | | | |
| ; APPLICANT: MASIGNANI Vega | | | | | | | | | |
| ; APPLICANT: MONACI Elisabetta | | | | | | | | | |
| ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEAR ACIDS | | | | | | | | | |
| ; FILE REFERENCE: | | | | | | | | | |
| ; CURRENT APPLICATION NUMBER: US/10/467,657 | | | | | | | | | |
| ; CURRENT FILING DATE: 2003-08-11 | | | | | | | | | |
| ; PRIOR APPLICATION NUMBER: GB-0103424.8 | | | | | | | | | |
| ; PRIOR FILING DATE: 2001-02-12 | | | | | | | | | |
| ; SOFTWARE: Seqwin99, version 1.04 | | | | | | | | | |
| ; SBQ ID NO: 6026 | | | | | | | | | |
| ; LENGTH: 792 | | | | | | | | | |
| ; TYPE: RT | | | | | | | | | |
| ; ORGANISM: Neisseria gonorrhoeae | | | | | | | | | |
| US-10-467-657-6026 | | | | | | | | | |
| ; Query Match Similarity 54.5%; Score 36; DB 6; Length 792; | | | | | | | | | |
| ; Best Local Similarity 75.0%; Pred. No. 27; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | |
| ; Matches 6; Conservative 2; Mismatches 0; | | | | | | | | | |
| ; SEQ ID: 4 ELVGYFDS 11 | | | | | | | | | |
| ; QY : ; | | | | | | | | | |
| ; DB 390 BLGGFDN 397 | | | | | | | | | |
| RESULT 2 | | | | | | | | | |
| US-10-467-657-7528 | | | | | | | | | |
| ; Sequence 7528, Application US/10467657 | | | | | | | | | |
| ; Publication No. US20050260581A1 | | | | | | | | | |
| ; GENERAL INFORMATION: | | | | | | | | | |
| ; APPLICANT: CHIRON SpA | | | | | | | | | |
| ; APPLICANT: FONTANA Maria Rita | | | | | | | | | |
| ; APPLICANT: PIZZA Mariagrazia | | | | | | | | | |
| ; APPLICANT: MASIGNANI Vega | | | | | | | | | |
| ; APPLICANT: MONACI Elisabetta | | | | | | | | | |
| ; TITLE OF INVENTION: GONOCCOCAL PROTEINS AND NUCLEAR ACIDS | | | | | | | | | |
| ; FILE REFERENCE: | | | | | | | | | |
| ; CURRENT APPLICATION NUMBER: US/10/467,657 | | | | | | | | | |
| ; CURRENT FILING DATE: 2003-08-11 | | | | | | | | | |
| ; PRIOR APPLICATION NUMBER: GB-0103424.8 | | | | | | | | | |

| | | | | | | | | | | |
|----|------|------|------|-----|---------------------|--|--|----------------------|----------------------|--|
| 1 | 36 | 54.5 | 792 | 6 | US-10-467-657-6026 | Sequence 6026, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 2 | 36 | 54.5 | 792 | 6 | US-10-467-657-7528 | Sequence 7528, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 3 | 35 | 53.0 | 356 | 6 | US-10-467-657-1210 | Sequence 1210, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 4 | 34 | 51.5 | 322 | 7 | US-11-074-176-35 | Sequence 35, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 5 | 34 | 51.5 | 723 | 6 | US-10-467-657-1916 | Sequence 1916, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 6 | 34 | 51.5 | 926 | 6 | US-10-841-129-2 | Sequence 129, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 7 | 33.5 | 50.8 | 478 | 7 | US-11-037-829A-4 | Sequence 829A-4, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 8 | 33 | 50.0 | 198 | 7 | US-11-082-389-302 | Sequence 389, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 9 | 33 | 50.0 | 281 | 7 | US-11-082-389-304 | Sequence 304, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 10 | 33 | 50.0 | 431 | 7 | US-11-055-822-75 | Sequence 75, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 11 | 33 | 50.0 | 724 | 6 | US-10-131-826A-60 | Sequence 60, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 12 | 33 | 50.0 | 1510 | 7 | US-11-133-822-72 | Sequence 72, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 13 | 33 | 50.0 | 2725 | 7 | US-11-133-424-52 | Sequence 52, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 14 | 32 | 48.5 | 456 | 6 | US-10-467-657-4150 | Sequence 4150, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 15 | 32 | 48.5 | 533 | 7 | US-11-147-047-33 | Sequence 33, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 16 | 32 | 48.5 | 771 | 7 | US-11-147-047-34 | Sequence 34, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 17 | 31.5 | 47.7 | 532 | 7 | US-11-184-380-6 | Sequence 6, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 18 | 31.5 | 47.7 | 544 | 6 | US-10-719-311-18 | Sequence 18, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 19 | 31.5 | 47.7 | 588 | 7 | US-11-184-380-5 | Sequence 5, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 20 | 31.5 | 47.7 | 598 | 6 | US-10-719-311-16 | Sequence 16, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 21 | 31.5 | 47.7 | 724 | 7 | US-11-184-380-4 | Sequence 4, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 22 | 31.5 | 47.7 | 734 | 6 | US-10-719-311-4 | Sequence 3, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 23 | 31.5 | 47.7 | 735 | 7 | US-11-184-380-24 | Sequence 2, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 24 | 31.5 | 47.7 | 735 | 7 | US-11-184-380-24 | Sequence 1, Application US/10467657 | Publication No. US20050260581A1 | GENERAL INFORMATION: | | |
| 25 | 31 | 47.0 | 142 | 6 | US-10-821-234-030 | CURRENT FILING DATE: 2003-08-11 | PRIOR APPLICATION NUMBER: GB-0103424.8 | GENERAL INFORMATION: | | |
| 26 | 31 | 47.0 | 290 | 6 | US-10-793-626-214 | SEQUENCE 214, APP | SEQUENCE 214, APP | GENERAL INFORMATION: | | |
| 27 | 31 | 47.0 | 393 | 6 | US-10-821-234-1292 | SEQUENCE 1222, APP | SEQUENCE 1222, APP | GENERAL INFORMATION: | | |
| 28 | 31 | 47.0 | 490 | 6 | US-10-131-826-310 | SEQUENCE 310, APP | SEQUENCE 310, APP | GENERAL INFORMATION: | | |
| 29 | 31 | 47.0 | 626 | 6 | US-10-467-657-6426 | SEQUENCE 6426, APP | SEQUENCE 6426, APP | GENERAL INFORMATION: | | |
| 30 | 31 | 47.0 | 625 | 6 | US-11-109-657-618 | SEQUENCE 618, APP | SEQUENCE 618, APP | GENERAL INFORMATION: | | |
| 31 | 31 | 47.0 | 745 | 7 | US-11-109-657-618 | SEQUENCE 618, APP | SEQUENCE 618, APP | GENERAL INFORMATION: | | |
| 32 | 31 | 47.0 | 766 | 6 | US-10-522-789-2 | SEQUENCE 216, APP | SEQUENCE 216, APP | GENERAL INFORMATION: | | |
| 33 | 30 | 45.5 | 30 | 6 | US-10-467-657-2188 | SEQUENCE 80, APP | SEQUENCE 80, APP | GENERAL INFORMATION: | | |
| 34 | 30 | 45.5 | 180 | 7 | US-11-055-822-80 | SEQUENCE 871, APP | SEQUENCE 871, APP | GENERAL INFORMATION: | | |
| 35 | 30 | 45.5 | 221 | 7 | US-11-055-822-82 | SEQUENCE 8, APP | SEQUENCE 8, APP | GENERAL INFORMATION: | | |
| 36 | 30 | 45.5 | 389 | 6 | US-10-850-730-8 | SEQUENCE 2, APP | SEQUENCE 2, APP | GENERAL INFORMATION: | | |
| 37 | 30 | 45.5 | 400 | 6 | US-10-793-626-3116 | SEQUENCE 116, APP | SEQUENCE 116, APP | GENERAL INFORMATION: | | |
| 38 | 30 | 45.5 | 450 | 6 | US-10-467-657-2126 | SEQUENCE 2126, APP | SEQUENCE 2126, APP | GENERAL INFORMATION: | | |
| 39 | 30 | 45.5 | 457 | 7 | US-11-055-822-80 | SEQUENCE 80, APP | SEQUENCE 80, APP | GENERAL INFORMATION: | | |
| 40 | 30 | 45.5 | 479 | 6 | US-10-821-234-871 | SEQUENCE 871, APP | SEQUENCE 871, APP | GENERAL INFORMATION: | | |
| 41 | 30 | 45.5 | 934 | 6 | US-10-850-730-8 | SEQUENCE 8, APP | SEQUENCE 8, APP | GENERAL INFORMATION: | | |
| 42 | 30 | 45.5 | 1857 | 7 | US-11-109-657-217-2 | SEQUENCE 17, APP | SEQUENCE 17, APP | GENERAL INFORMATION: | | |
| 43 | 30 | 45.5 | 29 | 6 | US-10-930-890-116 | SEQUENCE 32, APP | SEQUENCE 32, APP | GENERAL INFORMATION: | | |
| 44 | 29 | 45.5 | 44.7 | 178 | 6 | US-10-508-263-46 | SEQUENCE 46, APP | SEQUENCE 46, APP | GENERAL INFORMATION: | |
| 45 | 29 | 45.5 | 44.7 | 178 | 6 | US-10-508-263-46 | SEQUENCE 46, APP | SEQUENCE 46, APP | GENERAL INFORMATION: | |

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; PRIORITY FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO: 7528
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7328

Query Match Score 54.5%; Score 36; DB 6; Length 792;
Best Local Similarity 75.0%; Pred. No. 27; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY          4 ELVGFYFD 11
Db          390 ELVGFYFDN 397

RESULT 3
US-10-467-657-1210
; Sequence 1210, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO: 1210
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1210

Query Match Score 53.0%; Score 35; DB 6; Length 356;
Best Local Similarity 62.5%; Pred. No. 19; Mismatches 5; Indels 2; Gaps 0;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY          1 GPWELVGY 8
Db          45 GWEMLGY 52

RESULT 4
US-11-074-176-36
; Sequence 36, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIORITY FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 36
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-36

Query Match Score 51.5%; Score 34; DB 7; Length 322;
Best Local Similarity 65.7%; Pred. No. 25; Mismatches 6; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          4 ELVGFYFD 10
Db          43 ELVGFYFD 49

RESULT 5
US-10-467-657-1916
; Sequence 1916, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO: 1916
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1916

Query Match Score 51.5%; Score 34; DB 6; Length 723;
Best Local Similarity 53.3%; Pred. No. 55; Mismatches 8; Indels 1; Gaps 6;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 6;

QY          1 GPWELV-----GYF 9
Db          260 GNWELVNLNSAAGYF 274

RESULT 6
US-10-841-129-2
; Sequence 2, Application US/10841129
; Publication No. US20050250113A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Erlenbach, Isolda
; APPLICANT: Hoon, Mark A.
; APPLICANT: Ryba, Nicholas J. P.
; APPLICANT: Zhang, Yileng
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the Department of Health and Human Services
; TITLE OF INVENTION: A Mammalian Magnesium/Manganese Sensing G Protein
; TITLE OF INVENTION: Coupled Receptor
; FILE REFERENCE: 02307E-145400US
; CURRENT APPLICATION NUMBER: US/10/841,129
; CURRENT FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 926
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: human magnesium/manganese sensing G protein
; OTHER INFORMATION: coupled receptor (GPCR) R5.24, Mg receptor, Mn
```

; OTHER INFORMATION: receptor
US-10-841-129-2

Query Match 51.5%; Score 34; DB 6; Length 926;
Best Local Similarity 83.3%; Pred. No. 70; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PWELVG 7
Db 443 PWELVG 448

RESULT 7

US-11-037-829A-4

; Sequence 4, Application US/11037829A
; Publication No. US2005025551A1

; GENERAL INFORMATION:

; APPLICANT: Taracept, Inc
; APPLICANT: Catholic Healthcare West

; APPLICANT: Bencherif, Merouane

; TITLE OF INVENTION: Methods and Compositions Relating to Chimeric
TITLE OF INVENTION: Nicotinic Receptor Subunits

; CURRENT APPLICATION NUMBER: US/11/037,829A
; CURRENT FILING DATE: 2005-01-18

; PRIOR APPLICATION NUMBER: US 60/397,380
; PRIOR FILING DATE: 2002-07-19

; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4
; LENGTH: 478

; TYPE: PRT
; ORGANISM: Homo sapien

; US-11-037-829A-4

Query Match 50.8%; Score 33.5; DB 7; Length 478;
Best Local Similarity 58.3%; Pred. No. 45; Mismatches 1; Indels 3; Gaps 1;

Qy 1 GPWELVG--YF 9
Db 207 GEWEILGVLPV 218

RESULT 8
US-11-082-389-302

; Sequence 9, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krogger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131.CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487,4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489,0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549,3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550,7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134,5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379,7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19930489,0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487,4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489,0
; PRIOR FILING DATE: 1999-07-01

; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 4
; LENGTH: 478

; TYPE: PRT
; ORGANISM: Homo sapien

; US-11-082-389-302

Query Match 50.0%; Score 33; DB 7; Length 198;
Best Local Similarity 66.7%; Pred. No. 24; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WELVG 8
Db 99 WOLIGY 104

RESULT 9
US-11-082-389-304

; Sequence 10, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krogger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131.CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487,4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489,0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549,3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550,7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134,5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379,7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19930489,0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487,4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489,0
; PRIOR FILING DATE: 1999-07-01

; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 4
; LENGTH: 281

; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum

; US-11-082-389-304

Query Match 50.0%; Score 33; DB 7; Length 281;
 Best Local Similarity 66.7%; Pred. No. 33;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WELVGY 8
 Db 153 WQLTGY 158

RESULT 10
 US-11-055-822-76 Application US/11055822
 ; Sequence 76, Application US/11055822
 ; Publication No. US2005026070A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pompejus, Markus
 ; APPLICANT: Kroger, Burkhard
 ; APPLICANT: Schroder, Hartwig
 ; APPLICANT: Zelzer, Oskar
 ; APPLICANT: Haberhauer, Gregor
 ; TITLE OF INVENTION: CORNYBACTERIUM GLUTAMICUM GENES ENCODING
 ; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
 ; FILE REFERENCE: BGI-121CPCN
 ; CURRENT APPLICATION NUMBER: US/11/055, 822
 ; CURRENT FILING DATE: 2005-02-11
 ; PRIOR APPLICATION NUMBER: 09/606, 740
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: 60/141, 031
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: 60/142, 101
 ; PRIOR FILING DATE: 1999-07-02
 ; PRIOR APPLICATION NUMBER: 60/148, 613
 ; PRIOR FILING DATE: 1999-08-12
 ; PRIOR APPLICATION NUMBER: 60/187, 970
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: DE 19930476.9
 ; PRIOR FILING DATE: 1999-07-01
 ; PRIOR APPLICATION NUMBER: DE 19931415.2
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931418.7
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931419.5
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931420.9
 ; PRIOR FILING DATE: 1999-07-08
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1158
 ; SEQ ID NO 76
 ; LENGTH: 431
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 ; US-11-055-822-76

Query Match 50.0%; Score 33; DB 7; Length 431;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPWEL 5
 Db 284 GPWEL 288

RESULT 11
 US-10-131-826A-60 Application US/10131826A
 ; Sequence 60, Application US/10131826A
 ; Publication No. US20050245730A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Bersini Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.

Query Match 50.0%; Score 33; DB 7; Length 281;
 Best Local Similarity 66.7%; Pred. No. 33;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WELVGY 8
 Db 153 WQLTGY 158

RESULT 12
 US-11-055-822-72 Application US/11055822
 ; Sequence 72, Application US/11055822
 ; Publication No. US2005026070A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pompejus, Markus
 ; APPLICANT: Kroger, Burkhard
 ; APPLICANT: Schroder, Hartwig
 ; APPLICANT: Zelzer, Oskar
 ; APPLICANT: Haberhauer, Gregor
 ; TITLE OF INVENTION: CORNYBACTERIUM GLUTAMICUM GENES ENCODING
 ; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
 ; FILE REFERENCE: BGI-121CPCN
 ; CURRENT APPLICATION NUMBER: US/11/055, 822
 ; CURRENT FILING DATE: 2005-02-11
 ; PRIOR APPLICATION NUMBER: 09/606, 740
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: 60/141, 031
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: 60/142, 101
 ; PRIOR FILING DATE: 1999-07-02

Db 503 GPWYLAFYND 512
; Sequence 4150; Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabeta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-010324.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO: 4150
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-115-822-72
; Query Match 50.0%; Score 33; DB 7; Length 1510;
; Best Local Similarity 100.0%; Pred. No. 1.6e-02;
; Matches 5; Conservative 0; Mismatches 0;
; Qy 1 GPWEL 5 Db 1063 GPWEL 1067
; Indels 0; Gaps 0;
; RESULT 13
; US-11-113-424-52
; Sequence 52; Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolfi et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/286,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 52
; LENGTH: 2745
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-113-424-52
; Query Match 50.0%; Score 33; DB 7; Length 2725;
; Best Local Similarity 60.0%; Pred. No. 2.9e+02; Mismatches 4; Indels 0; Gaps 0;
; Qy 1 GPWELGYFD 10 Db 503 GPWYLAFYND 512
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-147-047-33
; Query Match 48.5%; Score 32; DB 7; Length 533;
; Best Local Similarity 83.3%; Pred. No. 90; Mismatches 1; Indels 0; Gaps 0;

Mon Dec 5 10:18:13 2005

usb-10-632-706-128.rapbn

Page 6

QY 2 PWELVG 7
| | |
Db 178 PWEEAVG 183

Search completed: December 4, 2005, 04:37:49
Job time : 4.20833 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:09:54 (without alignments)
50.576 Million cell updates/sec

Title: US-10-632-706-197
Perfect score: 89

Sequence: 1 EPDWLWLNGDRLGALDV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_21,*
1: geneseqqp1980s;**
- 2: geneseqqp1990s;**
- 3: geneseqqp2000s;**
- 4: geneseqqp2001s;**
- 5: geneseqqp2002s;**
- 6: geneseqqp2003as;*
- 7: geneseqqp2003bs;*
- 8: geneseqqp2004as;*
- 9: geneseqqp2005s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description | RESULT 1 |
|------------|-------|--------------------|-------|--------------|------------------------------------|
| 1 | 89 | 100.0 | 15 | 8 ADR38727 | ADR38727 |
| 2 | 89 | 100.0 | 15 | 8 ADR38728 | ADR38727 standard; peptide; 15 AA. |
| 3 | 89 | 100.0 | 15 | 8 ADR38792 | XX |
| 4 | 89 | 100.0 | 15 | 8 ADR38795 | XX |
| 5 | 89 | 100.0 | 15 | 8 ADR38798 | XX |
| 6 | 89 | 100.0 | 15 | 8 ADR38729 | XX |
| 7 | 75 | 84.3 | 15 | 8 ADR38801 | XX |
| 8 | 51 | 57.3 | 334 | 4 ABG20331 | XX |
| 9 | 48 | 53.9 | 201 | 8 ADJ91819 | XX |
| 10 | 48 | 53.9 | 7 | ADP66019 | XX |
| 11 | 48 | 53.9 | 229 | 7 ADP66015 | XX |
| 12 | 47 | 52.8 | 59 | 2 AAB13560 | XX |
| 13 | 47 | 52.8 | 455 | 4 ABG22524 | XX |
| 14 | 46 | 51.7 | 52.8 | 904 ABG23387 | XX |
| 15 | 46 | 51.7 | 186 | 4 AAM24399 | XX |
| 16 | 45 | 50.6 | 54 | 5 ABP03542 | XX |
| 17 | 45 | 50.6 | 372 | 6 ABP04048 | XX |
| 18 | 45 | 50.6 | 450 | 8 ADN47951 | XX |
| 19 | 45 | 50.6 | 614 | 7 ADP06781 | XX |
| 20 | 44 | 49.4 | 49.4 | 49.4 ADG1847 | XX |
| 21 | 44 | 49.4 | 137 | 6 ADG21119 | XX |
| 22 | 44 | 49.4 | 342 | 3 AAB51737 | XX |
| 23 | 44 | 49.4 | 409 | 4 AAB6593 | XX |
| 24 | 44 | 49.4 | 472 | 7 ADC86881 | XX |

ALIGNMENTS

| | | | | | |
|----|------|------|------|------------|--------------------|
| 25 | 44 | 49.4 | 687 | 8 ADS42446 | Ad42446 Bacterial |
| 26 | 43 | 48.3 | 100 | 8 ADQ65091 | Ad65091 Novel hum |
| 27 | 43 | 48.3 | 345 | 2 AAY8595 | Aay8595 Neisseria |
| 28 | 43 | 48.3 | 345 | 9 AEB4036 | Aeb4036 N. gonorr |
| 29 | 43 | 48.3 | 383 | 2 AAY8596 | Aay8596 Neisseria |
| 30 | 43 | 48.3 | 383 | 5 ABB79536 | Ab79536 N. gonorr |
| 31 | 43 | 48.3 | 383 | 9 ABB4038 | Abb4038 N. gonorr |
| 32 | 43 | 48.3 | 546 | 2 AAW6164 | AAW6164 KP-1 prot |
| 33 | 43 | 48.3 | 582 | 4 AAU30396 | AAU30396 Novel hum |
| 34 | 43 | 48.3 | 616 | 8 ADR0416 | Ad820416 Crab-eat |
| 35 | 43 | 48.3 | 683 | 2 AAW26163 | AAW26163 Mouse KP- |
| 36 | 43 | 48.3 | 683 | 9 ABM04210 | Ad04210 Novel apo |
| 37 | 43 | 48.3 | 685 | 2 AAW26165 | AAW26165 Human KP- |
| 38 | 43 | 48.3 | 685 | 9 ADX07646 | Adx07646 Cyclin-de |
| 39 | 43 | 48.3 | 685 | 9 ADZ04207 | Adz04207 Novel apo |
| 40 | 43 | 48.3 | 732 | 9 ABM9422 | Abm9422 M. xanthu |
| 41 | 43 | 48.3 | 2519 | 7 ABM80218 | Rice abio |
| 42 | 42.5 | 47.8 | 315 | 4 ABU15664 | Abu15664 Protein e |
| 43 | 42.5 | 47.8 | 320 | 7 ABO65555 | Ab65555 Pseudomon |
| 44 | 42.5 | 47.8 | 320 | 7 ABO65794 | Aau65794 Propionib |

| Result No. | Score | Query Match Length | DB ID | Description | RESULT 1 |
|------------|-------|--------------------|-------|--------------|---------------------------|
| 1 | 89 | 100.0 | 15 | 8 ADR38727 | ADR38727 |
| 2 | 89 | 100.0 | 15 | 8 ADR38728 | ADR38727; peptide; 15 AA. |
| 3 | 89 | 100.0 | 15 | 8 ADR38792 | XX |
| 4 | 89 | 100.0 | 15 | 8 ADR38795 | XX |
| 5 | 89 | 100.0 | 15 | 8 ADR38798 | XX |
| 6 | 89 | 100.0 | 15 | 8 ADR38729 | XX |
| 7 | 75 | 84.3 | 15 | 8 ADR38801 | XX |
| 8 | 51 | 57.3 | 334 | 4 ABG20331 | XX |
| 9 | 48 | 53.9 | 201 | 8 ADJ91819 | XX |
| 10 | 48 | 53.9 | 7 | ADP66019 | XX |
| 11 | 48 | 53.9 | 229 | 7 ADP66015 | XX |
| 12 | 47 | 52.8 | 59 | 2 AAB13560 | XX |
| 13 | 47 | 52.8 | 455 | 4 ABG22524 | XX |
| 14 | 46 | 51.7 | 52.8 | 904 ABG23387 | XX |
| 15 | 46 | 51.7 | 186 | 4 AAM24399 | XX |
| 16 | 45 | 50.6 | 54 | 5 ABP03542 | XX |
| 17 | 45 | 50.6 | 372 | 6 ABP04048 | XX |
| 18 | 45 | 50.6 | 450 | 8 ADN47951 | XX |
| 19 | 45 | 50.6 | 614 | 7 ADP06781 | XX |
| 20 | 44 | 49.4 | 49.4 | 49.4 ADG1847 | XX |
| 21 | 44 | 49.4 | 137 | 6 ADG21119 | XX |
| 22 | 44 | 49.4 | 342 | 3 AAB51737 | XX |
| 23 | 44 | 49.4 | 409 | 4 AAB6593 | XX |
| 24 | 44 | 49.4 | 472 | 7 ADC86881 | XX |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Example 3 : SEQ ID NO 129; 110pp; English.

The invention describes an isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a specific clone where (I) binds to and neutralizes botulinum neurotoxin type A (BoNT/A). An isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone S25, C25, C39, IC6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1, 3-8, 3-10 and INGL, where (I) binds to and neutralizes botulinum neurotoxin type A (BoNT/A). Also described are: a polypeptide comprising BoNT/A neutralising epitope having an epitope that is

CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC , producing (I), and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (II). (II) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the single
 CC antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain variable region complementarity determining
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.
 XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BPDWLWGDGRGALDV 15
 1 BPDWLWGDGRGALDV 15
 Db

RESULT 2

ADR38728

ID ADR38728 standard; peptide; 15 AA.

XX

AC ADR38728;

XX

DT 02-DEC-2004 (first entry)

XX

DB Mouse heavy chain variable region CDR3 seqid 130.

XX

KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;

KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;

KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;

KW heavy chain variable region; complementarity determining region; CDR3.

OS Mus sp.

PN US2004175385-A1.

XX

PD 09-SEP-2004.

XX

PR 31-AUG-1998; 98US-00144886.

XX

PR 01-AUG-2002; 2002US-0400721P.

XX

PR (REGC) UNIV CALIFORNIA.

XX

PI Marks JD, Amerstorfer P;

XX

DR WPI; 2004-652009/63.

XX

PT New isolated antibody that neutralizes botulinum neurotoxin type A'

PT useful for diagnosing botulism or for treating pathologies associated

PT with botulinum neurotoxin poisoning.

XX

Example 3; SEQ ID NO 130; 110pp; English.

XX

The invention describes an isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a specific clone where (I) binds to and neutralises botulinum neurotoxin type A (BONT/A). An isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone S25, C25, C39, IC6, 3D12, B4, 1F3, huc25, ARI, AR2, WRI(V), WRI(T), J-1,

CC 3-8 3-10 and ING1, where (I) binds to and neutralises botulinum
 CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
 CC comprising BONT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC comprising (II); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (II); and a kit comprising (II). (II) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (II) in surplus, where each of (II) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (II) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (II) exhibits specificity and affinity towards BONT/A. (II)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain variable region complementarity determining
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.
 XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BPDWLWGDGRGALDV 15
 1 BPDWLWGDGRGALDV 15
 Db

RESULT 3

ADR38792

ID ADR38792 standard; peptide; 15 AA.

XX

AC ADR38792;

XX

DT 02-DEC-2004 (first entry)

XX

DB Mouse heavy chain anti-BONT-antibody CD3 seqid 194.

XX

KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;

KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;

KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;

KW CDR3; complementarity determining region 1.

OS Mus sp.

PN US2004175385-A1.

XX

PD 09-SEP-2004.

XX

PR 31-AUG-1998; 98US-00144886.

XX

PR 01-AUG-2002; 2002US-0400721P.

XX

PR (REGC) UNIV CALIFORNIA.

XX

PI Marks JD, Amerstorfer P;

XX

DR WPI; 2004-652009/63.

XX

PT New isolated antibody that neutralizes botulinum neurotoxin type A'

PT useful for diagnosing botulism or for treating pathologies associated

PT with botulinum neurotoxin poisoning.

XX

Example 4; SEQ ID NO 194; 110pp; English.

The invention describes an isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a specific clone where (I) binds to and neutralises botulinum neurotoxin type A (BONT/A). An isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone S25, C25, C39, IC6, 3D12, B4, 1F3, huc25, ARI, AR2, WRI(V), WRI(T), J-1,

CC (BONT/A). An isolated antibody, (I) that specifically binds to an epitope CC specifically bound by an antibody expressed by a clone chosen from clone CC C25, C25, C39, IC6, B4, 1F3, huC5, Ar1, Ar2, WRI(V), WRI(T), 3-1, CC 3-8, 3-10 and INGL, where (I) binds to and neutralizes botulinum CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II) CC comprising BONT/A neutralising epitope having an epitope that is CC specifically bound by an antibody expressed by clones as mentioned in (I) CC ; producing (I); and a composition (III) comprising several anti- CC botulinum neurotoxin antibodies, where each antibody is specific for a CC different epitope of a botulinum neurotoxin and the combination of CC antibodies shows greater toxin neutralisation than the single antibodies CC in surplus. The following are disclosed: a pharmaceutical composition CC comprising (II); and a kit comprising (I). (I) is useful for neutralising CC BONT/A antibody and for neutralising a botulinum neurotoxin which CC involves contacting neurotoxin with (I) in surplus, where each of (I) is CC specific for a different epitope of the botulinum neurotoxin and the CC combination of antibodies shows greater toxin neutralisation than the CC single antibodies in surplus. (I) is useful for diagnosing the botulism CC or for treating pathologies associated with botulinum neurotoxin CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I) CC enables rapid detection or diagnosis of botulism. This is the amino acid CC sequence of mouse heavy chain anti-BONT-antibody CDR3. XX SQ Sequence 15 AA:

Query Match 100.0%; Score 89; DB 8; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDWLWGDGALDV 15
Db 1 EPDWLWGDGALDV 15

RESULT 4
ADR38795

ID ADR38795 standard; peptide; 15 AA.
XX

AC ADR38795;

XX DT 02-DEC-2004 (first entry)

XX DE Mouse heavy chain anti-BONT-antibody CDR3 seqid 197.

XX KW anti-bacterial; antibody; botulinum neurotoxin type A; BONT/A;
KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;

KW CDR3; complementarity determining region 1.
XX OS Mus sp.

XX PN US2004175385-A1.

XX PD 09-SEP-2004.

XX PF 01-AUG-2003; 2003US-00632706.

XX PR 31-AUG-1998; 98US-00144886.

XX PR 01-AUG-2002; 2002US-0400721P.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Marks JD; Amerb dorfer P;

XX DR WPI; 2004-652009/63.

PT New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
XX with botulinum neurotoxin poisoning.

PS Example 4; SEQ ID NO 197; 110pp; English.

CC The invention describes an isolated antibody (I) that specifically binds

CC to an epitope specifically bound by an antibody expressed by a specific CC clone where (I) binds to and neutralises botulinum neurotoxin type A CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope CC specifically bound by an antibody expressed by a clone chosen from clone CC S25, C25, C39, IC6, B4, 1F3, huC5, Ar1, Ar2, WRI(V), WRI(T), 3-1, CC 3-8, 3-10 and INGL, where (I) binds to and neutralises botulinum CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II) CC comprising BONT/A neutralising epitope having an epitope that is CC specifically bound by an antibody expressed by clones as mentioned in (I) CC ; producing (I); and a composition (III) comprising several anti- CC botulinum neurotoxin antibodies, where each antibody is specific for a CC different epitope of a botulinum neurotoxin and the combination of CC antibodies shows greater toxin neutralisation than the single antibodies CC in surplus. The following are disclosed: a pharmaceutical composition CC comprising BONT/A neutralising epitope that is useful for neutralising CC BONT/A antibody and for neutralising a botulinum neurotoxin which CC involves contacting neurotoxin with (I) in surplus, where each of (I) is CC specific for a different epitope of the botulinum neurotoxin and the CC combination of antibodies shows greater toxin neutralisation than the CC single antibodies in surplus. (I) is useful for diagnosing the botulism CC or for treating pathologies associated with botulinum neurotoxin CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I) CC enables rapid detection or diagnosis of botulism. This is the amino acid CC sequence of mouse heavy chain anti-BONT-antibody CDR3.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDWLWGDGALDV 15
Db 1 EPDWLWGDGALDV 15

RESULT 5
ADR38798

ID ADR38798 standard; peptide; 15 AA.
XX

AC ADR38798;

XX DT 02-DEC-2004 (first entry)

XX DE Mouse heavy chain anti-BONT-antibody CDR3 seqid 200.

XX KW anti-bacterial; antibody; botulinum neurotoxin type A; BONT/A;
KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;

KW CDR3; complementarity determining region 1.
XX OS Mus sp.

XX PN US2004175385-A1.

XX PD 09-SEP-2004.

XX PF 01-AUG-2003; 2003US-00632706.

XX PR 31-AUG-1998; 98US-00144886.

XX PR 01-AUG-2002; 2002US-0400721P.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Marks JD; Amerb dorfer P;

XX DR WPI; 2004-652009/63.

PT New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
XX with botulinum neurotoxin poisoning.

PS Example 4; SEQ ID NO 200; 110pp; English.

XX
 CC The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, Ic6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WRI(V), WRI(T), 3-1,
 CC 3-8, 3-10 and INGL, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC specifically for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain anti-BoNT antibody CDR3.
 XX
 SQ sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY ||||| ||||| |||||
 Db 1 EPDWLWGDGRGALDV 15

RESULT 5
 ADR38729

ID ADR38729 standard; peptide; 15 AA.
 AC ADR38729;
 XX DT 02-DEC-2004 (first entry)

DE Mouse heavy chain variable region CDR3 seqid 131.

XX
 KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
 KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KW heavy chain variable region; complementarity determining region; CDR3.
 OS Mus sp.
 XX
 PN US2004175385-A1.
 XX
 PD 09-SEP-2004.
 XX
 PR 01-AUG-2003; 2003US-00632706.
 XX
 PR 31-AUG-1998; 98US-00144886.
 PR 01-AUG-2002; 2002US-0400721P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PT Marks JD, Amerstorfer P;
 XX
 DR MPI; 2004-652009/63.

New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.

XX

Example 3; SEQ ID NO 131; 110pp; English.

XX
 CC The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, Ic6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WRI(V), WRI(T), 3-1,
 CC 3-8, 3-10 and INGL, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain variable region complementarity determining
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDWLWGDGRGALDV 15
 Db 1 EPDWLWGDGRGALDV 15

RESULT 7
 ADR38801

ID ADR38801 standard; peptide; 15 AA.
 AC ADR38801;
 XX DT 02-DEC-2004 (first entry)

XX
 DE Mouse heavy chain anti-BoNT-antibody CDR3 seqid 203.
 KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
 KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
 KW CDR3; complementarity determining region 1.
 OS Mus sp.
 XX
 PN US2004175385-A1.
 XX
 PD 09-SEP-2004.
 XX
 PR 01-AUG-2003; 2003US-00632706.
 XX
 PR 31-AUG-1998; 98US-00144886.
 PR 01-AUG-2002; 2002US-0400721P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PT Marks JD, Amerstorfer P;
 XX
 DR MPI; 2004-652009/63.

PT New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.
 XX Example 4; SEQ ID NO 203; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 clone where (I) binds to and neutralizes botulinum neurotoxin type A
 (BONT/A). An isolated antibody (I), that specifically binds to an epitope
 specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C39, IC6, 3D12, B4, 1F3, huCC5, Ar1, Ar2, WRL(V), WR1(T), 3-1,
 3-8, 3-10 and INGL, where (I) binds to and neutralizes botulinum
 neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
 comprising BONT/A neutralising epitope having an epitope that is
 specifically bound by an antibody expressed by clones as mentioned in (I)
 ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 involves contacting neurotoxin with (I) in surplus, where each of (I) is
 specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain anti-BONT-antibody CDR3.
 XX SQ Sequence 15 AA;

Query Match 84.3%; Score 75; DB 8; Length 15;
 Best Local Similarity 93.3%; Pred. No. 0.00023; Mismatches 1; Indels 0; Gaps 0;

| | |
|----|-----------------------|
| Qy | 1 EPDWLWGDGRGALDV 15 |
| Db | 1 EPDRLLWGDGRGALDV 15 |

RESULT 8

| | |
|----|--|
| ID | ABG20331 |
| XX | |
| AC | ABG20331; |
| XX | |
| DT | 13-FEB-2002 (first entry) |
| XX | |
| DE | Novel human diagnostic protein #20322. |
| XX | |
| KW | Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | WO200175067-A2. |
| XX | |
| PD | 11-OCT-2001. |
| XX | |
| PF | 30-MAR-2001; 2001WO-US008631. |
| XX | |
| PR | 31-MAR-2000; 2000US-0050217. |
| XX | |
| PR | 23-AUG-2000; 2000US-00649167. |
| XX | |
| PA | (HYSE-) HYSEQ INC. |
| XX | |
| PI | Drmanc RT, Liu C, Tang YT; |
| XX | |
| DR | WPI; 2001-639362/73. |
| XX | |
| DR | N-PSDB; AAS84518. |

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

CLAIM 20; SEQ ID NO 50690; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probe, polymerase chain
 reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 in diagnostics as expressed sequence tags for identifying expressed
 genes. (I) is useful in gene therapy techniques to restore normal
 activity of (II) or to treat disease states involving (II). (II) is
 useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 supplement. (II) and its binding partners are useful in medical imaging
 CC of bites expressing (II). (I) and (II) are useful for treating disorders
 involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG3077 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 334 AA;

Query Match 57.3%; Score 51; DB 4; Length 334;
 Best Local Similarity 53.3%; Pred. No. 23; Mismatches 5; Indels 0; Gaps 0;

| | |
|----|-------------------------|
| Qy | 1 EPDWLWGDGRGALDV 15 |
| Db | 263 KPWSSWGPSPGWIDV 277 |

RESULT 9

| | |
|----|--|
| ID | ADJ98189 |
| XX | |
| AC | ADJ98189; |
| XX | |
| DT | 06-MAY-2004 (first entry) |
| XX | |
| DE | Prochlorococcus marinus str MIT 9313 phytol kinase protein. |
| XX | |
| KW | phytol kinase; tocopherol biosynthesis; plant; drought resistance; enzyme. |
| XX | |
| OS | Prochlorococcus marinus str. MIT 9313. |
| XX | |
| PN | WO2004013312-A2. |
| XX | |
| PD | 12-FEB-2004. |
| XX | |
| PF | 05-AUG-2003; 2003WO-US025276. |
| XX | |
| PR | 05-AUG-2002; 2002US-0400683P. |
| XX | |
| PR | 05-AUG-2003; 2003US-0063458. |
| XX | |
| PA | (MONS) MONSANTO TECHNOLOGY LLC. |
| XX | |
| PI | Norris SR, Lincoln K, Abd MS, Eilers R, Hartsvyker KK; |
| PI | Hirschberg J, Karunandaa B, Moshiri F, Stein JC, Valentin HB; |
| PI | Venkatesh TV; |
| XX | |
| DR | WPI; 2004-157125/15. |

PT New phytol kinase polynucleotides, useful in mediating tocopherol biosynthesis and in producing plants with increased drought resistance.

PT biosynthesis and in producing plants with increased drought resistance.

PX

PS Claim 1; SEQ ID NO 27; 189pp; English.

XX

CC The invention relates to a novel substantially purified nucleic acid molecule encoding a phytol kinase. The nucleic acid molecules and polypeptides of the invention may be useful in mediating tocopherol biosynthesis and in producing plants with increased drought resistance. The current sequence is that of a phytol kinase protein of the invention.

XX

SQ Sequence 201 AA;

| | | | | | | | |
|-----------------------|-------|----------------|----|------------|---|--------|-----|
| Query Match | 53.9% | Score | 48 | DB | 8 | Length | 201 |
| Best Local Similarity | 50.0% | Pred. No. | 39 | | | | |
| Matches | 6 | Conservative | 4 | Mismatches | 2 | Indels | 0 |
| Qy | 2 | PDWLMGDRLG 13 | | Gaps | 0 | | |
| Db | 123 | PNWLWQKRSI 134 | | | | | |

RESULT 10

ID ABO66015 standard; protein, 229 AA.

XX

AC ABO66015;

XX

DT 29-JUL-2004 (first entry)

XX

DB Klebsiella pneumoniae polypeptide seqid 12532.

XX

KW Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; Vaccine.

OS Klebsiella pneumoniae.

XX

PN US6610836-B1.

XX

PD 26-AUG-2003.

XX

PP 27-JAN-2000; 2000US-00489039.

PR 29-JAN-1999; 99US-011774P.

XX

PA (GENO-) GENOME THERAPEUTICS CORP.

PI Bretton GL, Osborne M;

XX

DR WPI: 2003-895346/82.

DR N-PSDB; ACH99566.

XX

PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.

XX

PS Disclosure; SEQ ID NO 12532; 932pp; English.

XX

The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention.

XX

SQ Sequence 229 AA;

| | | | | | | | |
|-----------------------|-------|-----------------|---------|------------|---|--------|-----|
| Query Match | 53.9% | Score | 48 | DB | 3 | Length | 775 |
| Best Local Similarity | 53.8% | Pred. No. | 1.6e-02 | | | | |
| Matches | 7 | Conservative | 1 | Mismatches | 5 | Indels | 0 |
| Qy | 2 | PDWLMGDRLG 14 | | Gaps | 0 | | |
| Db | 195 | PDWQIWAKSGR 207 | | | | | |

RESULT 11

ID AAB13560 standard; protein, 775 AA.

XX

AC AAB13560;

XX

DT 06-MAR-2001 (first entry)

XX

DE Streptomyces globisporus C-1027 gene cluster ORF -1.

XX

PR 06-JAN-1999; 99US-0115434P.

PR 05-JAN-2000; 2000US-00477962.

XX

(REGC) UNIV CALIFORNIA.

XX

PI Shen B, Liu W, Christenson SD, Standage S;

XX

WPI: 2000-465947/40.

DR N-PSDB; AAA63348, AAA63349.

XX

PT Isolated nucleic acid comprising a nucleic acid encoding any of C-1027 open reading frames (ORFs) -7 to 42, excluding ORF 9 (cagA), useful for the production of enediyne C-1027 antitumor antibiotics.

XX

PS Claim 15; Page 87-91; 160pp; English.

XX

The present sequence is the protein which is encoded by open reading frame -1 of the Streptomyces globisporus enediyne C-1027 gene cluster. Enediyne C-1027 is an antibiotic, consisting of an apoprotein and a non-peptide chromophore, which acts by damaging DNA. The sequences within the gene cluster, and the proteins they encode, can be used in the treatment of cancer, along with antagonists of the protein. This protein is an ABC transport/UVRA-like protein

XX

SQ Sequence 775 AA;

| | | | | | | | |
|-----------------------|-------|-----------------|---------|------------|---|--------|-----|
| Query Match | 53.9% | Score | 48 | DB | 3 | Length | 775 |
| Best Local Similarity | 53.8% | Pred. No. | 1.6e-02 | | | | |
| Matches | 7 | Conservative | 1 | Mismatches | 5 | Indels | 0 |
| Qy | 2 | PDWLMGDRLG 14 | | Gaps | 0 | | |
| Db | 195 | PDWQIWAKSGR 207 | | | | | |

RESULT 12

ID AAY48365

XX

AC AAY48365 standard; protein, 59 AA.

XX

AAAY48365;

XX

DT 08-DCC-1999 (first entry)

XX

DR Human prostate cancer-associated protein 62.

XX

PR Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy;

XX

KW cancer; tissue specificity; human.

XX

OS Homo sapiens.

XX
PN DE19811194-A1.
XX
PD 16-SEP-1999.

XX
PR 10-MAR-1998; 98DB-01011194.

XX
PT 10-MAR-1998; 98DE-01011194.

XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX
PI Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
XX DR WPI; 1999-519629/44.
XX N-PSDB; AAS86711.

XX
PT New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX
PS Claim 20; SEQ ID NO 52883; 103pp; English.

XX
CC This invention describes novel nucleic acid sequences (A) that are
CC expressed at high level in normal prostatic tissue. Polypeptides (I)
CC encoded by (A) are used: (a) for identifying agents for treatment of
CC prostatic cancer and (b) for therapy of prostate cancer, optionally where
CC expressed by gene therapy methods. (A) is also used to isolate full-
CC length genes (for gene therapy) and for recombinant production of (I),
CC which can be used to raise specific antibodies. (A) are identified by
CC assembly of ESTs (expressed sequence tags) before these are analyzed for
CC expression pattern (tissue specificity). This approach eliminates many of
CC the false results, as regards tissue specificity, associated with known
CC methods that use single (usually short) ESTs. Any8304-Y48456 represent
CC peptides encoded by the expressed sequence tags described in the method
of the invention

XX
SQ Sequence 59 AA:
XX

Query Match 52.8%; Score 47; DB 2; Length 59;
Best Local Similarity 87.5%; Pred. No. 15; Mismatches 7; Conservative 0; Indels 1; Gaps 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 WLWGDGRG 11
Db 44 WLWGSGRG 51.

XX
SQ Sequence 59 AA:
XX

Query Match 52.8%; Score 47; DB 2; Length 59;
Best Local Similarity 87.5%; Pred. No. 15; Mismatches 7; Conservative 0; Indels 1; Gaps 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EPDNWLWGDGRGAL 13
Db 93 EQNWLLWCBRGMV 105

XX
SQ Sequence 455 AA:
XX

Query Match 52.8%; Score 47; DB 4; Length 455;
Best Local Similarity 53.8%; Pred. No. 1.3e+02; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EPDNWLWGDGRGAL 13
Db 93 EQNWLLWCBRGMV 105

RESULT 13

ABG2252⁴
ID ABG2252 standard; protein; 455 AA.

AC ABG2252;
XX
DT 18-FEB-2002 (first entry)

DB Novel human diagnostic protein #22515.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo Sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PP 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.

Pi Drmanac RT, Liu C, Tang YI;
XX
WPI: 2001-639362/73.
DR N-PSDB; AAS86711.

XX
PT New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX
PS Claim 20; SEQ ID NO 52883; 103pp; English.

XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridization probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 455 AA:
XX

Query Match 52.8%; Score 47; DB 4; Length 455;
Best Local Similarity 53.8%; Pred. No. 1.3e+02; Mismatches 3; Indels 0; Gaps 0;

XX
AC ADS23387;
XX
DT 02-DEC-2004 (first entry)

DB Bacterial polypeptide #12420.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.

XX
PN US2003233675-A1.

XX
PD 18-DEC-2003.

XX
PT 20-FEB-2003; 2003US-00369493.

XX
PR 21-FEB-2002; 2002US-0360039P.

PA (CAO/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 PI Cao Y., Hinkle GJ, Slater SC, Chen X, Goldman BS;
 DR WPI; 2004-061375/06.

PT New recombinant DNA construct comprising a promoter positioned to provide expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
 PT Claim 1; SEQ ID NO 12420; 122Pp; English.
 XX
 CC The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. An method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway, modified seed oil or protein yield and/or homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 904 AA;
 Query Match 52.8%; Score 47; DB 8; Length 904;
 Best Local Similarity 70.0%; Pred. No. 2.6e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 WLWGRGAL 13
 Db 460 WLLWGDKTS 469

RESULT 15
 AAM24399
 ID AAM24399 Standard; protein; 186 AA.
 XX
 AC AAM24399;
 DT 12-OCT-2001 (first entry)
 XX
 DB Human EST encoded protein SEQ ID NO: 1924.
 XX
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
 XX
 OS Homo sapiens.
 XX
 PN WO200154477-A2.
 XX
 PD 02-AUG-2001.

PF 25-JAN-2001; 200100-US002687.
 XX
 PR 25-JAN-2000; 200000S-00491404.
 PR 17-JUL-2000; 200000S-00517746.
 PR 03-AUG-2000; 200000S-00531451.
 PR 15-SEP-2000; 200000S-0063870.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Zhou P, Oian XB, Wang Z, Chen R, Asundi V;
 XX
 DR N-PSDB; AAH99056.
 XX
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use.
 XX
 PS Claim 20; Page 1235; 1275pp; English.

CC The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention

SQ Sequence 186 AA;

Query Match 51.7%; Score 46; DB 4; Length 186;
 Best Local Similarity 53.3%; Pred. No. 71;
 Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;
 Qy 2 PDWLWGG--DRGALD 14
 Db 168 PGWLWGGKGRRGLN 182

Search completed: December 4, 2005, 04:44:59
 Job time : 132.312 Secs

| | | | | | | | | | |
|---|--|--|----|--------|---------------------------|-------|------------------|---------------|-------------|
| Copyright (c) 1993 - 2005 | GenCore version 5.1.6 | | | | | | | | |
| Run on: | December 4, 2005, 04:31:45 ; Search time 21.25 Seconds | | | | | | | | |
| Title: | US-10-632-706-197 | | | | | | | | |
| Perfect score: | 89 | | | | | | | | |
| Sequence: | 1 EPDWLWGDRCALDV 15 | | | | | | | | |
| Scoring table: | BLOSUM62 | | | | | | | | |
| | Gapop 10.0 , Gapext 0.5 | | | | | | | | |
| Searched: | 283416 seqs, 96216763 residues | | | | | | | | |
| Total number of hits satisfying chosen parameters: | 283416 | | | | | | | | |
| Minimum DB seq length: | 0 | | | | | | | | |
| Maximum DB seq length: | 200000000 | | | | | | | | |
| Post-processing: | Minimum Match 0% | | | | | | | | |
| | Maximum Match 100% | | | | | | | | |
| Database : | Listing first 45 summaries | | | | | | | | |
| | PIR 80.0* | | | | | | | | |
| 1: | pir1:* | | | | | | | | |
| 2: | pir2:* | | | | | | | | |
| 3: | pir3:* | | | | | | | | |
| 4: | pir4:* | | | | | | | | |
| Pred. No. | is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | | | | | | | | |
| SUMMARIES | | | | | | | | | |
| Result No. | Score | | | | | | | | |
| | Query | | | | | | | | |
| | Match Length DB ID | | | | | | | | |
| 1 | 46 51.7 373 2 D71142 | | | | | | | | |
| 2 | 45.5 51.1 298 2 AE3234 | | | | | | | | |
| 3 | 45 50.6 203 2 G70595 | | | | | | | | |
| 4 | 45 50.6 601 2 AG0565 | | | | | | | | |
| 5 | 44.5 50.0 1076 2 T30842 | | | | | | | | |
| 6 | 44 49.4 237 2 G82768 | | | | | | | | |
| 7 | 44 49.4 409 2 BT5010 | | | | | | | | |
| 8 | 44 49.4 491 2 T10930 | | | | | | | | |
| 9 | 44 49.4 601 2 E95296 | | | | | | | | |
| 10 | 43 48.3 321 2 ST77614 | | | | | | | | |
| 11 | 43 48.3 462 2 TS50422 | | | | | | | | |
| 12 | 43 48.3 683 2 JC5393 | | | | | | | | |
| 13 | 43 48.3 685 2 JC5392 | | | | | | | | |
| 14 | 43 48.3 698 2 AB2593 | | | | | | | | |
| 15 | 42.5 47.8 315 2 H83256 | | | | | | | | |
| 16 | 42 47.2 71 2 G98356 | | | | | | | | |
| 17 | 42 47.2 139 2 AG2925 | | | | | | | | |
| 18 | 42 47.2 397 2 BS53240 | | | | | | | | |
| 19 | 42 47.2 408 1 A69819 | | | | | | | | |
| 20 | 42 47.2 482 2 AI0554 | | | | | | | | |
| 21 | 42 47.2 482 2 E90688 | | | | | | | | |
| 22 | 42 47.2 482 2 T46944 | | | | | | | | |
| 23 | 42 47.2 482 2 A85539 | | | | | | | | |
| 24 | 42 47.2 482 2 G64771 | | | | | | | | |
| 25 | 42 47.2 486 2 T51431 | | | | | | | | |
| 26 | 42 47.2 486 2 H87311 | | | | | | | | |
| 27 | 42 47.2 492 2 T38156 | | | | | | | | |
| 28 | 42 47.2 566 2 H884037 | | | | | | | | |
| 29 | 42 47.2 604 2 T49577 | | | | | | | | |
| ALIGNMENTS | | | | | | | | | |
| RESULT 1 | D71142 | | | | | | | | |
| | hypothetical protein PH0351 - Pyrococcus horikoshii | | | | | | | | |
| C;Species: | Pyrococcus horikoshii | | | | | | | | |
| C;Date: | 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004 | | | | | | | | |
| C;Accession: | D71142 | | | | | | | | |
| R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Ohtoku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kubida, N.; Oguchi, A.;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a | | | | | | | | | |
| A;Reference number: | AY1000; PMID:9834137; PMID:9679194 | | | | | | | | |
| A;Accession: | D71142 | | | | | | | | |
| A;Status: | preliminary; nucleic acid sequence not shown; translation not shown | | | | | | | | |
| A;Molecule type: | DNA | | | | | | | | |
| A;Residues: | 1-373 < KAN> | | | | | | | | |
| A;Cross-references: | UNIPROT:058089; UNIPARC:UP10000062DB7; GB:AP000002; NID:93236129; PII: A;Experimental source: | strain OR3 | | | | | | | |
| A;Note: | this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics: | | | | | | | | |
| A;Gene: | PH0351 | | | | | | | | |
| Query | Match | Score | DB | Length | Best Local Similarity | DB 2; | Score 46; | DB 2; | Length 373; |
| | | | | | 43.5% | 1; | Pred. No. 19; | Mismatches 1; | Indels 10; |
| | | | | | | | Conserveative 1; | | Gaps 1; |
| OY | 2 | PDWLIW-----GIRGALD 14 | Db | 318 | PGWLIWGLLLMGRIGNGPALD 340 | | | | |
| RESULT 2 | AE3234 | | | | | | | | |
| | | transcriptional regulator, LYBR family | | | | | | | |
| C;Species: | Agrobacterium tumefaciens | | | | | | | | |
| C;Date: | 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 | | | | | | | | |
| C;Accession: | AE3234 | | | | | | | | |
| R;Knod, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, L.; Erge, G.; Gillet, W.; Guelthner, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClellan, Karp, P.; Romero, P.; Zhang, S. | | | | | | | | | |
| A;Reference number: | AB2577; MUIB:21608550; PMID:11743193 | | | | | | | | |
| A;Accession: | AE3234 | | | | | | | | |
| A;Status: | preliminary | | | | | | | | |
| A;Molecule type: | DNA | | | | | | | | |
| A;Residues: | 1-298 < KAR> | | | | | | | | |
| A;Cross-references: | UNIPROT:Q8U680; UNIPARC:UP1000002764; GB:AE008690; PIDN:AA146291.1; A;Experimental source: | strain CS8 (Dupont) | | | | | | | |
| C;Genetics: | | | | | | | | | |
| A;Gene: | gcva | | | | | | | | |

A;genome: plasmid
C;Superfamily: regulatory protein ampr

Query Match 51.1%; Score 45.5; DB 2; Length 298;

Best Local Similarity 56.2%; Pred. No. 18; Mismatches 9; Conservative 0; Indels 1; Gaps 1;

Qy 1 RPPMLW-GDRGALDV 15
Db 199 EPDMLRWCAQAGVADY 214

RESULT 3

G70595 probable entD protein - *Mycobacterium tuberculosis* (strain H37Rv)

C;Species: *Mycobacterium tuberculosis*

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C;Accession: G70595

R;Cole, S.T.; Brosh, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

R;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

R;Rajandream, M.A.; Rogers, J.; Rutteer, S.; Seeger, K.; Skelton, S.; Square, S.

Nature 393, 537-544, 1998

A;Authors: Sparreboom, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: G70595

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-203 <COL>

A;Experimental source: strain H37Rv

C;Genetics:

A;Gene: entD

C;Superfamily: cofactor-dependent phosphoglycerate mutase; phosphoglycerate mutase homolog

Query Match 50.6%; Score 45; DB 2; Length 203;

Best Local Similarity 85.7%; Pred. No. 15; Mismatches 6; Conservative 1; Indels 0; Gaps 0;

Qy 1 EPDMLW 7
Db 103 EPDMLW 109

RESULT 4

G0066 probable AMP-binding enzyme-family protein YPO0537 [imported] - *Yersinia pestis* (strain

C;Species: *Yersinia pestis*

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C;Accession: AG0066

R;Pilkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

R;de Jong, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

R;deno-Tarraga, A.M.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AG0066

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-237 <SM>

A;Cross-references: UNIPROT:Q9PFC4; UNIPARC:UPI0000024F4; GB:AB003916; GB:AB003849; NID

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arrieta, P.; Abreu, F.A.; Aencencio, M.; Alvaranga, R.; A

R;Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carrero, D.M.; Carter, H.

R;as-Feto, E.; Docena, C.; Bl-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

R;submitted to GenBank, June 2000

R;A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, S.C.; Franca, M.C.; Frohm

R;J.D.; Junqueira, M.L.; Kempfer, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuramitsu, E.E.; Laigr

R;chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, R.

R;A;Authors: Martins, E.M.F.; Matsumura, A.Y.; Menck, C.F.M.; Mikacki, C.Y.; Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A.

R;Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Swasek

R;A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; da Silva Jr., W.A.; da Silveir

R;M.; Tsuhako, M.H.; Valladares, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

R;A;Reference number: A59328

R;A;Contents: annotation

R;A;Gene: YPO0537

C;Genetics:

C;Superfamily: *Synechocystis* long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homolog

Query Match 50.6%; Score 45; DB 2; Length 601;

Best Local Similarity 64.3%; Pred. No. 42; Mismatches 9; Conservative 0; Indels 5; Gaps 0;

Qy 1 EPDWLWGGDRGALDV 14
Db 440 EDGLWLKGDAQGALD 453

RESULT 5
T30842 berine-repeat antigen 3 - *Plasmodium vivax*

C;Species: *Plasmodium vivax*

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C;Accession: T30842

R;Klefer, M.C.; Crawford, K.A.; Boley, L.J.; Landsberg, K.E.; Gibson, H.L.; Kaslow, D.C.; Mol. Biochem. Parasitol. 78, 55-65, 1996

A;Title: Identification and cloning of a locus of serine repeat antigen (bera)-related genes

A;Reference number: Z20898; MUID:96408670; PMID:8813677

A;Accession: T30842

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-1076 <KIE>

A;Cross-references: UNIPROT:Q26154; UNIPARC:UPI00000809B3; EMBL:U51723; NID:91381087; PII

C;Genetics:

A;Intron: 12/1; 253/1; 302/1

A;Note: V-SERA 3

C;Superfamily: *Plasmodium vivax* serine-repeat antigen

Query Match 50.0%; Score 44.5; DB 2; Length 1076;

Best Local Similarity 40.9%; Pred. No. 87; Mismatches 9; Conservative 2; Indels 7; Gaps 1;

Matches 9; Indels 7; Gaps 1;

Qy 1 EPDMIL-----WGDRGALDV 15
Db 743 KPYWNLLQNSWKGKHWGDKGTPKV 764

RESULT 6

G87768 virulence protein XP0754 [imported] - *Xylella fastidiosa* (strain 9a5c)

C;Species: *Xylella fastidiosa*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: G82768

R;anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequenc

R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc

A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: G82768

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-237 <SM>

A;Cross-references: UNIPROT:Q9PFC4; UNIPARC:UPI0000024F4; GB:AB003916; GB:AB003849; NID

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arrieta, P.; Abreu, F.A.; Aencencio, M.; Alvaranga, R.; A

R;Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carrero, D.M.; Carter, H.

R;as-Feto, E.; Docena, C.; Bl-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

R;submitted to GenBank, June 2000

R;A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, S.C.; Franca, M.C.; Frohm

R;J.D.; Junqueira, M.L.; Kempfer, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuramitsu, E.E.; Laigr

R;chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, R.

R;A;Authors: Martins, E.M.F.; Matsumura, A.Y.; Menck, C.F.M.; Mikacki, C.Y.; Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A.

R;Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Swasek

R;A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; da Silva Jr., W.A.; da Silveir

R;M.; Tsuhako, M.H.; Valladares, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

R;A;Reference number: A59328

R;A;Contents: annotation

R;A;Gene: XP0754

C;Genetics:

C;Superfamily: type IV secretory pathway, VirJ component

Query Match 49.4%; Score 44; DB 2; Length 237;

Best Local Similarity 58.3%; Pred. No. 24; Mismatches 7; Conservative 1; Indels 4; Gaps 0;

Matches 7; Indels 0; Gaps 0;

Qy 4 WLWLGDRGALDV 15
Db 151 WLWLGDRGALDV 162

RESULT 7
 B75010 hypothetical protein PAB1063 - Pyrococcus abyssi (strain Orsay)
 C;Species: Pyrococcus abyssi
 C;Accession: B75010 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 R;Anonymous, Genoscope submitted to the EMBL Data library, July 1999
 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
 A;Reference number: A75001
 A;Accession: B75010
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-409 <KOR>
 A;Cross-references: UNIPROT:Q9Y92; UNIPARC:UPI000034560; GB:AJ248288; GB:AL096836; NID
 A;Experimental source: strain Orsay
 C;Genetics:
 A;Gene: PAB1063

Query Match 49.4%; Score 44; DB 2; Length 409;
 Best Local Similarity 39.1%; Pred. No. 41;
 Matches 9; Conservative 2; Mismatches 2; Indels 10; Gaps 1;

RESULT 8
 T10930 C2.21 protein - Streptomyces coelicolor
 C;Species: Streptomyces coelicolor
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C;Accession: T10930
 R;Parkhill, J.; Barrell, B.G.; Ralston, M.A.
 submitted to the EMBL Data Library, August 1998
 A;Reference number: Z17215
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-491 <PRA>
 A;Cross-references: UNIPROT:Q86654; UNIPARC:UPI0000DAD67; EMBL:AL031231; NID:e1315070;
 A;Experimental source: strain A3(2)
 A;Gene: 3C3.21

Query Match 49.4%; Score 44; DB 2; Length 491;
 Best Local Similarity 61.5%; Pred. No. 49;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 3 DMU1WGDRGALDV 15
 Qy ::|||:|||||:|||:
 Db 413 EFW1WGDRGALDV 425

RESULT 9
 E93296 probable ABC-type iron transport system protein SMA0525 [imported] - Sinorhizobium meliloti
 C;Species: Sinorhizobium meliloti
 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C;Accession: E93296
 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barlow-Hubler, F.; Bowe
 ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
 Proc. Natl. Acad. Sci. U.S.A., 98, 9883-9888, 2001
 A;Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*
 A;Reference number: A95262; MUID:21396509; PMID:11481432
 A;Accession: E93296
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-601 <KOR>
 A;Cross-references: UNIPROT:Q930C1; UNIPARC:UPI0000CB03E; GB:AE006469; PIDN:AAK64935.1;
 A;Experimental source: strain 1021; megaplasmid psymA

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 pala, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federpel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelauze,
 heault, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Weiss, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A;Reference number: A96039; MUID:21368234; PMID:11474104
 A;Contents: annotation
 C;Genetics:
 A;Gene: SMA0525
 A;Genome: plasmid

Query Match 49.4%; Score 44; DB 2; Length 601;
 Best Local Similarity 85.7%; Pred. No. 59;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 169 PDWLAWG 175
 Qy 2 PDWLAWG 8
 Db 169 PDWLAWG 175

RESULT 10
 S77614 phosphoribosylformylglycaminidine synthase (EC 6.3.5.3) component II - Synechococcus sp.
 N;Alternate names: FGAM synthetase
 C;Species: Synechococcus sp.
 A;Variety: PCC 7942
 C;Date: 29-Jul-1997 #sequence_revision 24-Oct-1998 #text_change 31-Dec-2004
 C;Accession: S77614; S77613
 R;Liu, Y.; Trainor, N.F.
 submitted to the EMBL Data Library, August 1995
 A;Description: Unusual gene arrangement for the putative chromosome replication origin a:
 A;Reference number: S77614
 A;Accession: S77614
 A;Molecule type: DNA
 A;Residues: 1-112 <LIW>
 A;Cross-references: UNIPROT:Q55037; UNIPARC:UPI000176276; EMBL:U33322; NID:9974613; PIDN:
 A;Experimental source: PCC 7942
 R;Liu, Y.; Trainor, N.F.; Golden, S.S.; Kondo, T.; Johnson, C.H.
 Mol. Microbiol. 20, 1071-1081, 1996
 A;Title: Circadian expression of genes involved in the purine biosynthetic pathway of cyanobacteria
 A;Reference number: S77612; MUID:96405630; PMID:8809759
 A;Accession: S77613
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 113-321 <LIW>
 A;Cross-references: UNIPARC:UPI0000BBE4A4; EMBL:U33221
 A;Experimental source: PCC 7942
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
 C;Genetics:
 A;Gene: purL
 C;Function:
 A;Description: catalyzes the condensation of 5'-phosphoribosylformylglycaminide with ATP,
 A;Pathway: purine nucleotide biosynthesis
 A;Note: fourth step in pathway
 C;Keywords: ligase; purine nucleotide biosynthesis

Query Match 48.3%; Score 43; DB 2; Length 321;
 Best Local Similarity 63.6%; Pred. No. 46;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 2 PDWLWGREGA 12
 Qy |||||: :|||:
 Db 240 PDWLFAASGA 250

RESULT 11
 T50422 homolog to yeast orf Yor166c. [imported] - fission yeast (*Schizosaccharomyces pombe*)
 C;Species: Schizosaccharomyces pombe
 C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
 C;Accession: T50422

R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, February 2000

A;Reference number: Z225039

A;Accession: T50422

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-462 <SEE>

A;Cross-references: UNIPROT:Q9P7J1; UNIPARC:UPI00006FA1B; EMBL:AL157991; PIDN:CAB76224

A;Experimental source: strain 972h(-); cosmid c24B10

C;Genetics:

A;Gene: SPDB:SPCC24B10.15

A;Map position: 3

Query Match 48.3%; Score 43; DB 2; Length 462;

Best Local Similarity 55.6%; Pred. No. 65; Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DWLWGDGRG 11

Db 394 EPMLWAERG 402

RESULT 12

JC3393 zinc finger protein KF-1 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 04-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004

C;Accession: JC3393

R;Yasojima, K.; Tsujimura, A.; Miuno, T.; Shigejoshi, Y.; Inazawa, J.; Kikuno, R.; Kuroki, T.

Biochem. Biophys. Res. Commun. 231, 481-487, 1997

Title: Cloning of human and mouse cDNAs encoding novel zinc finger proteins expressed

A;Reference number: JC3392; MUID:97223484; PMID:9070305

A;Accession: JC3393

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-683 <YAS>

A;Experimental source: brain

C;Comment: This protein is involved in membranous protein-sorting apparatus similarly to

C;Genetics:

A;Gene: kfl-1

A;Superfamily: zinc finger protein KF-1 precursor, RING finger homology

F;1-19/Domain: signal sequence #status predicted <SIG>

F;325-344/Domain: transmembrane #status predicted <TM1>

F;352-380/Domain: transmembrane #status predicted <TM2>

F;617-668/Domain: RING finger homology <RNG>

Query Match 48.3%; Score 43; DB 2; Length 685;

Best Local Similarity 85.7%; Pred. No. 95; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPDNLW 7

Db 605 EPDNLW 611

RESULT 14

A82593 hypothetical protein Xf2169 [imported] - Xylella fastidiosa (strain 945c)

C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: A82593

R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A83328 below

A;Accession: A82593

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-698 <SM>

A;Cross-references: UNIPROT:Q9PBH5; UNIPARC:UPI0000C2968; GB:AE004030; GB:AB003849; NID

A;Experimental source: strain 945c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acecio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, H

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froeh

J.D.; Jungueira, M.L.; Kemper, B.I.; Kitajima, J.P.; Krieger, J.B.; Kuramata, M.V.; Martins, S

Chado, M.A.; Madeira, M.H.F.; Madeira, C.L.; Marinho, E.C.; Miyaki, C.Y.;

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmeri, R.; Rodrigues, V.V.; Rosa, A.J. de M.; de Rosa, H.V.; Santelli, R.V.; Swasak

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsunhao, M.H.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

Query Match 48.3%; Score 43; DB 2; Length 683;

Best Local Similarity 85.7%; Pred. No. 95; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPDNLW 7

Db 603 EPDNLW 609

RESULT 13

JC3392 zinc finger protein KF-1 precursor - human

C;Species: Homo sapiens (man)

C;Date: 04-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004

C;Accession: JC3392

R;Yasojima, K.; Tsujimura, A.; Mizuno, T.; Shigeyoshi, Y.; Inazawa, J.; Kikuno, R.; Kume

Biochem. Biophys. Res. Commun. 231, 481-487, 1997

Title: Cloning of human and mouse cDNAs encoding novel zinc finger proteins expressed

A;Reference number: JC3392; MUID:97223484; PMID:9070305

A;Accession: JC3392

A;Status: nucleic acid sequence not shown

RESULT 15

H83276 probable lipase PA2949 [imported] - Pseudomonas aeruginosa (strain PA01)

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 12-Jul-2004

C;Accession: H83276

R;Stover, C.K.; Pham, X.Q.; Brin, A.L.; Mizoguchi, S.D.; Warren, P.; Rickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.; Nature 406, 959-964, 2000
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A;Reference number: A82950; MOID:2043737; PMID:10984043
A;Accession: H83276
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-315 <STO>
A;Cross-references: UNIPROT:Q9KJG6; UNIPARC:UPI0000C4EC6; GB:AE004721; GB:AE004091; NCBI
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2949
C;Superfamily: tropinesterase

Query Match 47.8%; Score 42.5; DB 2; Length 315;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 10; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 2 PDWLLWGDGRG-ALDV 15
Db 249 ||||| ||||| |||||
PTLLLWGDRDRVLDV 263

Search completed: December 4, 2005, 04:53:46
Job time : 33.25 sec

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| OM protein - protein search, using sw model | | | | | | | | | |
|--|-------------------|-------------------------------|-------------------------|--------------------------|--|--|------------------------------------|-----------------------------------|----------------------------|
| Run on: December 4, 2005, 04:31:36 ; Search time 136.875 seconds | | | | | | | | | |
| Maximum DB seq length: 0 77.318 Million cell updates/sec | | | | | | | | | |
| Title: US-10-632-706-197 | Perfect score: 89 | Sequence: 1 EPDWLWGDGRGLDV 15 | Scoring table: BLOSUM62 | Gapop 10.0 , Gapext: 0.5 | Searched: 2166443 Seqs, 705528306 residues | Total number of hits satisfying chosen parameters: 2166443 | Maximum DB seq length: 0 200000000 | Post-processing: Minimum Match 0% | Listing first 45 summaries |
| Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | 1: | uniprot_sprot:* | 2: | uniprot_trembl:* | | | | | |
| SUMMARIES | | | | | | | | | |
| Result No. | Score | Query Match | Length | DB ID | Description | RESULT 1 | RESULT 2 | ALIGMENTS | |
| 1 | 50 | 56.2 | 441 | 2 Q5IQ90_SILPO | Q5IQ90_SILPO PRELIMINARY; PRT; 441 AA. | Q5IQ90_SILPO | Q5IQ90_SILPO | Q5IQ90_SILPO | Q5IQ90_SILPO |
| 2 | 49 | 55.1 | 208 | 2 Q5YQ86_NOCTA | Q5YQ86_NOCTA / DSM 15171; RT STRAIN-DSS-3 / ATCC 700808 / DOI=10.1038/nature0170; | Q5YQ86_NOCTA | Q5YQ86_NOCTA | Q5YQ86_NOCTA | Q5YQ86_NOCTA |
| 3 | 49 | 55.1 | 405 | 2 Q5NqJ9_SYN66 | Moran M.A., Buchan A., Gonzalez J.M., Heidelberg J.F., Whitman W.B., Kiene R.P., Henriksen J.R., King G.M., Belas R., Fugua C., Brinkac L.M., Lewis M., Johni S., Weaver B., Pai G., Eisen J.A., Rane E., Sheldon W.M., Ye W., Miller T.R., Carlton J., Rakoc D.A., Paulsen I.T., Ren O., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Robovitz M.J., Haft D.H., Selengut J., Ward N.; RT "Genome sequence of Silicibacter pomeroyi reveals adaptations to the marine environment."; Nature 432:910-913(2004). | Q5NqJ9_SYN66 | Q5NqJ9_SYN66 | Q5NqJ9_SYN66 | Q5NqJ9_SYN66 |
| 4 | 49 | 55.1 | 779 | 2 Q6h084_FREDI | DR EMBL:CP000031; AAV95831.1; -; Genomic_DNA. | Q6h084_FREDI | Q6h084_FREDI | Q6h084_FREDI | Q6h084_FREDI |
| 5 | 48 | 53.9 | 217 | 2 Q7V3U3_PROMI | DR InterPro: IPR010556; DCTM; DR InterPro: IPR00282; Deda; DR Pfam: PRO6808; DCDM; I. | Q7V3U3_PROMI | Q7V3U3_PROMI | Q7V3U3_PROMI | Q7V3U3_PROMI |
| 6 | 48 | 53.9 | 262 | 2 Q8E7F9_SHEDR | DR Pfam: PR00597; Deda; I. | Q8E7F9_SHEDR | Q8E7F9_SHEDR | Q8E7F9_SHEDR | Q8E7F9_SHEDR |
| 7 | 48 | 53.9 | 426 | 2 Q5SS00_CRIME | KW Complete proteome. | Q5SS00_CRIME | Q5SS00_CRIME | Q5SS00_CRIME | Q5SS00_CRIME |
| 8 | 48 | 53.9 | 448 | 2 Q9S423_SALEN | DR | Q9S423_SALEN | Q9S423_SALEN | Q9S423_SALEN | Q9S423_SALEN |
| 9 | 48 | 53.9 | 775 | 2 Q5PSA1_CANAL | DR | Q5PSA1_CANAL | Q5PSA1_CANAL | Q5PSA1_CANAL | Q5PSA1_CANAL |
| 10 | 48 | 53.9 | 784 | 2 Q8GM13_STRLG | DR | Q8GM13_STRLG | Q8GM13_STRLG | Q8GM13_STRLG | Q8GM13_STRLG |
| 11 | 48 | 53.9 | 793 | 2 Q59S70_CANAL | DR | Q59S70_CANAL | Q59S70_CANAL | Q59S70_CANAL | Q59S70_CANAL |
| 12 | 48 | 53.9 | 804 | 2 Q8ZP90_SALTY | DR | Q8ZP90_SALTY | Q8ZP90_SALTY | Q8ZP90_SALTY | Q8ZP90_SALTY |
| 13 | 47.5 | 53.4 | 527 | 2 Q62D26_ORYSA | DR | Q62D26_ORYSA | Q62D26_ORYSA | Q62D26_ORYSA | Q62D26_ORYSA |
| 14 | 47 | 52.8 | 61 | 2 Q6JHZB_HUMAN | DR | Q6JHZB_HUMAN | Q6JHZB_HUMAN | Q6JHZB_HUMAN | Q6JHZB_HUMAN |
| 15 | 47 | 52.8 | 364 | 2 Q7UG34_RHOMA | DR | Q7UG34_RHOMA | Q7UG34_RHOMA | Q7UG34_RHOMA | Q7UG34_RHOMA |
| 16 | 47 | 52.8 | 369 | 2 Q5KQW7_CRYNE | DR | Q5KQW7_CRYNE | Q5KQW7_CRYNE | Q5KQW7_CRYNE | Q5KQW7_CRYNE |
| 17 | 47 | 52.8 | 375 | 2 Q5SB22_CRYNE | DR | Q5SB22_CRYNE | Q5SB22_CRYNE | Q5SB22_CRYNE | Q5SB22_CRYNE |
| 18 | 47 | 52.8 | 471 | 2 QTPV5_9SPEN | DR | QTPV5_9SPEN | QTPV5_9SPEN | QTPV5_9SPEN | QTPV5_9SPEN |
| 19 | 47 | 52.8 | 1517 | 2 Q5A1P5_EWEKI | DR | Q5A1P5_EWEKI | Q5A1P5_EWEKI | Q5A1P5_EWEKI | Q5A1P5_EWEKI |
| 20 | 47 | 52.8 | 1547 | 2 Q9C1A0_ASPTU | DR | Q9C1A0_ASPTU | Q9C1A0_ASPTU | Q9C1A0_ASPTU | Q9C1A0_ASPTU |
| 21 | 47 | 52.8 | 1547 | 2 Q4WDD4_ASPTU | DR | Q4WDD4_ASPTU | Q4WDD4_ASPTU | Q4WDD4_ASPTU | Q4WDD4_ASPTU |
| 22 | 45 | 51.7 | 214 | 2 Q4WDD4_ASPTU | DR | Q4WDD4_ASPTU | Q4WDD4_ASPTU | Q4WDD4_ASPTU | Q4WDD4_ASPTU |
| 23 | 46 | 51.7 | 350 | 1 QCBT_FBSRM | DR | QCBT_FBSRM | QCBT_FBSRM | QCBT_FBSRM | QCBT_FBSRM |
| 24 | 46 | 51.7 | 356 | 2 Q6C1B2_YARII | DR | Q6C1B2_YARII | Q6C1B2_YARII | Q6C1B2_YARII | Q6C1B2_YARII |
| 25 | 46 | 51.7 | 373 | 2 Q5B089_PYRHO | DR | Q5B089_PYRHO | Q5B089_PYRHO | Q5B089_PYRHO | Q5B089_PYRHO |
| 26 | 46 | 51.7 | 396 | 2 Q7OGM6_CHLRE | DR | Q7OGM6_CHLRE | Q7OGM6_CHLRE | Q7OGM6_CHLRE | Q7OGM6_CHLRE |
| 27 | 46 | 51.7 | 1562 | 2 Q9YB40_MYCGR | DR | Q9YB40_MYCGR | Q9YB40_MYCGR | Q9YB40_MYCGR | Q9YB40_MYCGR |
| 28 | 45.5 | 51.1 | 266 | 2 Q7D2MB_AGRTS | DR | Q7D2MB_AGRTS | Q7D2MB_AGRTS | Q7D2MB_AGRTS | Q7D2MB_AGRTS |
| 29 | 45.5 | 51.1 | 298 | 2 Q8U680_AGRTS | DR | Q8U680_AGRTS | Q8U680_AGRTS | Q8U680_AGRTS | Q8U680_AGRTS |
| 30 | 45 | 50.6 | 941 | 2 Q854E3_9CAUD | DR | Q854E3_9CAUD | Q854E3_9CAUD | Q854E3_9CAUD | Q854E3_9CAUD |
| 31 | 45 | 50.6 | 954 | 2 Q9NU66_HUMAN | DR | Q9NU66_HUMAN | Q9NU66_HUMAN | Q9NU66_HUMAN | Q9NU66_HUMAN |

OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;
 OC Corynebacterineae; Nocardiaceae; Nocardiidae.
 OC NCBI_TaxID=37329;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=IFM 10152;
 RX PubMed=15466710; DOI=10.1073/pnas.0406410101;
 RA Ichikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
 RA Shiba T., Hattori M.;
 RT "The complete genomic sequence of *Nocardia farcinica* IFM 10152.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
 DR EMBL; AP006618; BAD9655.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 208 AA; 22565 MW; EBB3243D9B52094E CRC64;

Query Match 55.1%; Score 49; DB 2; Length 208;
 Best Local Similarity 46.7%; Pred. No. 16;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 EPDWMLWGDGRALDY 15
 Db 111 DPDWVYMLNRBDIDV 125

RESULT 3
 Q5NAJ9 SYNP6
 ID Q5NAJ9_SYNP6 PRELIMINARY; PRT; 405 AA.
 AC Q5NAJ9;
 DT 01-FEB-2005 (TREMBLrel. 29, Created)
 DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
 DE Sun protein.
 GN Name=Sun; Order=LocusNames=BYC0580_d;
 OS Synechococcus sp. (strain PCC 6301) (*Anacystis nidulans*).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX [1]
 RP NUCLEOTIDE SEQUENCE.

Sugita M.;
 RT "Complete genome structure of the unicellular cyanobacterium *Anacystis nidulans* 6301 (Synechococcus sp. PCC6301)."; databases.
 DR Submitted (DBC-2004) to the EMBL/GenBank/DDBJ databases.
 EMBL; AP00821; BAD9870.1; -; Genomic DNA.
 GO; GO:0008649; tRNA methyltransferase activity; IEA.
 GO; GO:0006364; tRNA processing; IEA.
 DR InterPro; IPR04573; Fmu_mt_fbase.
 DR InterPro; IPR01678; Fmu_NOL1_Nop2P.
 DR InterPro; IPR006027; NusB_Rmb3_TIM4.
 DR InterPro; IPR006174; RsmB_mt_fbase.
 DR InterPro; IPR00051; SAM_Bind.
 PFAM; PF00189; Nol1_Nop2_Fmu; 1.
 DR ProDom; PDD05242; NusB_region; 1.
 DR TIGR4MS; TIGR00563; rmbB; 1.
 KW Complete proteome.
 SQ SEQUENCE 405 AA; 44708 MW; 89F6CS1BB86590C4 CRC64;

Query Match 55.1%; Score 49; DB 2; Length 405;
 Best Local Similarity 66.7%; Pred. No. 31;
 Matches 10; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
 Qy 2 PDWL-LWGDGRAL 14
 Db 110 PDWLQVQLWSRDLGLD 124

RESULT 4
 Q6H084_FREDI
 ID Q6H084_FREDI PRELIMINARY; PRT; 779 AA.
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

Query Match 53.9%; Score 48; DB 2; Length 217;
 Best Local Similarity 50.0%; Pred. No. 24;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PDWLWGDGRAL 13
 Db 139 PNWLWGGQRKSI 150

RESULT 5
 Q7V3U3 PROMM
 ID Q7V3U3_PROMM PRELIMINARY; PRT; 217 AA.
 AC Q7V3U3;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Hypothetical protein precursor.
 GN Order=LocusNames=PWT2347;
 OS Prochlorococcus marinus (strain MIT 9313).
 OC Bacteria; Cyanobacteria; prochlorobiales; prochlorococcaceae;
 Prochlorococcus;
 OX [1]
 RP NUCLEOTIDE SEQUENCE.
 MEDLINE=22825598; PubMed=12917642; DOI=10.1038/nature01947;
 RX Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
 RA Ahlgren N.A., Arellano A., Coleman M., Hauer L., Hess W.R.,
 RA Johnson Z.I., Land M.L., Lindell D., Post A.P., Regala W., Shah M.,
 RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
 RA Webb E.R., Chisholm S.W.;
 RT "Genome divergence in two *Prochlorococcus* ecotypes reflects oceanic
 niche differentiation.";
 RL Nature 424:1042-1047 (2003);
 DR EMBL; BX572101; CAB22421.1; -; Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004605; F:phosphatidate cytidylyltransferase activity; IEA.
 DR GO; GO:0008651; P:phospholipid biosynthesis; IEA.
 DR InterPro; IPR000374; PC_trans.
 DR InterPro; IPR01148; CTP_transf_1.
 KW Complete proteome; Hypothetical protein; Signal.
 PT SIGNAL 1
 SQ SEQUENCE 217 AA; 23892 MW; 522AA448403FBC CRC64;

| | | Best Local Similarity 53.3%; Pred. No. 47; Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0; | |
|---|---|---|---|
| Q8BPF9 SHEON | | PRT; 262 AA. | AC Q8BPF9; SHEN PRELIMINARY; |
| AC | | | DT 01-MAR-2003 (TREMBLrel. 23, Created) |
| DT | 01-MAR-2003 (TREMBLrel. 23, Last sequence update) | | DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update) |
| DE | Hypothetical protein S00508. | | DE Hypothetical protein S00508. |
| GN | OrderedLocusNames=S00508; | | OS Shewanella oneidensis. |
| OS | Shewanella oneidensis. | | OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; |
| OC | Sheanellaceae; Shewanella. | | OC NCBI_TaxID=70863; |
| RN | [1] | | RN NUCLEOTIDE SEQUENCE. |
| RP | STRAIN=MR-1; | | RX MEDLINE-2229786; PubMed=1236813; DOI=10.1038/nbt749; |
| RX | Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Yamathavan J.J., Weidman J.P., Imprain M., Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J., Utterback T.R., McCollum L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nelson K.H., Fraser C.M., "Genomic sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis.", Nat. Biotechnol. 20:1118-1123 (2002). | RA [1] | |
| RL | EMBL; AE051498; AACN3589.1; -, Genomic_DNA. | | DR TIGR; S00508; -. |
| DR | Complete proteome. | | DR Sequence 262 AA; 29556 MW; 5E5B6EF4D52DC44C CRC64; |
| DR | SEQUENCE 262 AA; 29556 MW; 5E5B6EF4D52DC44C CRC64; | | SQ Query Match 53.9%; Score 48; DB 2; Length 262; Best Local Similarity 61.5%; Pred. No. 29; Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0; |
| QY | 2 PDWLWGDGRGND 14 | | Db 58 PDWLWGDGRGND 70 |
| RESULT 7 | | | |
| Q5SS0 CRVNE | | | |
| ID 05SS0- CRVNE PRELIMINARY; | PRT; 426 AA. | | |
| AC Q5SS0; | | | |
| DT 13-SEP-2005 (TREMBLrel. 31, Created) | | | |
| DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update) | | | |
| DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update) | | | |
| DE Hypothetical protein. | | | |
| GN ORFName=cCNBE1140; | | | |
| OS Cryptococcus neoformans var. neoformans B-3501A. | | | |
| OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; | | | |
| OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella. | | | |
| OX NCBI_TaxID=283643; | | | |
| RN [1] | | | |
| RP NUCLEOTIDE SEQUENCE. | | | |
| RC STRAIN=B-3501A; | | | |
| RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M., Wickes B.M., Fu J., Davis R.W., | | | |
| RT "Cryptococcus neoformans serotype D sequencing". | | | |
| RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases. | | | |
| CC - CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data. | | | |
| CC EMBL; AAEL0100024; EAL20751.1; -, Genomic_DNA. | | | |
| DR Hypothetical protein. | | | |
| SEQUENCE 426 AA; 47024 MW; A0FD1F268A28310 CRC64; | | | |
| RN 53.9%; Score 48; DB 2; Length 426; | | | |
| QY Query Match | 53.9%; Score 48; DB 2; Length 448; Best Local Similarity 87.5%; Pred. No. 49; Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | | |
| QY 1 EPDNLWLG 8 | | | |
| Db 408 EPDNLWLG 415 | | | |
| RESULT 9 | | | |
| Q5SSA1 CANAL | | | |
| ID 05SSA1- CANAL PRELIMINARY; | PRT; 775 AA. | | |
| AC Q5SSA1; | | | |
| DT 10-MAY-2005 (TREMBLrel. 30, Created) | | | |
| DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update) | | | |
| DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update) | | | |
| DE Hypothetical protein. | | | |
| GN ORFName=cCa019.10074; | | | |
| OS Candida albicans SC5314. | | | |
| OC Buxaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; | | | |
| OC Saccharomycetales; mitosporic Saccharomycetales; Candida. | | | |
| OX NCBI_TaxID=237561; | | | |
| RN [1] | | | |
| RP NUCLEOTIDE SEQUENCE. | | | |
| RC STRAIN=SC5314; | | | |
| RA PubMed=1512389; DOI=10.1073/pnas.0401648101; | | | |
| RA Jones T., Peterspiel N.A., Chibana H., Dungan J., Kalman S., Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T., Davis R.W., Scherer S., "The diploid genome sequence of Candida albicans.", Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004). | | | |
| RN [2] | | | |
| RP NUCLEOTIDE SEQUENCE. | | | |
| RC STRAIN=SC5314; | | | |
| RA Dungan J., Kuo A., Newport G., Ian C.-Y., Iijima C., Adegbola O., Robert S.J., Persson K., Donnelly S., Favoretto S., Trung K.-W., Jones T., Scherer S., Agabian N., | | | |

RT "Annotation of the Genome of *Candida albicans*.";
 RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
 CC -|- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL; AAC001000154; EAK93359_1; -; Genomic_DNA.
 KW Hypothetical protein.
 SEQUENCE 775 AA; 88474 MW; 685118C6B2C914A8 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 775;
 Best Local Similarity 54.5%; Pred. No. 88;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PDWLWGDGCA 12
 Db 718 PEAVWNGSOGA 728

RESULT 10
 Q8GM13 STRGL
 ID Q8GM13_STRL PRELIMINARY; PRT; 784 AA.
 AC 08GM13;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DB UvrA-like drug resistance pump.
 OS Streptomyces globisporus.
 OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1908;
 RN [1]
 RP NUCLEOTIDE_SEQUENCE.
 RC STRAIN=C-1027;
 RX MEDLINE=22171413; PubMed=12183628; DOI=10.1126/science.1072110;
 RA Liu W., Christensen S.D., Standage S., Shen B.;
 RT "Biosynthesis of the enediyne antitumor antibiotic C-1027.";
 RL Science 297:1170-1173 (2002).
 CC -|- SIMILARITY Belongs to the ABC transporter family.
 DR EMBL; AY088670; AAL06654_1; -; Genomic_DNA.
 GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:005524; F:ATP binding; IEA.
 GO; GO:005687; F:ATPase activity; IEA.
 GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:006810; P:transport; IEA.
 DR InterPro; IPR003439; ABC_tranP_like.
 PTM; PF00005; ABC_tran; 2.
 PROTE; PS00211; ABC_TRANSPORTER_1; 1.
 PROTE; PS5083; ABC_TRANSPORTER_2; 2.
 KW ATP-binding; Membrane; Nucleotide-binding; Transport.
 SEQUENCE 784 AA; 83960 MW; DABC2D965720A5E7 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 784;
 Best Local Similarity 53.8%; Pred. No. 87;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 PDWLWGDGAL 14
 Db 204 PDWQIWAWSGRLL 216

RESULT 11
 Q59ST0 CANAL
 ID Q59ST0_CANAL_PRBLIMINARY; PRT; 793 AA.
 AC 059ST0;
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DB Hypothetical protein.
 ORFNames=c2019_347;
 GN Candida albicans SC3314.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=237561;

RESULT 12
 Q8ZK90 SALTY
 ID Q8ZK90_SALTY_PRELIMINARY; PRT; 804 AA.
 AC 08ZK90;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Putative inner membrane protein.
 GN Name=ybbP; Order=dicoccusNames=STM0508;
 OG Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonellae.
 OX NCBI_TaxID=602;
 RN [1]
 RP NUCLEOTIDE_SEQUENCE.
 RC STRAIN=LIT;
 RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101014;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvane E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoenkting T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 LT2.";
 RL Nature; 413:852-856(2001).
 DR EBD08719; AAL19462_1; -; Genomic_DNA.
 GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR003838; DUR214.
 PTM; PF02687; FtBX; 2.
 KW Complete_proteome.
 SEQUENCE 804 AA; 88772 MW; 72A29069A7021F11 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 804;
 Best Local Similarity 87.5%; Pred. No. 89;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPDWLWGG 8
 Db 764 EPDWLWGG 771

RESULT 13
 Q6ZD22 ORYSA PRELIMINARY; PRT; 527 AA.
 ID Q6ZD22; ORYSA PRELIMINARY; PRT; 527 AA.
 AC Q6ZD22;
 DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
 DE Hypothetical protein.
 GN OrderidocussRB8157;
 OS Rhodopirellula baltica.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellulidae.
 OX NCBI_TaxID=117;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto K.; Yamamoto T.,
 RT "Oryza sativa nipponbare (Ga3) genomic DNA, chromosome 7, PAC
 clone: P0507H12";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP014338; BAC03511.1; -; Genomic_DNA.
 DR Gramene; Q6ZD22; -.
 DR GO:0004519; F: endonuclease activity; IEA.
 DR GO:0016787; F: nucleobase activity; IEA.
 DR GO:0006281; P: DNA repair; IEA.
 DR InterPro: IPR004843; M-pesterase.
 DR Pfam; PF00149; Metallophospho; 1.
 KW Hypothetical protein.
 SEQUENCE 527 AA; 61478 MW; 2658E1451BC92BB6 CRC64;

Query Match 53.4%; Score 47.5%; DB 2; Length 527;
 Best Local Similarity 50.0%; Pred. No. 70;
 Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

Qy 1 EPPDWL--WDRGALDV 15
 Db 86 EPNWLDWYWMDKTKGTV 103

RESULT 14
 Q6JH28_HUMAN PRELIMINARY; PRT; 61 AA.
 ID Q6JH28_HUMAN PRELIMINARY; PRT; 61 AA.
 AC Q6JH28;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
 DE HCV-52 binding protein 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Zhang J., Cheng J., Wang L., Shao Q., Lu Y., Chen T., Hong Y.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY459290; AAC03235.1; -; mRNA.
 SQ SEQUENCE 61 AA; 6607 MW; 4B162AA344EB7A56 CRC64;

Query Match 52.8%; Score 47; DB 2; Length 61;
 Best Local Similarity 87.5%; Pred. No. 93;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 WILWGDRG 11
 Db 46 WDLWGSRG 53

RESULT 15
 Q7UG34_RH0BA PRELIMINARY; PRT; 364 AA.
 ID Q7UG34_RH0BA PRELIMINARY; PRT; 364 AA.
 AC Q7UG34;

Query Match 53.4%; Score 47.5%; DB 2; Length 61;
 Best Local Similarity 87.5%; Pred. No. 93;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Description

Sequence 12532, A
Sequence 7066, AP
Sequence 22630, A
Sequence 196, APP
Sequence 984, AP
Sequence 13627, A
Sequence 18301, A
Sequence 426, APP
Sequence 80, APP
Sequence 80, APP
Sequence 12903, A
Sequence 4, App1
Sequence 7786, AP
Sequence 20574, A
Sequence 29, App1
Sequence 27798, A
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Sequence 22, App1
Sequence 23, App1
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Sequence 38, App1
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Sequence 42, App1
Sequence 43, App1
Sequence 44, App1
Sequence 45, App1

RESULT 1
US-09-489-039A-12532

; Sequence 12532, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709_1002-001

; CURRENT APPLICATION NUMBER: US/09/489, 039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 12532

; LENGTH: 229

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-12532

Query Match Score: 48; DB: 2; Length: 229;

| | | | | | |
|--------------------|--------------------|----------------|---------------|-----------|---------|
| Best Local Matches | Similarity: 57.1% | Pred. No.: 7.8 | Mismatches: 1 | Indels: 5 | Gaps: 0 |
| Qy | 1 EPDWLUWGDRALD 14 | | | | |
| Db | 32 ERSWCKWGRDFR 45 | | | | |

RESULT 2
US-09-543-681A-7066

; Sequence 7066, Application US/09543681A

; Patent No. 6610709

; GENERAL INFORMATION:

; APPLICANT: GARY BRETON

; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRAB

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709_1002-001

; CURRENT APPLICATION NUMBER: US/09/543, 681A

; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/128, 706

; PRIOR FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 7066

; LENGTH: 614

; TYPE: PRT

; ORGANISM: Proteus mirabilis

US-09-543-681A-7066

Query Match Score: 45; DB: 2; Length: 614;

Best Local Similarity 64.3%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

RESULT 3
US-09-248-796A-22630
; Sequence 22630, Application US/09248796A
; Patent No. 6747137

GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 22630
LENGTH: 80
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-22630

Query Match 49.4%; Score 44; DB 2; Length 80;
Best Local Similarity 54.5%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PDWLWGDGRGA 12
Db 12 PDWAVNGSQA 22

RESULT 4
US-09-303-518D-194
; Sequence 194, Application US/09303518D
; Patent No. 6914131

GENERAL INFORMATION:
APPLICANT: Scariato, Vincenzo
APPLICANT: Massignani, Vega
APPLICANT: Rappoli, Rino
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Neisseria meningitidis

CURRENT APPLICATION NUMBER: US/09/303-518D-194
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: 60/160,160
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 1088
SEQ ID NO 160,160
LENGTH: 383
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-303-518D-196

Query Match 48.3%; Score 43; DB 2; Length 383;
Best Local Similarity 70.0%; Pred. No. 72;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PDWLWGDGRGA 12
Db 12 PDWAVNGSQA 22

RESULT 5
US-09-949-016-9984
; Sequence 9984, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: Venter, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231, 498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9984
LENGTH: 638
TYPE: PRT
ORGANISM: Human
US-09-949-016-9984

Query Match 48.3%; Score 43; DB 2; length 638;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPDWLW 7
Db 558 EPDWLW 564

RESULT 7
US-09-902-540-13627
; Sequence 13627, Application US/09902540
; Patent No. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

RESULT 5
US-09-303-518D-196
; Sequence 196, Application US/09303518D

CURRENT APPLICATION NUMBER: US/09/902,540
 CURRENT FILING DATE: 2001-07-10
 PRIOR APPLICATION NUMBER: 60/217,883
 PRIOR FILING DATE: 2000-07-10
 NUMBER OF SEQ ID NOS: 16825
 SEQ ID NO: 13627
 LENGTH: 732
 TYPE: PRT
 ORGANISM: *Myxococcus xanthus*
 US-09-902-540-13627

RESULT 8
 Query Match 48.3%; Score 43; DB 2; Length 732;
 Best Local Similarity 63.6%; Pred. No. 1.6e+02; 1; Mismatches
 Matches 7; Conservative 1; Indels 0; Gaps 0;
 Qy 4 WLLWDGRGALD 14
 Db 126 WLLWGTRRAAE 136

RESULT 9
 US-09-252-991A-18301
 Sequence 18301, Application US/09252991A
 ;
 GENERAL INFORMATION:
 ;
 ; APPLICANT: Marc J. Rubenstein et al.
 ; PATENT NO. 6551795
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 18301
 ; LENGTH: 320
 ; TYPE: PRT
 ; ORGANISM: *Pseudomonas aeruginosa*
 ;
 ; US-09-252-991A-18301

Query Match 47.8%; Score 42.5; DB 2; Length 320;
 Best Local Similarity 66.7%; Pred. No. 79; 10; Mismatches 0; Indels 4; Gaps 1;
 Matches 10; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 2 PDWLLWGDRG-ALDV 15
 Db 254 PTLLWGDRDRVLDV 268

RESULT 9
 US-09-854-133-426
 ; Sequence 426, Application US/09854133
 ;
 ; Patent No. 6759508
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Monamath, Raodon
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Secrist, Heather
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 ; THERAPY AND DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.475C10
 ; CURRENT APPLICATION NUMBER: US/09/854,133
 ; CURRENT FILING DATE: 2001-05-11
 ; NUMBER OF SEQ ID NOS: 735
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 426
 ; LENGTH: 174
 ; TYPE: PRT
 ; ORGANISM: *Homo sapiens*

RESULT 10
 US-08-290-448A-80
 Sequence 80, Application US/08290448A
 ;
 ; Patent No. 5679354
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Rogers, Bruce
 ; APPLICANT: Klapper, David G.
 ; APPLICANT: Rafnar, Thorunn
 ; APPLICANT: Kuo, Mei-chang
 ; TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
 ; NUMBER OF SEQ ID NOS: 93
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LATHIVE & COCKFIELD
 ; STREET: 60 State Street, suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ;
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patient Release #1.0, Version #1.25
 ;
 ; CURRENT APPLICATION DATA:
 ;
 ; APPLICATION NUMBER: US/08/290,448A
 ; FILING DATE: August 15, 1994
 ;
 ; PRIOR APPLICATION DATA:
 ;
 ; APPLICATION NUMBER: US 07/529, 951
 ; FILING DATE: May 29, 1990
 ;
 ; APPLICATION NUMBER: US 07/325, 365
 ; FILING DATE: March 17, 1989
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ;
 ; NAME: Amy E. Mandrigoras
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: IMI-018CN
 ;
 ; TELECOMMUNICATION INFORMATION:
 ;
 ; TELEPHONE: (617)227-7400
 ;
 ; TELEFAX: (617)227-5941
 ;
 ; INFORMATION FOR SEQ ID NO: 80:
 ;
 ; SEQUENCE CHARACTERISTICS:
 ;
 ; LENGTH: 388 amino acids
 ;
 ; TYPE: amino acid
 ;
 ; TOPOLOGY: linear
 ;
 ; MOLECULE TYPE: protein
 ;
 ; US-08-290-448A-80

RESULT 11
 US-08-290-448A-80
 ; Sequence 80, Application US/08290448A
 ;
 ; Patent No. 5698304
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Rogers, Bruce
 ; APPLICANT: Klapper, David G.
 ; APPLICANT: Rafnar, Thorunn

APPLICANT: Kuo, Mei-chang
 TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
 NUMBER OF SEQUENCES: 93
 CORRESPONDENCE ADDRESS:
 ADDRESSE: LAHIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/290,448A
 FILING DATE: August 15, 1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/529,951
 FILING DATE: May 29, 1990
 APPLICATION NUMBER: US 07/325,365
 FILING DATE: March 17, 1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragouras
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IMI-018CN
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 80:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 388 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 80:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 388 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-175-069A-80

Query Match Score 42; DB 1; Length 388;
 Best Local Similarity 46.7%; Pred. No. 1.2e+02;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

| Qy | 1 | EPDWLWGGDGLADV 15 |
|----|-----|--------------------|
| Db | 323 | EPPEMTWNWRQNDV 337 |

RESULT 12

US-08-175-069A-80

Sequence 80, Application US/08175069A
 Patent No. 577671

GENERAL INFORMATION:

APPLICANT: Rogers, Bruce
 APPLICANT: Klapper, David G.
 APPLICANT: Rahnar, Thorunn
 APPLICANT: Kuo, Mei-chang
 TITLE OF INVENTION: Methods For Treating Sensitivity To A Title
 NUMBER OF INVENTION: Protein Allergen Using Peptides Which Include A T Cell Epitope
 CORRESPONDENCE ADDRESS:
 ADDRESSE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/461,939B
 FILING DATE:

PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/464,000
 FILING DATE: 05-JUN-1995
 APPLICATION NUMBER: US 08/290,448A
 FILING DATE: 15-AUG-1994
 APPLICATION NUMBER: US 07/529,951
 FILING DATE: 29-MAY-1990
 APPLICATION NUMBER: US 07/325,365
 FILING DATE: 17-MAR-1989

ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragouras
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IMI-018CN
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 80:

INFORMATION FOR SEQ ID NO: 80:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 388 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-175-069A-80

Query Match Score 42; DB 1; Length 388;
 Best Local Similarity 46.7%; Pred. No. 1.2e+02;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

| Qy | 1 | EPDWLWGGDGLADV 15 |
|----|-----|--------------------|
| Db | 323 | EPPEMTWNWRQNDV 337 |

RESULT 13

US-08-461,939B-80

Sequence 80, Application US/08461939B
 Patent No. 6335019

GENERAL INFORMATION:

APPLICANT: Rogers, Bruce
 APPLICANT: Klapper, David G.
 APPLICANT: Rahnar, Thorunn
 APPLICANT: Kuo, Mei-chang
 TITLE OF INVENTION: Methods For Treating Sensitivity To A Title
 NUMBER OF INVENTION: Protein Allergen Using Peptides Which Include A T Cell Epitope
 CORRESPONDENCE ADDRESS:
 ADDRESSE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/461,939B
 FILING DATE:

PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/464,000
 FILING DATE: 05-JUN-1995
 APPLICATION NUMBER: US 08/290,448A
 FILING DATE: 15-AUG-1994
 APPLICATION NUMBER: US 07/529,951
 FILING DATE: 29-MAY-1990
 APPLICATION NUMBER: US 07/325,365
 FILING DATE: 17-MAR-1989

ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragouras
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IMI-018CN
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 80:

RESULT 15
 Query Match 47.2%; Score 42; DB 2; Length 388;
 Best Local Similarity 46.7%; Pred. No. 1.2e-02;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 Molcule Type: protein
 US-08-461-939B-80

Qy 1 EPPDWLWGDGRALDV 15
 Db 323 EPENNMTWNWRQNDV 337

RESULT 14
 Sequence 80, Application US/08464000
 Patent No. 6335020

GENERAL INFORMATION:
 APPLICANT: Rogers, Bruce
 APPLICANT: Klapper, David G.
 APPLICANT: Rafnar, Thorunn
 APPLICANT: Kuo, Mei-chang
 TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen
 NUMBER OF SEQUENCES: 93
 CORRESPONDENCE ADDRESS:
 ADDRESSE: LAHTI & COCKFIELD, LLP
 STREET: 60 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,000
 FILING DATE: 05-JUN-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/290,448
 FILING DATE: 15-AUG-1994
 APPLICATION NUMBER: US 07/529,951
 FILING DATE: 29-MAY-1990
 APPLICATION NUMBER: US 07/325,365
 FILING DATE: 17-MAR-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragoras
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: INN1-018CN2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 80:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 388 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-464-000-80

Query Match 47.2%; Score 42; DB 2; Length 388;
 Best Local Similarity 46.7%; Pred. No. 1.2e-02;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

RESULT 15
 Query Match 47.2%; Score 42; DB 2; Length 493;
 Best Local Similarity 60.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Molcule Type: protein
 US-09-489-039A-12903

Qy 4 WILMGDRGAL 13
 Db 463 WLMCERGM 472

Search completed: December 4, 2005, 04:09:44
 Job time : 33.1875 sec

Query Match 47.2%; Score 42; DB 2; Length 388;
 Best Local Similarity 46.7%; Pred. No. 1.2e-02;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 Molcule Type: protein
 US-09-489-039A-12903

Qy 1 EPPDWLWGDGRALDV 15
 Db 323 EPENNMTWNWRQNDV 337

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GenCore version 5.1.6

OM protein - protein search, using sw model
Run on: December 4, 2005, 04:07:28 ; Search time 107.5 Seconds
Sequence: 1 EPDWLWGDRGALDV 15
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Title: US-10-632-706-197
Perfect score: 89
Sequence: 1 EPDWLWGDRGALDV 15
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 18757569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

1: /cgn2_6/pctodata/1/pupbaa/us07_pubcomb.pep: *
2: /cgn2_6/pctodata/1/pupbaa/us08_pubcomb.pep: *
3: /cgn2_6/pctodata/1/pupbaa/us09_pubcomb.pep: *
4: /cgn2_6/pctodata/1/pupbaa/us10_pubcomb.pep: *
5: /cgn2_6/pctodata/1/pupbaa/us10b_pubcomb.pep: *
6: /cgn2_6/pctodata/1/pupbaa/us11_pubcomb.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Match Length

DB ID

Description

No.

Score

Query

RESULT 1
US-10-632-706-129
; Sequence 159, Application US/10632706
; Publication No. US20040175385A1

GENERAL INFORMATION:

APPLICANT: MARX, JAMES D.

INVENTOR: AMERSDORFER, PETER

TITLE OF INVENTION: THERAPEUTIC MONOClonal ANTIBODIES THAT NEUTRALIZE BOTULINUM

TITLE OF INVENTION: NEUROTOXINS

FILE REFERENCE: 4077-89520US

CURRENT APPLICATION NUMBER: US/10/632,706

CURRENT FILING DATE: 2003-05-01

PRIOR APPLICATION NUMBER: US 60/400,721

PRIOR FILING DATE: 2002-08-01

PRIOR APPLICATION NUMBER: US 09/144,806

NUMBER OF SEQ ID NOS: 278

SOFTWARE: Patentin version 3.2

SEQ ID NO: 129
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: single chain antibody fragment
US-10-632-706-129
Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDWLWGDRGALDV 15
Dy 1 EPDWLWGDRGALDV 15

RESULT 2
US-10-632-706-130
Sequence 130, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: MARX, JAMES D.
APPLICANT: AMERSDORFER, PETER
APPLICANT: THERAPEUTIC MONOClonal ANTIBODIES THAT NEUTRALIZE BOTULINUM
TITLE OF INVENTION: NEUROTOXINS
FILE REFERENCE: 4077-89520US
CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT FILING DATE: 2003-05-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806

ALIGNMENTS

| | | | | | | |
|----|------|------|-----|---|----------------------|-------------------|
| 28 | 42.5 | 47.8 | 315 | 4 | US-10-282-122A-43588 | Sequence 43588, A |
| 29 | 42 | 47.2 | 77 | 3 | US-09-762-847-922 | Sequence 922, APP |
| 30 | 42 | 47.2 | 77 | 4 | US-09-925-154-922 | Sequence 925, APP |
| 31 | 42 | 47.2 | 116 | 4 | US-10-424-599-206931 | Sequence 206931, |
| 32 | 42 | 47.2 | 131 | 3 | US-09-864-4084-4566 | Sequence 456, APP |
| 33 | 42 | 47.2 | 154 | 4 | US-10-312-354-26 | Sequence 26, APP |
| 34 | 42 | 47.2 | 174 | 3 | US-09-738-973-426 | Sequence 426, APP |
| 35 | 42 | 47.2 | 174 | 3 | US-09-854-133-426 | Sequence 425, APP |
| 36 | 42 | 47.2 | 174 | 4 | US-10-144-6494-426 | Sequence 3129, A |
| 37 | 42 | 47.2 | 175 | 5 | US-10-450-763-31629 | Sequence 34331, A |
| 38 | 42 | 47.2 | 198 | 4 | US-10-767-701-34131 | Sequence 3778, A |
| 39 | 42 | 47.2 | 211 | 5 | US-10-457-761-37978 | Sequence 10592, |
| 40 | 42 | 47.2 | 245 | 4 | US-10-431-963-108592 | Sequence 6625, A |
| 41 | 42 | 47.2 | 275 | 4 | US-10-425-114-66625 | Sequence 50322, A |
| 42 | 42 | 47.2 | 363 | 4 | US-10-282-122A-50322 | Sequence 20944, A |
| 43 | 42 | 47.2 | 380 | 4 | US-10-365-493-20944 | Sequence 97, APP |
| 44 | 42 | 47.2 | 397 | 3 | US-09-847-208-17 | Sequence 97, APP |
| 45 | 42 | 47.2 | 397 | 5 | US-10-801-689-97 | Sequence 97, APP |

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; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 130
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-130

Query Match          100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 EPDWLWGDGALDV 15
Db      1 EPDWLWGDGALDV 15

RESULT 3
US-10-632-706-131
; Sequence 131, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR APPLICATION NUMBER: 2003-08-01
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR FILING NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SEQ ID NO: 131
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-131

Query Match          100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 EPDWLWGDGALDV 15
Db      1 EPDWLWGDGALDV 15

RESULT 4
US-10-632-706-194
; Sequence 194, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 200
; LENGTH: 15
; TYPE: PRT

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; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
; US-10-632-706-200

Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2; 8e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPDWLWGDGRGALDV 15
Db 1 EPDWLWGDGRGALDV 15

;

RESULT 7
US-10-632-706-203
; Sequence 203, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS
; CURRENT APPLICATION NUMBER: US 10/632-706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 203
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
; US-10-632-706-203

Query Match 84.3%; Score 75; DB 4; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00033; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPDWLWGDGRGALDV 15
Db 1 EPDWLWGDGRGALDV 15

;

RESULT 8
US-10-450-763-50690
; Sequence 50690, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: HYBEQ, INC.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 770C1P3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO: 50690
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN

;

RESULT 9
US-10-634-548-27
; Sequence 27, Application US/10634548
; Publication No. US2004045051A1
; GENERAL INFORMATION:
; APPLICANT: NO. US2004045051Airs, Susan R
; APPLICANT: Lincoln, Kim
; APPLICANT: Akad, Mark Scott
; APPLICANT: Ellers, Robert
; APPLICANT: Hartsuyker, Karen Kindle
; APPLICANT: Hirshberg, Joseph
; APPLICANT: Karunananand, Balasubojini
; APPLICANT: Mohbiri, Farhad
; APPLICANT: Stein, Joshua C.
; APPLICANT: Valentim, Henry B.
; APPLICANT: Venkatesh, Tyamagondlu V.
; TITLE OF INVENTION: Tocopherol biosynthesis related genes and uses thereof
; CURRENT APPLICATION NUMBER: US/10/634,548
; FILE REFERENCE: Ren-01-125
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: US 60/400,689
; PRIOR FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 27
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Prochlorococcus marinus-MIT9313
; US-10-634-548-27

Query Match 53.9%; Score 48; DB 4; Length 201;
Best Local Similarity 50.0%; Pred. No. 37; Mismatches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PDWLWGDGRAL 13
Db 123 PNWLWGDGRAL 134

;

RESULT 10
US-10-159-257A-160
; Sequence 160, Application US/10159257A
; Publication No. US20040161828A1
; GENERAL INFORMATION:
; APPLICANT: SHEN, BEN
; APPLICANT: LIU, WEN
; APPLICANT: CHRISTENSON, STEVEN D.
; APPLICANT: STANDAGE, SCOTT
; TITLE OF INVENTION: GENE CLUSTER FOR PRODUCTION OF THE ENEDIYNE ANTITUMOR

```

; TITLE OF INVENTION: ANTIBIOTIC C-1027
; FILE REFERENCE: 4077-896020US
; CURRENT APPLICATION NUMBER: US/10/159, 257A
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 09/478, 188
; PRIOR FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/615, 434
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 160
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Streptomyces globisporus
; FEATURE:
; OTHER INFORMATION: off(-1)
; US-10-159-257A-160

Query Match      53.9%; Score 48; DB 4; Length 775;
Best Local Similarity 53.8%; Pred. No. 1.3e+02; Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy   2 PDWLWLGDRGALD 14
Db   |||| :||| :||| 207

RESULT 11
US-10-437-963-134355
; Sequence 114365, Application US/10437963
; Publication No. US20040123343A1
GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbuzuk, Brad

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/437, 963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO: 134365
LENGTH: 992
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_36146C.1.pep
; US-10-437-963-134365

Query Match      53.4%; Score 47.5%; DB 4; Length 992;
Best Local Similarity 50.0%; Pred. No. 2e+02; Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 1;
Qy   1 EPPDWLU--WGDGRGALD 15
Db   |||| :||| :||| :||| 568

RESULT 12
US-10-450-763-52883
; Sequence 52883, Application US/10450763
; Publication No. US20050196754A1
GENERAL INFORMATION:
; APPLICANT: Rysaq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790C19/US
; CURRENT APPLICATION NUMBER: US/10/450, 763
; CURRENT FILING DATE: 2003-06-11

Query Match      53.4%; Score 47.5%; DB 4; Length 992;
Best Local Similarity 50.0%; Pred. No. 2e+02; Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 1;
Qy   1 EPPDWLU--WGDGRGALD 15
Db   |||| :||| :||| :||| 568

RESULT 13
US-10-369-493-12420
; Sequence 12420, Application US/10369493
; Publication No. US20030233675A1
GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369, 493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 6/360, 039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO: 12420
LENGTH: 904
TYPE: PRT
ORGANISM: Aspergillus nidulans
; US-10-369-493-12420

Query Match      52.8%; Score 47; DB 4; Length 904;
Best Local Similarity 70.0%; Pred. No. 2.1e+02; Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy   4 WLLWLGDRGAL 13
Db   |||| :||| :||| 469

RESULT 14
US-10-425-115-240160
; Sequence 240160, Application US/10425115
; Publication No. US20040214272A1
GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425, 115

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CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 369326
 SEQ ID NO: 240160
 LENGTH: 159
 TYPE: PRT
 ORGANISM: *zea mays*
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)..(159)
 OTHER INFORMATION: unsure at all xaa locations
 FEATURE:
 OTHER INFORMATION: Clone ID: MRT4577_150607C.1.pep
 US-10-425-115-240160

Query Match Best Local Similarity 50.6%; Score 45; DB 4; Length 372;
 Matches 7; Conservative 70.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
 Qy 2 PDWLIWGDRGAL 13
 Db 35 PGRLIWGRRGAL 46

RESULT 15
 US-10-282-122A-68332
 ; Sequence 68332, Application US/10282122A
 ; GENERAL INFORMATION:
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Ryskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trwick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forbyth, R.
 ; APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: BLTRIA_04A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-15
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 68332
 LENGTH: 372
 TYPE: PRT
 ORGANISM: *Pseudomonas putida*
 US-10-282-122A-68332

Query Match Best Local Similarity 50.6%; Score 45; DB 4; Length 372;
 Matches 7; Conservative 70.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
 Qy 2 PDWLIWGDRGAL 11
 Db 221 PDWLWTPAG 230

Search completed: December 4, 2005, 04:37:43
 Job time : 121.5 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 4, 2005, 04:08:08 ; Search time: 4.375 Seconds

Perfect score: 89 US-10-632-706-197 (without alignments)

Sequence: 1 ERDMLWGDGALDV 15

Scoring table: BUCSUM62 Gapext 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New: *

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2: /cgn2_6/podata/1/pubpa/us09_NEW_PUB.PEP:*

3: /cgn2_6/podata/1/pubpa/us07_NEW_PUB.PEP:*

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6: /cgn2_6/podata/1/pubpa/us10_NEW_PUB.PEP:*

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8: /cgn2_6/podata/1/pubpa/us60_NEW_PUB.PEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

* SUMMARIES

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| 1 | 43 | 48.3 | 383 | 6 US-10-467-657-5602 Sequence 5602, Ap |
| 2 | 41 | 46.1 | 251 | 7 US-11-054-515-1084 Sequence 1084, Ap |
| 3 | 40.5 | 45.5 | 125 | 6 US-10-821-234-1277 Sequence 1277, Ap |
| 4 | 38.5 | 43.3 | 1075 | 7 US-11-174-150-34 Sequence 34, Appl |
| 5 | 38.5 | 43.3 | 1114 | 7 US-11-174-150-35 Sequence 35, Appl |
| 6 | 38 | 42.7 | 248 | 7 US-11-054-515-1079 Sequence 1079, Ap |
| 7 | 38 | 42.7 | 251 | 7 US-11-054-515-944 Sequence 944, App |
| 8 | 37 | 41.6 | 344 | 6 US-10-967-522A-24 Sequence 225, Ap |
| 9 | 36 | 40.4 | 225 | 6 US-10-81-234-1116 Sequence 1006, Ap |
| 10 | 36 | 40.4 | 322 | 6 US-10-467-657-1006 Sequence 484, App |
| 11 | 36 | 40.4 | 428 | 6 US-10-793-626-484 Sequence 60, Appl |
| 12 | 36 | 40.4 | 1857 | 7 US-11-057-058-61 Sequence 61, Appl |
| 13 | 36 | 40.4 | 1857 | 7 US-11-057-058-61 Sequence 128, App |
| 14 | 35.5 | 39.9 | 158 | 6 US-10-510-386-128 Sequence 1466, Ap |
| 15 | 35.5 | 39.9 | 247 | 6 US-793-626-156 Sequence 923, App |
| 16 | 35.5 | 39.9 | 344 | 6 US-10-821-534-923 Sequence 20, Appl |
| 17 | 35.5 | 39.9 | 380 | 6 US-10-624-932-20 Sequence 54, Appl |
| 18 | 35 | 39.3 | 239 | 6 US-10-957-569-54 Sequence 5824, Ap |
| 19 | 35 | 39.3 | 350 | 6 US-10-467-657-5824 Sequence 68, Appl |
| 20 | 35 | 39.3 | 401 | 6 US-10-510-386-68 Sequence 62, Appl |
| 21 | 35 | 39.3 | 503 | 6 US-10-590-388-62 Sequence 1668, Ap |
| 22 | 35 | 39.3 | 551 | 6 US-10-793-626-1668 Sequence 86, Appl |
| 23 | 34.5 | 38.8 | 1613 | 7 US-11-108-228-84 Sequence 86, Appl |
| 24 | 34.5 | 38.8 | 1613 | 7 US-11-228-86 Sequence 1079, Ap |
| 25 | 38.2 | 41.2 | 251 | 7 US-11-054-515-1079 Sequence 1079, Ap |

* ALIGNMENTS

RESULT 1
US-10-467-657-5602

; Sequence 5602, Application US/10467657

; Publication No. US20050260581A1

; GENERAL INFORMATION:

; APPLICANT: CHIRION SPA

; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariarazia

; APPLICANT: MASIGNANI Vega

; APPLICANT: MONACI Elisabetta

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEAR

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-05-11

; PRIOR APPLICATION NUMBER: GB-01013424.8

; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 5602

; LENGTH: 383

; TYPE: PRT

; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-5602

Query Match Score: 48.3%; Score: 43; DB: 6;

Best Local Similarity: 70.0%; Pred. No.: 3-8;

Matches: 7; Conservative: 2; Mismatches: 2

Qy 2 PDMILWGRG 11

Db 181 PEWILFGYRG 190

RESULT 2
US-11-054-515-1084

; Sequence 1084, Application US/11054515

; Publication No. US2005025532A1

; GENERAL INFORMATION:

; APPLICANT: RUBEN et al.

; TITLE OF INVENTION: Antibodies that Immunospecific

; FILE REFERENCE: P523P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; CURRENT FILING DATE: 2005-02-10

; CURRENT FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: P523P3, 296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

Sequence 1793, APP
Sequence 2, APP1
Sequence 1069, APP
Sequence 10, APP1
Sequence 12, APP1
Sequence 1063, APP
Sequence 190, APP
Sequence 206, APP
Sequence 31, APP1
Sequence 52, APP1
Sequence 882, APP
Sequence 645, APP
Sequence 1052, APP
Sequence 95, APP1
Sequence 1307, APP
Sequence 877, APP
Sequence 953, APP
Sequence 965, APP
Sequence 980, APP
Sequence 984, APP

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; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO: 1084
; LENGTH: 251
; ORGANISM: Homo sapiens
; US-11-054-515-1084
; Query Match 46.1%; Score 41; DB 7; Length 251;
; Best Local Similarity 46.2%; Pred. No. 5.1;
; Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 2 PWDWLWGDGRGA 14
Db 45 PEWMGWNNGRSD 57

RESULT 3
US-10-821-234-1277
; Sequence 1277, Application US/10821234
; Publication No. US2005225514A1
; GENERAL INFORMATION:
; APPLICANT: labat, ivan
; APPLICANT: Stache-Crein, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; NUMBER OF SEQ ID NOS: 1704
; SEQ ID NO: 1277
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-1277

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; Best Local Similarity 63.6%; Pred. No. 3.1;
; Matches 7; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
Qy 1 EDDWLWGDGRG 11
Db 101 DDDWLWGDGRGA 110

RESULT 4
US-11-174-150-34
; Sequence 34, Application US/11174150
; Publication No. US20050260714A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: QP50022
; CURRENT APPLICATION NUMBER: US/11/174,150
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/257,174
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: PCT/US01/11797
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/196,603
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/199,417
; PRIOR FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ For Windows Version 3.0
; SEQ ID NO: 35
; LENGTH: 1114
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-174-150-34

Query Match 43.3%; Score 38.5; DB 7; Length 1114;
; Best Local Similarity 53.8%; Pred. No. 53;
; Matches 7; Conservative 2; Mismatches 1; Indels 3; Gaps 1;
Qy 3 DWLWG---DRGA 12
Db 961 EWSWMGSWYDRGA 973

RESULT 6
US-11-054-515-1679
; Sequence 1679, Application US/11054515
; Publication No. US200525532A1

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; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/233,499
; PRIOR FILING DATE: 2001-03-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO: 1679
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapienB
; US-11-054-515-1679
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Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 4; Mismatches 4;
Qy 1 EPPDWLWGDRGALD 14
Db 44 EPERNMGWINGGSGD 57
; RESULT 7
; Sequence 944, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO: 1679
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapienB
; US-11-054-515-1679
Query Match 42.7%; Score 38; DB 7; Length 251;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 4; Mismatches 4;
Qy 1 EPPDWLWGDRGALD 14
Db 44 EPERNMGWINGGSGD 57
; RESULT 8
; Sequence 944, Application US/11054515
; Publication No. US2005025604A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Shippard, Paul O.
; TITLE OF INVENTION: Ztnr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 24
; LENGTH: 344
; TYPE: PRT
; ORGANISM: mus musculus
; US-10-967-527A-24
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Best Local Similarity 83.3%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 1;
Qy 2 PDWLW 7
Db 3 PSWLW B
; RESULT 9
; Sequence 1116, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-03-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO: 1116
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-1116
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Best Local Similarity 62.5%; Pred. No. 27; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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; Sequence 1005, Application US/10467657
; Publication No. US2005260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLBIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin9, version 1.04
; SEQ ID NO 1006
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1006

Query Match 40.4%; Score 36; DB 6; Length 322;
Best Local Similarity 63.6%; Pred. No. 38; Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PDWLLNGDRGA 12
Db 251 PDWLFLVLDRSA 261

RESULT 11
US-10-793-626-484
; Sequence 484, Application US/10793626
; Publication No. US2005255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMELLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUJ480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/1164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 484
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-484

Query Match 40.4%; Score 36; DB 6; Length 428;
Best Local Similarity 62.5%; Pred. No. 50; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 WDRGALD 14
Db 333 WGDGVVD 340

RESULT 12
US-11-057-058-60
; Sequence 60, Application US/11057058
; Publication No. US2005024440A1
; GENERAL INFORMATION:
; APPLICANT: LeBowitz, Jonathan
; APPLICANT: Maga, John
; TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
; FILE REFERENCE: SYM-011
; CURRENT APPLICATION NUMBER: US/11/057,058
; PRIOR APPLICATION NUMBER: US 60/543,812
; PRIOR FILING DATE: 2004-02-10
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 1857
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-057-058-60

Query Match 40.4%; Score 36; DB 7; Length 1857;
Best Local Similarity 45.5%; Pred. No. 2.1e+02; Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 WLLNGDRGA 14
Db 1749 WLFWDDGQSID 1759

RESULT 13
US-11-057-058-61
; Sequence 61, Application US/11057058
; Publication No. US2005024400A1
; GENERAL INFORMATION:
; APPLICANT: LeBowitz, Jonathan
; APPLICANT: Maga, John
; TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
; FILE REFERENCE: SYM-011
; CURRENT APPLICATION NUMBER: US/11/057,058
; PRIOR APPLICATION NUMBER: US 60/543,812
; PRIOR FILING DATE: 2004-02-10
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 1857
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-057-058-61

Query Match 40.4%; Score 36; DB 7; Length 1857;
Best Local Similarity 45.5%; Pred. No. 2.1e+02; Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 WLLNGDRGA 14
Db 1749 WLFWDDGQSID 1759

RESULT 14
US-10-510-386-128
; Sequence 128, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjørke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus host Cell
; FILE REFERENCE: 10294 204-US
; CURRENT APPLICATION NUMBER: US/10/510,386

; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 128
; LENGTH: 158
; ORGANISM: *Bacillus licheniformis*
US-10-510-386-128

Query Match 39.9%; Score 35.5; DB 6; Length 158;
Best Local Similarity 72.7%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 5 ULW-GDREGALD 14
Db 65 LYWTGDRGKUD 75

RESULT 15

US-10-793-626-1466

; Sequence 1466, Application US/10793626

; Publication No. US20050255478A1

; GENERAL INFORMATION:

; APPLICANT: KIMMERMAYER, WILLIAM JOHN

; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

; FILE REFERENCE: PU3490US

; CURRENT APPLICATION NUMBER: US/10/793,626

; CURRENT FILING DATE: 2004-03-04

; PRIOR APPLICATION NUMBER: 60/164,258

; PRIOR FILING DATE: 1999-11-09

; NUMBER OF SEQ ID NOS: 4472

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 1466

; LENGTH: 247

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: amino acid sequence

US-10-793-626-1466
Query Match 39.9%; Score 35.5; DB 6; Length 247;
Best Local Similarity 63.6%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 4 WL-JMDRGAL 13
Db 186 WMLLNGNNGVGL 196

Search completed: December 4, 2005, 04:37:50
Job time : 5.375 sec8

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 4, 2005, 04:31:36 ; Search time 100.375 Seconds
77.318 Million cell updates/sec

Title: US-10-632-706-198

Perfect score: 59

Sequence: 1 WGQGTTVTVSS 11

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Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt; 05.80;*
1: uniprot_sprot;*
2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------------|---|
| 1 | 59 | 100.0 | 119 | 2 QGYZ2_MOUSE | QGYZ2_MOUSE |
| 2 | 59 | 100.0 | 121 | 2 Q8CGS2_MOUSE | Q8CGS2_MOUSE PRELIMINARY; |
| 3 | 59 | 100.0 | 146 | 1 HV1_C_HUMAN | AC QGYZ2; |
| 4 | 59 | 100.0 | 147 | 1 HV1_C_HUMAN | DT 01-MAR-2001 (TREMBrel. 16, Created) |
| 5 | 59 | 100.0 | 147 | 2 Q92583_MOUSE | DT 01-MAR-2001 (TREMBrel. 16, Last sequence update) |
| 6 | 59 | 100.0 | 159 | 2 Q96Q90_HUMAN | DT 01-OCT-2003 (TREMBrel. 25, Last annotation update) |
| 7 | 59 | 100.0 | 170 | 2 Q92582_MOUSE | DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30 heavy chain variable region (Fragment). |
| 8 | 59 | 100.0 | 218 | 2 Q92581_MOUSE | OS Mus musculus (Mouse). |
| 9 | 59 | 100.0 | 241 | 2 Q92146_MOUSE | OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |
| 10 | 59 | 100.0 | 348 | 2 Q6YXK1_HUMAN | OX NCBI_TaxID=10990; RN |
| 11 | 59 | 100.0 | 416 | 2 Q9NP86_HUMAN | RTP Song X.T.; Feng Z.Q.; Guan X.H.; RT "Amplification, cloning and sequence analysis of the heavy chain variable region gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma japonicum.", DR Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases. |
| 12 | 59 | 100.0 | 472 | 2 Q6IN09_HUMAN | DR EMBL; AR28262; ARGO1452.1; -; mRNA. |
| 13 | 59 | 100.0 | 573 | 2 Q8WU38_HUMAN | DR HSSP; R01751; IAW. |
| 14 | 59 | 100.0 | 576 | 2 Q6PA41_HUMAN | DR SIRP; QGYZ2; 1-119. |
| 15 | 59 | 100.0 | 595 | 2 Q8WU54_HUMAN | DR InterPro; IPR007110; Ig-like. |
| 16 | 59 | 100.0 | 597 | 2 Q9BU10_HUMAN | DR SMART; SM00406; Ig_V. |
| 17 | 59 | 100.0 | 597 | 2 Q9BQB8_HUMAN | DR PROSITE; PSS0835; Ig_LIKE; 1. |
| 18 | 59 | 100.0 | 597 | 2 Q6GMZ5_HUMAN | DR FT NON_TER 1 119 119 |
| 19 | 59 | 100.0 | 605 | 2 Q6GMY2_HUMAN | DR SEQ; QGYZ2; 1-119. |
| 20 | 59 | 100.0 | 625 | 2 Q96AA6_HUMAN | DR InterPro; IPR003396; Ig_V. |
| 21 | 59 | 98.3 | 465 | 2 Q6PJ22_MOUSE | DR SMART; SM00406; Ig_V. |
| 22 | 58 | 98.3 | 468 | 2 Q5F9W9_MOUSE | DR PROSITE; PSS0835; Ig_LIKE; 1. |
| 23 | 58 | 98.3 | 468 | 2 Q505N9_MOUSE | DR FT NON_TER 1 119 119 |
| 24 | 58 | 98.3 | 471 | 2 Q61K04_MOUSE | DR SEQ; QGYZ2; 1-119 AA; BA893073FD5FA6AB CRC64; |
| 25 | 58 | 98.3 | 472 | 2 Q6P1X7_MOUSE | DR Query Match 100.0%; Score 59; DB 2; Length 119; Best Local Similarity 100.0%; Pred. No. 0; 0.053; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| 26 | 58 | 98.3 | 473 | 2 Q91205_MOUSE | DR Db 109 WGQGTTVTVSS 11 |
| 27 | 58 | 98.3 | 476 | 2 Q561X5_MOUSE | DR RESULT 2 |
| 28 | 58 | 98.3 | 477 | 2 Q58E56_MOUSE | DR Q8CGS2_MOUSE PRELIMINARY; PRT; 121 AA. |
| 29 | 58 | 98.3 | 486 | 2 Q91207_MOUSE | DR AC Q8CGS2; |
| 30 | 58 | 98.3 | 487 | 2 Q9J1K4_MOUSE | DR DT 01-MAR-2003 (TREMBrel. 23, Created) |
| 31 | 58 | 98.3 | 487 | 2 Q9J175_MOUSE | DR DT 01-MAR-2004 (TREMBrel. 26, Last annotation update) |

ALIGNMENTS

| | | | | | |
|----|----|------|-----|----------------|--------------------|
| 32 | 56 | 94.9 | 111 | 1 HV35_MOUSE | PO1804 mus musculu |
| 33 | 56 | 94.9 | 114 | 2 Q9J181_MOUSE | Q9J181 mus musculu |
| 34 | 56 | 94.9 | 117 | 2 Q9DF0_MOUSE | Q9DF0 mus musculu |
| 35 | 56 | 94.9 | 118 | 1 HV39_MOUSE | PO180 mus musculu |
| 36 | 56 | 94.9 | 118 | 2 Q9ZIC4_MOUSE | Q9ZIC4 mus musculu |
| 37 | 56 | 94.9 | 120 | 1 HV03_MOUSE | PO1747 mus musculu |
| 38 | 56 | 94.9 | 121 | 1 HV01_MOUSE | PO1745 mus musculu |
| 39 | 56 | 94.9 | 134 | 2 Q65FR6_MOUSE | Q52R6 mus musculu |
| 40 | 56 | 94.9 | 136 | 1 HV15_MOUSE | PO1759 mus musculu |
| 41 | 56 | 94.9 | 137 | 1 HV11_MOUSE | PO1755 mus musculu |
| 42 | 56 | 94.9 | 137 | 1 HV46_MOUSE | PO1822 mus musculu |
| 43 | 56 | 94.9 | 137 | 2 Q924R6_MOUSE | Q924R6 mus musculu |
| 44 | 56 | 94.9 | 139 | 1 HV07_MOUSE | PO1751 mus musculu |
| 45 | 56 | 94.9 | 140 | 2 Q924P8_MOUSE | Q924P8 mus musculu |

OX NCBI_TAXID=10090;
 RN [1] NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/C;
 RA Wang Z., Munshi K., Osawa P., Pestka J. J., Hart L.P.;
 RL Submitted (SSEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY151140; AANT5452.1; -; mRNA.
 DR HSSP; P01751; INOB
 DR Ensemble; ENSMUSG0000021155; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00406; Ig_v.
 FT PROSITE; PS50835; Ig_LIKE; 1.
 FT NON_TER 1 121 121 AA; 13475 MW; 84FB6CFAB053F5D6 CRC64;
 SQ SEQUENCE 111 WQGQTIVVSS 11

Query Match Best Local Similarity 100.0%; Score 59; DB 1; Length 147;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WQGQTIVVSS 11

Db 136 WQGQTIVVSS 146

RESULT 3

| | | | |
|---|------------|-----------|---------|
| HV21_HUMAN | STANDARD; | PRT; | 146 AA. |
| ID HV21_HUMAN | | | |
| ID | HV21_HUMAN | STANDARD; | PRT; |
| AC P01744; | | | 147 AA. |
| DT 21-JUL-1986 (Rel. 01, Created) | | | |
| DT 16-OCT-2001 (Rel. 40, Last sequence update) | | | |
| DT 10-MAY-2005 (Rel. 47, Last annotation update) | | | |
| DE Ig heavy chain V-II region ARH-77 precursor. | | | |
| OS Homo sapiens (Human). | | | |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo sapiens (Human). | | | |
| OC OC | | | |
| OC NCBI_TAXID=9606; | | | |
| RN [1] | | | |
| RR NUCLEOTIDE SEQUENCE. | | | |
| RX MEDLINE:83065234; PubMed=6815656; | | | |
| RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J., Bell L.O., Gould H.J., | | | |
| RT "Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line.", | | | |
| RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982). | | | |
| RN [2] | | | |
| RP PROTEIN SEQUENCE OF 20-147. | | | |
| RA Bernmark H.H., Johansson S.G.O., von Bahr-Lindstrom H., (In) Bach M.K. (eds.); | | | |
| RL Immediate hypersensitivity: modern concepts and developments, pp.1-36, Marcel Dekker, New York (1978). | | | |
| RL -1. MISCELLANEOUS: This epsilon chain was isolated from a myeloma protein. | | | |
| CC -1. SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain. | | | |
| CC --- | | | |
| CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed. | | | |
| CC --- | | | |
| CC --- | | | |
| DR HSSP; P01751; INOB. | | | |
| DR GO; GO:0005576; C:extracellular region; NAS. | | | |
| DR GO; GO:0003823; F:antigen binding; NAS. | | | |
| DR InterPro; IPR007110; Ig-like. | | | |
| DR SMART; SM00406; Ig_v. | | | |
| DR PROSITE; PS50835; Ig_LIKE; 1. | | | |
| DR Direct protein sequencing; Immunoglobulin domain; Immunoglobulin v region; Pyrrolidone carboxylic acid; Signal. | | | |
| FT SIGNAL 1 19 | | | |
| FT CHAIN 20 147 Ig heavy chain V-I region ND. | | | |
| FT DOMAIN 20 131 Ig-like. | | | |
| FT MOD_RES 20 20 Pyrrolidone carboxylic acid. | | | |
| FT DISUFD 41 115 T -> V (in Ref. 2). | | | |
| FT CONFLICT 21 21 IH -> HI (in Ref. 2). | | | |
| FT CONFLICT 53 54 VG -> GV (in Ref. 2). | | | |
| FT CONFLICT 67 68 Missing (in Ref. 2). | | | |
| FT CONFLICT 125 125 | | | |
| FT NON_TER 147 147 | | | |
| SQ SEQUENCE 147 AA; 16496 MW; 94FP9P2A536C20 CRC64; | | | |

Query Match Best Local Similarity 100.0%; Score 59; DB 1; Length 147;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WQGQTIVVSS 11

Db 136 WQGQTIVVSS 146

RESULT 4

| | | | |
|---|------------|-----------|---------|
| HV21_HUMAN | STANDARD; | PRT; | 147 AA. |
| ID HV21_HUMAN | | | |
| ID | HV21_HUMAN | STANDARD; | PRT; |
| AC P01744; | | | 147 AA. |
| DT 21-JUL-1986 (Rel. 01, Created) | | | |
| DT 16-OCT-2001 (Rel. 40, Last sequence update) | | | |
| DT 10-MAY-2005 (Rel. 47, Last annotation update) | | | |
| DE Ig heavy chain V-I region ND precursor (Fragment(s). | | | |
| OS Homo sapiens (Human). | | | |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo sapiens (Human). | | | |
| OC OC | | | |
| OC NCBI_TAXID=9606; | | | |
| RN [1] | | | |
| RR NUCLEOTIDE SEQUENCE. | | | |
| RX MEDLINE:83065234; PubMed=6815656; | | | |
| RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J., Bell L.O., Gould H.J., | | | |
| RT "Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line.", | | | |
| RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982). | | | |
| RN [2] | | | |
| RP PROTEIN SEQUENCE OF 20-147. | | | |
| RA Bernmark H.H., Johansson S.G.O., von Bahr-Lindstrom H., (In) Bach M.K. (eds.); | | | |
| RL Immediate hypersensitivity: modern concepts and developments, pp.1-36, Marcel Dekker, New York (1978). | | | |
| RL -1. MISCELLANEOUS: This epsilon chain was isolated from a myeloma protein. | | | |
| CC -1. SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain. | | | |
| CC --- | | | |
| CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed. | | | |
| CC --- | | | |
| DR HSSP; P01751; INOB. | | | |
| DR GO; GO:0005576; C:extracellular region; NAS. | | | |
| DR GO; GO:0003823; F:antigen binding; NAS. | | | |
| DR InterPro; IPR007110; Ig-like. | | | |
| DR SMART; SM00406; Ig_v. | | | |
| DR PROSITE; PS50835; Ig_LIKE; 1. | | | |
| DR Direct protein sequencing; Immunoglobulin domain; Immunoglobulin v region; Pyrrolidone carboxylic acid; Signal. | | | |
| FT SIGNAL 1 19 | | | |
| FT CHAIN 20 147 Ig heavy chain V-I region ND. | | | |
| FT DOMAIN 20 131 Ig-like. | | | |
| FT MOD_RES 20 20 Pyrrolidone carboxylic acid. | | | |
| FT DISUFD 41 115 T -> V (in Ref. 2). | | | |
| FT CONFLICT 21 21 IH -> HI (in Ref. 2). | | | |
| FT CONFLICT 53 54 VG -> GV (in Ref. 2). | | | |
| FT CONFLICT 67 68 Missing (in Ref. 2). | | | |
| FT CONFLICT 125 125 | | | |
| FT NON_TER 147 147 | | | |
| SQ SEQUENCE 147 AA; 16496 MW; 94FP9P2A536C20 CRC64; | | | |

Query Match Best Local Similarity 100.0%; Score 59; DB 1; Length 147;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 137 | ||||| 147
RESULT 5
ID Q2553_MOUSE PRELIMINARY; **PRT;** 147 AA.
AC Q9553;
DT 01-DEC-2001 (TREMBrel. 19, Created)
DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
DB MR23;
OS Mus musculus (Mouse);
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TAXID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,
RA Yan X.J., Hou Y., Su C.Z.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
 the repair of intestinal epithelium after gamma-irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
 of the irradiated mice by treatment with the intestinal RNA of mice of
 the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240166; AAC43731.1; - ; mRNA.
DR HSPB; P01751; IABW;
SRP; Q2553; 3-139.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; Ig_LIKE; 1.
KW Immunoglobulin domain;
SQ SEQUENCE 147 AA; 16274 MW; 80059412B97191F CRC64;

Query Match 100.0%; Score 59; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.0067; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGQGTIVTVSS 11
Db 111 WGQGTIVTVSS 121

RESULT 6
OSQSO_HUMAN
ID OSQSO_HUMAN PRELIMINARY; **PRT;** 159 AA.
AC Q9550;
DT 01-DEC-2001 (TREMBrel. 19, Created)
DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
DE Putative matrix cell adhesion molecule-3.
OS Homo Sapiens (Human);
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo; Homo sapiens;
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wilson M.D.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBBJ databases.
DR EMBL; AV039025; AAC82649.1; - ; mRNA.
DR HSPB; P01869; IAB6;
DR InterPro; IPR007110; Ig-like.

Db 139 WGQGTIVTVSS 149
RESULT 7
ID Q9552_MOUSE PRELIMINARY; **PRT;** 170 AA.
AC Q9552;
DT 01-DEC-2001 (TREMBrel. 19, Created)
DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
DB MR24;
OS Mus musculus (Mouse);
OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TAXID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,
RA Yan X.J., Hou Y., Su C.Z.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
 the repair of intestinal epithelium after gamma-irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
 of the irradiated mice by treatment with the intestinal RNA of mice of
 the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240167; AAC43732.1; - ; mRNA.
DR HSPB; P01751; IABW;
SRP; Q2552; 3-124.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; Ig_LIKE; 1.
KW Immunoglobulin domain;
SQ SEQUENCE 170 AA; 17978 MW; 5042B23CC6C10F38 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.0078; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGQGTIVTVSS 11
Db 113 WGQGTIVTVSS 123

RESULT 8
ID Q9551_MOUSE PRELIMINARY; **PRT;** 218 AA.
AC Q9551;
DT 01-DEC-2001 (TREMBrel. 19, Created)
DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
DB MR25 (Fragment);
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mu_B.
 OX NCBI_TAXID=10090;
 RN [1] _NUCLEOTIDE SEQUENCE.
 RP STRAIN=BALB/c;
 RX PubMed=1819679;
 RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,
 RT Yan X.J., Hou Y., Su C.Z.,
 RT "Mechanism of exogenous nucleic acids and their precursors improving
 the repair of intestinal epithelium after gamma-irradiation in mice.";
 RL World J. Gastroenterol. 6:709-717(2000).
 RN [2] _NUCLEOTIDE SEQUENCE.
 RP STRAIN=BALB/c;
 RA Cui D., Zeng G., Yan X., Li X., Su C.;
 RT "Cloning of mouse genes related to repairing of intestinal epithelium
 of the irradiated mice by treatment with the intestinal RNA of mice of
 the same strain.";
 RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
 DR EMBL: AAF40168; AAK13733.1; -; mRNA.
 DR Ensemble; ENSMUSG0000005040; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR03596; Ig-v.
 DR SMART; SM00406; Ig_v.
 DR PROSITE; PS50035; Ig_LIKE; 1.
 DR PROSITE; PS50035; Ig_LIKE; 1.
 DR NON_TER 218 AA; 218
 SQ SEQUENCE 218 AA; 23013 MN; 527B4FA8F7982817 CRC64;
 Query Match 100.0%; Score 59; DB 2; Length 218;
 Best Local Similarity 100.0%; Pred. No. 0.01; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Non-TER 218 AA; 23013 MN; 527B4FA8F7982817 CRC64;
 QY 1 WGQGTTVTVSS 11
 DB 110 WGQGTTVTVSS 120

RESULT 9
 ID 0921A6_MOUSE PRELIMINARY; PRT; 241 AA.
 AC 0921A6;
 DT 01-JUL-2001 (TREMBrel. 19, Created)
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 DR Anti-CBA 79 single chain Fv (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mu_B.
 OX NCBI_TAXID=10090;
 RN [1] _NUCLEOTIDE SEQUENCE.
 RA Zhu N.S., Chen Y.Y.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 ID 0921A6_HUMAN PRELIMINARY; PRT; 348 AA.
 AC 0921A6_HUMAN PRELIMINARY;
 DT 05-JUL-2004 (TREMBrel. 27, Created)
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)
 DR Hepatitis B virus receptor binding protein (Fragment).
 DE Homo sapiens (Human).
 OC Bakaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TAXID=9606;
 RN [1] _NUCLEOTIDE SEQUENCE.
 RA Zhu N.S., Chen Y.Y.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 ID 0921A6_HUMAN PRELIMINARY; PRT; 348 AA.
 AC 0921A6_HUMAN PRELIMINARY;
 DT 05-JUL-2004 (TREMBrel. 27, Created)
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003591; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00407; IgE1; 3.
 DR PROSITE; PS50835; Ig_LIKE; 3.
 DR PROSITE; PS00290; Ig_MHC; UNKNOWN_2.
 DR Receptor.
 DR Non-TER 348 AA; 38162 MN; DD96C3D7E0BB5845 CRC64;
 SQ SEQUENCE 348 AA; 38162 MN; DD96C3D7E0BB5845 CRC64;
 Query Match 100.0%; Score 59; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 0.017; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Non-TER 348 AA; 38162 MN; DD96C3D7E0BB5845 CRC64;
 QY 1 WGQGTTVTVSS 11
 DB 8 WGQGTTVTVSS 18

RESULT 11
 ID QNPBP6_HUMAN PRELIMINARY; PRT; 416 AA.
 AC QNPBP6_HUMAN PRELIMINARY;
 DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 DE Immunoglobulin heavy chain variant (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.

Mon Dec 5 10:18:16 2005

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Page 7

Query Match 100.0%; Score 59; DB 2; Length 595;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WGGQTIVTVSS 11
Db 141 WGGQTIVTVSS 151

Search completed: December 4, 2005, 04:52:27
Job time : 102.375 secs

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/

Page 2

CC specifically bound by an antibody expressed by clone as mentioned in (I), producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain variable region complementarity determining
 XX region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum neurotoxin type A (BoNT/A). Also described are: a polypeptide (II) comprising BoNT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I); producing (I); and a composition (III) comprising several anti-botulinum toxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising (I); and a kit comprising (I). (I) is useful for neutralising BoNT/A antibody and for neutralising a botulinum neurotoxin which involves contacting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. (I) is useful for diagnosing the botulism or for treating pathologies associated with botulinum neurotoxin poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I) enables rapid detection or diagnosis of botulism. This is the amino acid sequence of mouse heavy chain variable region complementarity determining region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

| | Query | Match | Score | DB | Length | Indels | Gaps |
|---------|--------------|------------------|--------|-------|------------|---------|------|
| Matches | 11; | Local Similarity | 100.0% | Pred. | No | 0.0017; | 0 |
| Qy | 1 LATYYFGLDV | 11 | 100.0% | 0; | Mismatches | 0; | |
| Db | 1 LATYYFGLDV | 11 | | | | | |

```

Query Match          100.0%; Score 60; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017; Mismatches 0;
Matches 11; Conservative 0; Indels 0; Gaps 0;
Qy              1 LATYYFGIDV 11
Db              1 LATYYFGIDV 11

```

RESULT 2

XX

XX DECEMBER 2000

DE Mouse heavy chain variable region

KW antibacterial; antibody; Bontium

KW heavy chain variable region; compl

XX

XX
PD
09-SEB-2004

PF 01-AUG-2003; 2003US-00632706.

PR 01-AUG-2002; 2002US-0400721P.

PA
REGG UNIV CALIFORNIA.

xx

New illustrated anti-slavery tract published

PT with botulinum neurotoxin poisonin

xxii
THEORY AND PRACTICE

The invention describes an isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a specific

clone where β_1 binds to and neutralises botulinum neurotoxin type A (BONTA). An isolated antibody (β_1) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone S251, C59, 1C6, 3D12, B4, 1F3, huC55, Ar1, Ar2, WRI(V) WRI(T), 3-1, CC

PS Example 5; Fig 1; 167pp; English.

XX
CC The invention relates to a human monoclonal antibody or its antigen-
CC binding portion that specifically binds to mucosal addressin cell
CC adhesion molecule (MacCAM). The invention also relates to a hybridoma
CC cell line that produces the human monoclonal antibody, a pharmaceutical
composition comprising an amount of the monoclonal antibody or its
antigen-binding portion and a pharmaceutical carrier, a method of
treating inflammatory disease in a subject, an isolated cell line that
produces the monoclonal antibody or its antigen-binding portion or the
heavy chain or light chain of the antibody or of its portion, an isolated
nucleic acid molecule comprising a nucleotide sequence encoding the heavy
chain or its antigen-binding portion or the light chain or its antigen-
binding portion of an antibody described above, a vector comprising the
nucleic acid molecule, where the vector optionally comprises an
expression control sequence operably linked to the nucleic acid molecule,
CC a host cell comprising the vector or the nucleic acid molecule above, a
method of producing a human monoclonal antibody or its antigen-binding
portion that specifically binds MacCAM, a method of isolating an antibody
or its antigen-binding portion that specifically binds to MacCAM, a
method of treating a subject in need of a human antibody or its antigen-
binding portion that specifically binds to MacCAM and inhibits binding to
alpha4beta7, a method of inhibiting alpha4beta7 binding to cells
expressing human MacCAM, a method of inhibiting MacCAM-mediated leukocyte
-endothelial cell adhesion, migration and infiltration into tissues, a
method of inhibiting alpha4beta7/MacCAM-dependent cellular adhesion,
inhibiting the MacCAM-mediated recruitment of lymphocytes to
gastrointestinal lymphoid tissue, a method of diagnosing a disorder
characterized by circulating soluble human MacCAM and detecting
inflammation in a subject. The antibody, composition and methods are
useful for diagnosing and treating inflammatory disease, e.g.
inflammatory bowel disease, Crohn's disease, ulcerative colitis,
diverticular disease, gastritis, liver disease, primary biliary
cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and
CC graft versus host disease. This sequence represents a human monoclonal
anti-MacCAM antibody related protein of the invention.
XX
SQ Sequence 122 AA;

Query Match 80.0%; Score 48; DB 9; Length 122;
Best Local Similarity 63.6%; Pred. No. 2.5; Mismatches 7; Conservative 3; Misnmatches 1; Indels 0; Gaps 0;
Db 100 VVYYGGMDV 110

RESULT 4
ADD28082
ID ADD28082 standard; protein; 114 AA.

AC ADD28082;
XX DT 15-JAN-2004 (first entry)
XX Lymphoma related immunoglobulin variable region.

XX B-cell; malignant; immunoglobulin; immunoglobulin variable region;
Ig variable region; glycosylation site; lymphoma; B cell receptor;
cytotoxic; gene therapy; glycosylation inhibitor;
non-Hodgkin's lymphoma.
OS Synthetic.
OS Homo sapiens.
XX WO2003074059-A2.

XX 12-SEP-2003.
PD XX 24-FEB-2003; 2003WO-GB000783.

PR XX 07-MAR-2002; 2002GB-00005395.

XX (CANC-) CANCER RES TECHNOLOGY LTD.

PA XX Zhu D, Stevenbon P;

PI XX DR; MPI; 2003-902720/82.

PT XX PT Classifying a B-cell as malignant or normal by isolating a sequence
representing an Ig variable region from the B cell; detecting the
presence of a glycosylation site and classifying the cell as malignant or
normal.

DS XX Disclosure; Fig 3; 61pp; English.

The present invention describes a method for classifying a B-cell as
malignant or normal comprising: (a) isolating a sequence representing an
immunoglobulin (Ig) variable region from the B cell; (b) detecting the
presence of a glycosylation site; and (c) classifying the cell as
malignant or normal on the basis of the presence or absence of a
glycosylation site. Also described: (1) treating a patient suffering from
or at risk of having lymphoma; (2) screening for substances capable of
inhibiting glycosylation of the Ig variable region of the B cell receptor
; and (3) screening for substances (S) capable of inhibiting the
interaction between lectins of the type found in the germinal centre and
N-glycans found on the surface of Ig of lymphoma cells. (S) has
cytostatic activity, and can be used in gene therapy, and as a
glycosylation inhibitor. The method is useful in classifying a B-cell as
malignant or normal. The glycosylation inhibitor is useful in preparing a
medicament for treating non-Hodgkin's lymphoma. The present sequence
represents an Ig variable region sequence which is used in the
exemplification of the present invention.

XX Sequence 114 AA;

Query Match 78.3%; Score 47; DB 7; Length 114;
Best Local Similarity 77.8%; Pred. No. 3.4; Mismatches 7; Conservative 2; Misnmatches 0; Indels 0; Gaps 0;
Db 106 TTYYGMDV 114

RESULT 5
ADD2823
ID ADD2823 standard; protein; 129 AA.

AC XX ADD2823;
XX DT 15-JAN-2004 (first entry)
XX DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:101.

XX Human heterodimeric antibody heavy chain variable region SEQ ID NO:101.
KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
KW edema factor; lethal factor; virucide; antibacterial; immunotherapy;
KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
KW Venezuelan equine encephalomyelitis virus; VSBV; West Nile virus; WNV.
XX OS Synthetic.
OS Homo sapiens.
XX PN WO2003076568-A2.

XX PD 18-SEP-2003.
XX PR 11-FEB-2003; 2003WO-US004206.
PR 11-FEB-2002; 2002US-0356056P.
PR 29-APR-2002; 2002US-0376408P.
PR 27-SEP-2002; 2002US-0414033P.
PR 25-NOV-2002; 2002US-0428807P.
XX

PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Bowdish KS, Wild MA;
 XX
 DR WPI; 2003-722327/6B.

XX
 PT New human heterodimeric antibodies or their antibody fragments, useful as anti-toxins or anti-infectives with respect to infective agents, e.g. anti-anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West Nile virus.

XX
 PS Claim 11; SEQ ID NO 101; 67pp; English.

The present invention describes a human heterodimeric antibody (I) (fragment), having a binding affinity of at least 1×10^{-8} M to the protective antigen of *Bacillus anthracis* or a molecule involved in anthrax infection that blocks binding of the antigen or molecule to cell receptors, edema factor and lethal factor. (I) has virucide and antibacterial activities, and can be used in immunotherapy. The antibodies (I) are useful as anti-toxins or anti-infectives with respect to infective agents, such as anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The present sequence represents a human heterodimeric antibody heavy chain variable region amino acid sequence, which is used in the exemplification of the present invention.

SQ Sequence 129 AA;

| | | | | | | | | |
|-------|-----------------------|-------|-------|-----|--------|---------|------|----|
| Query | 3 TYYYFGIDV | Score | 47; | DB | 7; | Length | 129; | |
| QY | Best Local Similarity | 77.8% | Pred. | No. | 3.9; | Matches | | |
| Db | 105 TRYYGMDV | | | 0; | Indels | 0; | Gaps | 0; |

RESULT 6

ADD20237 DT
 ID ADD20237 standard; protein; 134 AA.

XX AC ADD20237;
 XX DT 15-JAN-2004 (first entry)
 XX DB Human heterodimeric antibody heavy chain variable region SSEQ ID NO:15.

XX KW protective antigen; *Bacillus anthracis*; anthrax infection; cell receptor; edema factor; lethal factor; virucide; antibacterial; immunotherapy; anti-toxin; anti-infective; anthrax; botulinum; smallpox; Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.

OS Synthetic.
 OS Homo sapiens.

XX WO2003076568-A2.

XX PD 18-SEP-2003.

XX PP 11-FEB-2003; 2003WO-US004206.

XX PR 11-FEB-2002; 2002US-0356086P.

XX PR 29-APR-2002; 2002US-0376408P.

XX PR 27-SEP-2002; 2002US-0414053P.

XX PR 25-NOV-2002; 2002US-0428807P.

XX PA (ALEX-) ALEXION PHARM INC.

XX (ALEX-) ALEXION PHARM INC.

XX PI Bowdish KS, Wild MA;

XX DR WPI; 2003-722327/6B.

XX
 PT New human heterodimeric antibodies or their antibody fragments, useful as anti-toxins or anti-infectives with respect to infective agents, e.g. anti-anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West Nile virus.

XX
 PS Claim 6; SEQ ID NO 15; 67pp; English.

The present invention describes a human heterodimeric antibody (I) (fragment) having a binding affinity of at least 1×10^{-8} M to the protective antigen of *Bacillus anthracis* or a molecule involved in anthrax infection that blocks binding of the antigen or molecule to cell receptors, edema factor and lethal factor. (I) has virucide and antibacterial activities, and can be used in immunotherapy. The antibodies (I) are useful as anti-toxins or anti-infectives with respect to infective agents, such as anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The present sequence represents a human heterodimeric antibody heavy chain variable region amino acid sequence, which is used in the exemplification of the present invention.

SQ Sequence 134 AA;

| | | | | | | | | |
|-------|-----------------------|-------|-------|-----|--------|---------|------|----|
| Query | 3 TYYYFGIDV | Score | 47; | DB | 7; | Length | 134; | |
| QY | Best Local Similarity | 77.8% | Pred. | No. | 4; | Matches | | |
| Db | 110 TRYYGMDV | | | 0; | Indels | 0; | Gaps | 0; |

RESULT 7

ADV86824 DT
 ID ADV86824 standard; protein; 134 AA.

XX AC ADV86824;
 XX DT 10-MAR-2005 (first entry)
 XX DB *Bacillus anthracis* toxin Fab 9 K 2e G pro heavy chain variable region.

XX KW Bioterrorism; *Bacillus anthracis* infection; vaccine; diagnosis; antibacterial; antibody; heavy chain variable region.

XX OS Homo sapiens.

XX FN WO2004110362-A2.

XX PD 23-DBC-2004.

XX FP 26-MAY-2004; 2004WO-US016557.

XX PR 02-JUN-2003; 2003US-00452593.

XX PA (ALEX-) ALEXION PHARM INC.

XX PI Bowdish KS, Frederickson S, Wild MA, Maruyama T, Nolan MJ;

XX DR WPI; 2005-057715/06.

XX
 PT Treating an animal with anthrax infection by administering an antibody to the protective antigen of *Bacillus anthracis*, and blocking binding to cell receptors, edema factor or lethal factor.

XX PS Claim 7, SEQ ID NO 15; 87pp; English.

XX
 PT A claimed method for treating an animal infected with *Bacillus anthracis* comprises administering an antibody or antibody fragment that binds to a molecule involved in anthrax infection and which has the ability to block the binding of the molecule to at least one of a cell receptor, PA63 heptamer, PA63, edema factor and lethal factor. A claimed method for determining exposure to B. anthracis comprises assaying a sample for the presence of a molecule selected from cell receptors, PA63, PA63 heptamer,

CC PA83, edema factor or lethal factor with an antibody that has binding
 CC affinity for the molecule, where the presence of elevated levels of the
 CC antibody correlates with the presence of a disease associated with B.
 CC anthracis. Alternatively, the method involves assaying for the presence
 CC of an antibody to a cell receptor, PA63, PA63 heptamer, PA83, edema
 CC factor or lethal factor with a secondary antibody having binding affinity
 CC for the antibody, where the presence of elevated levels of the secondary
 CC antibody correlates with the presence of B. anthracis in a subject. In
 CC all cases, the antibody (full length or functional fragment) may comprise
 CC a heavy chain variable region selected from a group of sequences ADV6810
 CC -ADV6827, a light chain kappa region selected from a group or sequences
 CC ADV6828-ADV8685 and a light chain lambda region selected from a group
 CC of sequences ADV8686-ADV8687. Diagnostic kits are provided. A claimed
 CC vaccine comprises a multimer of anthrax toxin PA63. The methods and
 CC compositions of the present invention are also useful for producing anti-
 CC toxins or anti-infectives to infective agents such as anthrax, botulinum,
 CC smallpox, Venezuelan equine encephalomyelitis and West Nile virus. The
 CC present sequence is that of the heavy chain variable region of a human
 CC Fab (designated 9 K 2e G Pro) with positive reactivity to anthrax
 CC proteins Pa63 and Pa83. Phage libraries were developed from mRNA isolated
 CC from blood and bone marrow samples of donors who had been vaccinated
 CC against anthrax. The libraries were panned against PA83 and PA63, and
 CC sequence analysis was performed on positive responders. Neutralization of
 CC anthrax toxin activity by purified Fab's was demonstrated.

SQ Sequence 134 AA;

Query Match 78.3%; Score 47; DB 9; Length 134;
 Best Local Similarity 77.8%; Pred. No. 4; Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TYYFGDV 11
 Db 110 TYYYGMDV 11B

RESULT 8

ADR28082
 ID ADR28082 standard; protein: 244 AA.
 AC :ADR28082;
 XX DT 07-OCT-2004 (first entry)

NPB polypeptide scFv27, seq id 29.
 Cytostatic; metastasis inhibitor; neuropilin binder; NPB; scFv;
 Single chain antibody; neuropilin-1; NP-1; angiogenesis; tumour; cancer.

Mus SP.
 Synthetic.
 Location/Qualifiers
 87..103
 /note="complementary determining region claimed under
 claim 5"
 WO2004056874-A2.

Key Region
 FT
 XX
 PN
 XX
 PD
 XX
 PR
 XX
 PR
 XX
 PA
 XX
 PA
 XX
 PT
 XX
 PI
 XX
 DR

08-JUL-2004.

22-DEC-2003; 2003WO-EP014756.

20-DEC-2002; 2002US-0435893P.

15-JAN-2003; 2003EP-00000615.

(XERI-) XERION PHARM AG.
 (TUFT) UNIV TUFTS.Unger CM, Beste G, Zehetmeier C, Iain B, Torella C, Niewoehner J;
 Jay DG, Eustace BK, Knauer R, Jensen KH;
 XX WPT; 2004-507700/4B.

N-PSDB; ADR28116.

DR

XX

PT

XX

The invention relates to a neuropilin binder (NPB) (I) which is a polypeptide, antibody, scFv, antibody fragment or bioconjugate, that modulates neuropilin-1 (NP-1) function or inhibits NP-1 dependent angiogenesis of endothelial cells and/or invasion of tumor cells useful for treating cancer.

Claim 3: SEQ ID NO 29; 120PP; English.

RESULT 8

ADR28082

ID ADR28082 standard; protein: 244 AA.

AC :ADR28082;

XX DT 07-OCT-2004 (first entry)

DE NPB polypeptide scFv27, seq id 29.

Cytostatic; metastasis inhibitor; neuropilin binder; NPB; scFv; Single chain antibody; neuropilin-1; NP-1; angiogenesis; tumour; cancer.

Mus SP.

Synthetic.

Location/Qualifiers

87..103
 /note="complementary determining region claimed under
 claim 5"
 WO2004056874-A2.

Key Region

FT

XX

PN

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PD

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PR

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PR

XX

PA

XX

PA

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PT

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PI

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DR

Sequence 244 AA;

Query Match 78.3%; Score 47; DB 8; Length 244;

Best Local Similarity 77.8%; Pred. No. 7.7; Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TYYFGDV 11

Db 95 TYYYGMDV 103

RESULT 9

AREB45991

ID AREB45991 standard; protein: 468 AA.

AC AEB45991;

XX

DE Human monoclonal anti-MADCAM antibody #27.

Monoclonal antibody; mucosal addressin cell adhesion molecule; MADCAM; inflammation; inflammatory bowel disease; Crohns disease; ulcerative colitis; diverticular disease; gastritis; liver disease; primary biliary cirrhosis; primary sclerosing cholangitis; insulin dependent diabetes; graft versus host disease; anti-inflammatory; gastrointestinal-gen.; antiulcer; hepatotropic; antidiabetic; immunosuppressive; antibody.

Homo sapiens.

OS

XX

PN WO200507620-A2.

XX

PD 28-JUL-2005.

XX

PR 07-JAN-2005; 2005WO-US000370.

XX

PR 09-JAN-2004; 2004US-0535490P.

XX

PA (PFIZ) PFIZER INC.

PA (ABGEN-) ABGENX INC.

PA (PFIZ) PFIZER LTD.

XX

PI Pollen N, Molloy E, Kellermann S, Green L, Haak-Frendscho M;

XX

DR WPI; 2005-554958/56.
DR N-PSDB; ABB45890.

XX New antibody to Mucosal Adressin Cell Adhesion Molecule, useful for PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel disease, ulcerative colitis, gastritis, insulin-dependent diabetes or PT graft versus host disease.

XX Claim 8; SEQ ID NO 56; 167PP; English.

The invention relates to a human monoclonal antibody or its antigen-binding portion that specifically binds to mucosal addressin cell adhesion molecule (MadCAM). The invention also relates to a hybridoma cell line that produces the human monoclonal antibody, a pharmaceutical composition comprising an amount of the monoclonal antibody or its antigen-binding portion and a pharmaceutical carrier, a method of treating inflammatory disease in a subject, an isolated cell line that produces the monoclonal antibody or its antigen-binding portion or the heavy chain or light chain of the antibody or of its portion, an isolated nucleic acid molecule comprising a nucleotide sequence encoding the heavy chain or its antigen-binding portion or the light chain or its antigen-binding portion of an antibody described above, a vector comprising the nucleic acid molecule, where the vector optionally comprises an expression control sequence operably linked to the nucleic acid molecule, a host cell comprising the vector or the nucleic acid molecule above, a method of producing a human monoclonal antibody or its antigen-binding portion that specifically binds MadCAM, a method of isolating an antibody or its antigen-binding portion that specifically binds to MadCAM, a method of treating a subject in need of a human antibody or its antigen-binding portion that specifically binds to MadCAM and inhibits binding to alpha4beta7, a method of inhibiting alpha4beta7 binding to cells expressing human MadCAM, a method of inhibiting MadCAM-mediated leukocyte -endothelial cell adhesion, migration and infiltration into tissues, a method of inhibiting alpha4beta7/MadCAM-dependent cellular adhesion, inhibiting the MadCAM-mediated recruitment of lymphocytes to gastrointestinal lymphoid tissue, a method of diagnosing a disorder characterized by circulating soluble human MadCAM and detecting inflammation in a subject. The antibody, composition and methods are useful for diagnosing and treating inflammatory disease, e.g. diverticular disease, Crohn's disease, ulcerative colitis, diverticular disease, gastritis, liver disease, primary biliary cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and graft versus host disease. This sequence represents a human monoclonal anti-MadCAM antibody of the invention.

XX Sequence 468 AA;

Query Match 78.3%; Score 47; DB 9; Length 468;
Best Local Similarity 77.8%; Pred. No. 15; Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY ||||:||| TYYFGIDV 11
OY ||||:||| Db 123 TYYFGIDV 131

RESULT 10

AEB45853 standard; protein: 469 AA.

AC AEB45853;
XX 06-OCT-2005 (first entry)

Human monoclonal anti-MadCAM antibody #9.

DR Monoclonal antibody; mucosal addressin cell adhesion molecule; MadCAM; XX inflammation; inflammatory bowel disease; Crohn's disease; XX ulcerative colitis; diverticular disease; gastritis; liver disease; XX primary biliary cirrhosis; primary sclerosing cholangitis; insulin dependent diabetes; graft versus host disease; antiinflammatory; XX gaстронтестиналь-ген; антиулcer; hepatotropic; antidiabetic; XX immunosuppressive; antibody.

XX Homo sapiens.
XX OS
XX PN WO20050620-A2.
XX PD 28-JUL-2005.

XX 07-JAN-2005; 2005WQ-US000370.
XX PR 09-JAN-2004; 2004US-0535490P.

XX DR (PFIZ) PFIZER INC.
PA (ABCB-) ABGENIX INC.
PA (PFIZ) PFIZER LTD.
XX PR Pullen N, Molloy E, Kellermann S, Green LL, Haak-Frendscho M;
XX DR WPI; 2005-554958/56.
XX N-PSDB; ABB45852.

XX Claim 8; SEQ ID NO 18; 167PP; English.

The invention relates to a human monoclonal antibody or its antigen-binding portion that specifically binds to mucosal addressin cell adhesion molecule (MadCAM). The invention also relates to a hybridoma cell line that produces the human monoclonal antibody, a pharmaceutical composition comprising an amount of the monoclonal antibody or its antigen-binding portion and a pharmaceutical carrier, a method of treating inflammatory disease in a subject, an isolated cell line that produces the monoclonal antibody or its antigen-binding portion or the heavy chain or light chain of the antibody or of its portion, an isolated nucleic acid molecule comprising a nucleotide sequence encoding the heavy chain or its antigen-binding portion or the light chain or its antigen-binding portion of an antibody described above, a vector comprising the nucleic acid molecule, where the vector optionally comprises an expression control sequence operably linked to the nucleic acid molecule, a host cell comprising the vector or the nucleic acid molecule above, a method of producing a human monoclonal antibody or its antigen-binding portion that specifically binds MadCAM, a method of isolating an antibody or its antigen-binding portion that specifically binds to MadCAM, a method of treating a subject in need of a human antibody or its antigen-binding portion that specifically binds to MadCAM and inhibits binding to alpha4beta7, a method of inhibiting alpha4beta7 binding to cells expressing human MadCAM, a method of inhibiting MadCAM-mediated leukocyte -endothelial cell adhesion, migration and infiltration into tissues, a method of inhibiting alpha4beta7/MadCAM-dependent cellular adhesion, inhibiting the MadCAM-mediated recruitment of lymphocytes to gastrointestinal lymphoid tissue, a method of diagnosing a disorder characterized by circulating soluble human MadCAM and detecting inflammation in a subject. The antibody, composition and methods are useful for diagnosing and treating inflammatory disease, e.g. diverticular disease, Crohn's disease, ulcerative colitis, diverticular disease, gastritis, liver disease, primary biliary cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and graft versus host disease. This sequence represents a human monoclonal anti-MadCAM antibody of the invention.

XX Sequence 469 AA;

Query Match 78.3%; Score 47; DB 9; Length 469;
Best Local Similarity 77.8%; Pred. No. 15; Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY ||||:||| TYYFGIDV 11
OY ||||:||| Db 123 TYYFGIDV 131

RESULT 11

ADR38712 standard; peptide: 13 AA.

XX

ID

ADR38712;

AC

XX

DT

02-DEC-2004 (first entry)

XX

DE

Mouse heavy chain variable region CDR3 seqid 114.

XX

PR

antibacterial; antibody: botulinum neurotoxin type A; BONT/A;

KW

BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;

KW

toxin neutralisation; botulinum neurotoxin poisoning; mouse;

KW

heavy chain variable region; complementarity determining region; CDR3.

OS

Mus sp.

XX

PN

US2004175385-A1.

XX

PR

09-SEP-2004.

XX

PD

01-AUG-2003; 2003US-00632706.

XX

PR

31-AUG-1998; 98US-00144886.

XX

PR

01-AUG-2002; 2002US-0400721P.

XX

PA

(REGC) UNIV CALIFORNIA.

XX

PI

Marks JD, Amersdorfer P;

XX

DR

WPI; 2004-652009/63.

XX

PT

New isolated antibody that neutralizes botulinum neurotoxin type A, useful for diagnosing botulism or for treating pathologies associated with botulinum neurotoxin poisoning.

XX

PS

Example 3; SEQ ID NO 114; 110pp; English.

XX

CC

The invention describes an isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a specific clone where (I) binds to and neutralises botulinum neurotoxin type A (BONT/A). An isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone S25, C25, C19, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1, 3-8, 3-10 and ING1, where (I) binds to and neutralises botulinum neurotoxin type A (BONT/A). Also described are: a polypeptide (II) comprising BONT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I); producing (I); and a composition (III) comprising several anti-different epitope or a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising (I); and a kit comprising (I). (I) is useful for neutralising BONT/A antibody and for neutralising a botulinum neurotoxin which involves contacting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. (I) is useful for diagnosing the botulism or for treating pathologies associated with botulinum neurotoxin poisoning. (I) exhibits specificity and affinity towards BONT/A. (I) enables rapid detection or diagnosis of botulism. This is the amino acid sequence of mouse heavy chain variable region complementarity determining region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

CC

CC

CC

CC

RESULT 12

ID ADW04316

ID ADW04316 standard; peptide: 21 AA.

XX ADW04316;

XX AC

XX DT 07-APR-2005 (first entry)

XX DE PAPP-A immunoglobulin variable domain AB b03 heavy chain CDR3 SEQ ID 141.

XX KW Cytostatic; Vasotropics; heavy chain variable domain; proliferative disorder; restenosis; glioblastoma; osteosarcoma.

XX OS Unidentified.

XX PN US2005009136-A1.

XX PD 13-JAN-2005.

XX PR 19-FEB-2004; 2004US-00783311.

XX PR 19-FEB-2003; 2003US-0448515P.

XX PA (DYAX-) DYAX CORP.

XX PI Nixon A, Hogan S;

XX DR WPI; 2005-080519/09.

XX PT New pregnancy-associated plasma protein-A (PAPP-A) binding protein comprising immunoglobulin variable domain sequences, useful for diagnosing, preventing or treating diseases such as cancer.

XX PT Example; SEQ ID NO 141; 160pp; English.

XX CC The present invention relates to novel proteins (I) that bind to pregnancy-associated plasma protein A (PAPP-A ADW04316). (I) comprises a first and second immunoglobulin variable domain sequence which binds to PAPP-A. Also claimed are proteins (II) which comprise light chain (LC) and heavy chain immunoglobulin variable domain sequences which binds to PAPP-A. The proteins are useful for diagnosing, preventing or treating proliferative diseases such as glioblastoma, osteosarcoma and overgrowth of vascular smooth muscle cells following e.g., balloon angioplasty (which may cause restenosis). The proteins are especially useful for useful for treating diseases involving IGF regulated growth. The present sequence is one such immunoglobulin variable domain sequence.

CC CC

CC Sequence 21 AA:

Query Match 76.7%; Score 46; DB 9; Length 21;

Best Local Similarity 63.6%; Pred. No. 0.83; Mismatches 2; Indels 0; Gaps 0;

Matches 7; Conservative 2; Mismatches 2;

Qy 1 LATYYFGFLDV 11

Db 11 LGNYYGMDV 21

AC AD241994;

XX AD241994

XX AC AD241994;

XX DT 30-JUN-2005 (first entry)

XX DE Ig H chain variable region, B-CU1 set II peptide #4.

XX KW Antibody; antibody engineering; antibody therapy; light chain variable region; heavy chain variable region;

Ov

2 ATIVYFGFLDV 11

Query Match 76.7%; Score 46; DB 8; Length 13;

Best Local Similarity 70.0%; Pred. No. 0.5; Mismatches 1; Indels 0; Gaps 0;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Sequence 13 AA:

AD241994

AD241994 standard; peptide: 126 AA.

AC AD241994;

Result 13

AD241994

AD241994

AC AD241994;

Query Match 76.7%; Score 46; DB 9; Length 21;

Best Local Similarity 63.6%; Pred. No. 0.83; Mismatches 2; Indels 0; Gaps 0;

Matches 7; Conservative 2; Mismatches 2;

Qy 1 LATYYFGFLDV 11

Db 11 LGNYYGMDV 21

AC AD241994;

AD241994

AD241994

AC AD241994;

DT 30-JUN-2005 (first entry)

DE Ig H chain variable region, B-CU1 set II peptide #4.

KW Antibody; antibody engineering; antibody therapy; light chain variable region; heavy chain variable region;

KW chronic lymphocytic leukemia; cytostatic; Hodgkins disease; lymphoma;
 KW Burkitt's lymphoma; multiple myeloma; systemic lupus erythematosus;
 KW antiinflammatory; dermatological; immunosuppressive; myasthenia gravis;
 KW muscular-gen.; neuroprotective; Graves disease; antithyroid;
 KW insulin dependent diabetes; diabetes mellitus; antidiabetic;
 KW autoimmune hemolytic anemia; anianemic.
 XX OS Homo sapiens.
 XX PN WO2005034733-A2.
 PD 21-APR-2005.
 XX PR 08-OCT-2004; 2004WO-US033176.
 XX PR 08-OCT-2003; 2003US-0509473P.
 PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RESS.
 XX PI Messmer BT, Chiorazzi N, Albessano E;
 XX DR WPI; 2005-306220/31.

PT New isolated and purified preparation of light chain and heavy chain antibody genes useful for diagnosing, preventing or treating B cell chronic lymphocytic leukemia (B-CLL). B-CLL is a disease of slowly proliferating CD5+ B lymphocytes. These cells express low levels of surface membrane Ig that serves as the receptor for antigen (BCR). Analysis of V region gene cassette usage has shown that distribution of variable region gene cassettes used by B-CLL clones differs from that in normal cells, with an increased frequency of VH3-07, VH4-34, and VH1-69 genes. This implies that the structure of the antibody molecule, and antigen specificity, play a role in the leukemic transformation of particular B cells. The present invention discloses that a significant proportion of B-CLL patients with aggressive disease share the same classes of VH, D, JH, VL and JL antibody genes, forming sets of patients with highly homologous B cell receptors. Alternatively, the patients have a disorder selected from Hodgkin's disease, non-Hodgkin's lymphoma, Burkitt's lymphoma, myeloma or systemic lupus erythematosus, myasthenia gravis, Grave's disease, type I diabetes mellitus, autoimmune peripheral neuropathy, and autoimmune hemolytic anemia. The new members of the antibody genes are: VH4-39/D5-13/JH5/Vlkappa012/2/Jlkappa1/kappa2 (Set I); VH4-34/D5-21/JH6/Vlkappa17/Jlkappa1/kappa2 (Set II); VH3-16/JH3/Vlkappa27/Jlkappa1/kappa4 (Set IV); VH1-69/D3-10/JH6/Vlkappa12/Jlkappa1/kappa4 (Set V); VH1-02/D5-19/JH4/Vlkappa012/2/Jlkappa1/kappa2 (Set VIa); VH1-03/D6-19/JH4/Vlkappa012/2/Jlkappa1/kappa2 (Set VIIb); VH1-18/D6-S1/D6-19/JH4/Vlkappa012/2/Jlkappa2 (Set VIIIc); VH1-45/D6-19/JH4/Vlkappa19/Jlkappa4 (Set VII); and VH1-69/D2-3/JH4/Vlkappa6/2/Jlkappa3 (Set VIII). Treating a patient having B-CLL with the above genes comprises administering an agent that binds to the antigen-binding region of an antibody encoded by the antibody genes. The agent is an anti-idiotypic antibody, a peptide antigen, or an aptamer. The present sequence is an Ig H chain variable region, B-CLL set II peptide. XX Sequence 126 AA;

Query Match 76.7%; Score 46; DB 9; Length 126;
 Best Local Similarity 72.7%; Pred. No. 5.6; Mismatches 8; Indels 1; Gaps 0;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 LATYYFFGLDV 11
 Db 109 LGNYYYYGMDV 119

RESULT 15
 ADW04952
 ID ADW04952 standard; peptide; 16 AA.
 AC ADW04952;
 XX DT 07-APR-2005 (first entry)
 XX DE PAPP-A immunoglobulin variable domain AB f03 heavy chain CDR3 SEQ ID 277.
 XX KW Cytostatic; Vasotropic; heavy chain variable domain;
 KW Proliferative disorder; restenosis; glioblastoma; osteosarcoma.

Ov 1 LATYYFFGLDV 11
 Db 105 LKRYYYYGLDV 115

RESULT 14
 ADW04910
 ID ADW04910 standard; protein; 140 AA.
 AC ADW04910;
 XX DT 07-APR-2005 (first entry)
 XX DE PAPP-A immunoglobulin variable domain AB b03 heavy chain SEQ ID 135.
 XX KW Cytostatic; Vacotropic; heavy chain variable domain;
 KW Proliferative disorder; restenosis; glioblastoma; osteosarcoma.
 OS Unidentified.
 XX US2005009136-A1.
 XX PR 13-JAN-2005.
 XX PR 19-FEB-2004; 2004US-00783311.
 XX PR 19-FEB-2003; 2003US-0448515P.
 XX PR (DYAX-) DYAX CORP.
 XX PI Nixon A, Hogan S;
 XX DR WPI; 2005-080519/09.
 XX New pregnancy-associated plasma protein-A (PAPP-A) binding proteins comprising immunoglobulin variable domain sequences, useful for diagnosing, preventing or treating diseases such as cancer.
 XX Example; SEQ ID NO 135; 168PP; English.
 XX The present invention relates to novel proteins (I) that bind to pregnancy-associated plasma protein A (PAPP-A ADW04676). (I) comprises a first and second immunoglobulin variable domain sequence which binds to PAPP-A. Also claimed are proteins (II) which comprise light chain (LC) and heavy chain immunoglobulin variable domain sequences which binds to PAPP-A. The proteins are useful for diagnosing, preventing or treating proliferative diseases such as glioblastoma, osteosarcoma and overgrowth of vascular smooth muscle cells following e.g., balloon angioplasty (which may cause restenosis). The proteins are especially useful for useful for treating diseases involving IGF regulated growth. The present sequence is one such immunoglobulin variable domain sequence.
 XX Sequence 140 AA;
 Query Match 76.7%; Score 46; DB 9; Length 140;
 Best Local Similarity 63.6%; Pred. No. 6.3; Mismatches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 LATYYFFGLDV 11
 Db 109 LGNYYYYGMDV 119

RESULT 15
 ADW04952
 ID ADW04952 standard; peptide; 16 AA.
 AC ADW04952;
 XX DT 07-APR-2005 (first entry)
 XX DE PAPP-A immunoglobulin variable domain AB f03 heavy chain CDR3 SEQ ID 277.
 XX KW Cytostatic; Vasotropic; heavy chain variable domain;
 KW Proliferative disorder; restenosis; glioblastoma; osteosarcoma.

OS Unidentified.
 XX
 PN US2005009136-A1.
 XX
 PD 13-JAN-2005.
 XX
 PP 19-FEB-2004; 2004US-00783311.
 XX
 PR 19-FEB-2003; 2003US-0448515P.

PA (DYAX-) DYAX CORP.
 XX
 PI Nixon A, Hogan S;
 XX
 DR WPI; 2005-080519/09.

XX
 PT New pregnancy-associated plasma protein-A (PAPP-A) binding proteins
 PT comprising immunoglobulin variable domain sequences, useful for
 XX diagnosing, preventing or treating diseases such as cancer.

PS Example: SEQ ID NO 277; 168pp; English.

XX
 CC The present invention relates to novel proteins (I) that bind to
 CC pregnancy-associated plasma protein A (PAPP-A RDW4676). (I) comprises a
 CC first and second immunoglobulin variable domain sequence which binds to
 CC PAPP-A. Also claimed are proteins (II) which comprise light chain (LC)
 CC and heavy chain immunoglobulin variable domain sequences which binds to
 CC PAPP-A. The proteins are useful for diagnosing, preventing or treating
 CC proliferative diseases such as glioblastoma, osteosarcoma and overgrowth
 CC of vascular smooth muscle cells following e.g., balloon angioplasty
 CC (which may cause restenosis). The proteins are especially useful for
 CC useful for treating diseases involving IGF regulated growth. The present
 CC sequence is one such immunoglobulin variable domain sequence.

XX
 SQ Sequence 16 AA;

Query Match 75.0%; Score 45; DB 9; Length 16;
 Best Local Similarity 63.6%; Pred. No. 0.92; Indels 0; Gaps 0;
 Matches 7; Conservative 3; Mismatches 1;

| | |
|----|------------------|
| Qv | 1 LATVYFGDNDV 11 |
| Db | 6 VAGYYYYGMDV 16 |

Search completed: December 4, 2005, 04:44:54
 Job time : 98.5625 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 4, 2005, 04:31:45 ; Search time 15.5833 Seconds
(without alignments)
67.918 Million cell updates/sec

Title: US-10-632-706-127

Perfect score: 60

Sequence: 1 LATYYFEGLDV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80;*
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|---|
| 1 | 43 | 71.7 | 19 | 2 PH1307 | Ig heavy chain DJ region (clone C96-119) - human (fragment) |
| 2 | 43 | 71.7 | 23 | 2 PH1361 | C;Species: Homo Sapiens (man) |
| 3 | 43 | 71.7 | 29 | 2 PH1328 | C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999 |
| 4 | 43 | 71.7 | 160 | 2 DY0189 | C;Accession: PH1307 |
| 5 | 43 | 71.7 | 160 | 2 SU5271 | R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G. |
| 6 | 43 | 71.7 | 408 | 2 ER0380 | J. Exp. Med. 176, 1577-1581, 1992 |
| 7 | 42 | 70.0 | 19 | 2 PH1304 | A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphocytes |
| 8 | 42 | 70.0 | 19 | 2 SU33960 | A;Reference number: PH1302; PMID:93094761; PMID:1460419 |
| 9 | 42 | 70.0 | 23 | 2 PH1364 | A;Accession: PH1307 |
| 10 | 42 | 70.0 | 24 | 2 PR0258 | A;Molecule type: DNA |
| 11 | 42 | 70.0 | 27 | 2 PH1371 | A;Residues: 1-19 <WAS> |
| 12 | 42 | 70.0 | 27 | 2 PH1355 | A;Cross-references: UNIPARC:UPI0000176935 |
| 13 | 42 | 70.0 | 74 | 2 SU26793 | C;Superfamily: immunoglobulin V region; immunoglobulin homology |
| 14 | 42 | 70.0 | 118 | 2 PH1666 | C;Keywords: heterotetramer; immunoglobulin |
| 15 | 42 | 70.0 | 119 | 2 PH0961 | Qy 3 TYYFGIDV 11 |
| 16 | 42 | 70.0 | 120 | 2 PH1650 | Db 6 SYYYGMDV 14 |
| 17 | 42 | 70.0 | 125 | 2 SU4686 | Query Match 71.7%; Score 43; DB 2; Length 23; |
| 18 | 42 | 70.0 | 128 | 2 SU4797 | Best Local Similarity 63.6%; Pred. No. 0-28; Mismatches 7; Conservative 2; Indels 0; Gaps 0; |
| 19 | 42 | 70.0 | 132 | 2 PH0954 | Matches 1 LATYYFEGLDV 11 |
| 20 | 42 | 70.0 | 133 | 2 C33548 | Qy 1 : |

| ALIGNMENTS | | | | | | | | | |
|--|------------------|--------------|-----------------|-------------|-------|-----------|-------|------------|----|
| Qy | 3 TYYFGIDV 11 | Db | 6 SYYYGMDV 14 | Query Match | 71.7% | Score 43; | DB 2; | Length 19; | |
| Matches | 6 | Conservative | 3; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
| RESULT 2 | | | | | | | | | |
| PH1361 | | | | | | | | | |
| Ig heavy chain DJ region (clone C178-122B) - human (fragment) | | | | | | | | | |
| C;Species: Homo Sapiens (man) | | | | | | | | | |
| C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999 | | | | | | | | | |
| C;Accession: PH1361 | | | | | | | | | |
| R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G. | | | | | | | | | |
| J. Exp. Med. 176, 1577-1581, 1992 | | | | | | | | | |
| A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphocytes | | | | | | | | | |
| A;Reference number: PH1302; PMID:93094761; PMID:1460419 | | | | | | | | | |
| A;Accession: PH1361 | | | | | | | | | |
| A;Molecule type: DNA | | | | | | | | | |
| A;Residues: 1-19 <WAS> | | | | | | | | | |
| A;Cross-references: UNIPARC:UPI0000176935 | | | | | | | | | |
| C;Superfamily: immunoglobulin V region; immunoglobulin homology | | | | | | | | | |
| C;Keywords: heterotetramer; immunoglobulin | | | | | | | | | |
| Qy | 1 LATYYFEGLDV 11 | Db | 8 LPPYYYGMDV 18 | Query Match | 71.7% | Score 43; | DB 2; | Length 23; | |
| Matches | 7 | Conservative | 2; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
| Qy | 1 LATYYFEGLDV 11 | Db | 8 LPPYYYGMDV 18 | Query Match | 71.7% | Score 43; | DB 2; | Length 23; | |
| Matches | 7 | Conservative | 2; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
| Qy | 1 LATYYFEGLDV 11 | Db | 8 LPPYYYGMDV 18 | Query Match | 71.7% | Score 43; | DB 2; | Length 23; | |
| Matches | 7 | Conservative | 2; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
| Qy | 1 LATYYFEGLDV 11 | Db | 8 LPPYYYGMDV 18 | Query Match | 71.7% | Score 43; | DB 2; | Length 23; | |
| Matches | 7 | Conservative | 2; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
| Qy | 1 LATYYFEGLDV 11 | Db | 8 LPPYYYGMDV 18 | Query Match | 71.7% | Score 43; | DB 2; | Length 23; | |
| Matches | 7 | Conservative | 2; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
| Qy | 1 LATYYFEGLDV 11 | Db | 8 LPPYYYGMDV 18 | Query Match | 71.7% | Score 43; | DB 2; | Length 23; | |
| Matches | 7 | Conservative | 2; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
| Qy | 1 LATYYFEGLDV 11 | Db | 8 LPPYYYGMDV 18 | Query Match | 71.7% | Score 43; | DB 2; | Length 23; | |
| Matches | 7 | Conservative | 2; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
| Qy | 1 LATYYFEGLDV 11 | Db | 8 LPPYYYGMDV 18 | Query Match | 71.7% | Score 43; | DB 2; | Length 23; | |
| Matches | 7 | Conservative | 2; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
| Qy | 1 LATYYFEGLDV 11 | Db | 8 LPPYYYGMDV 18 | Query Match | 71.7% | Score 43; | DB 2; | Length 23; | |
| Matches | 7 | Conservative | 2; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
| Qy | 1 LATYYFEGLDV 11 | Db | 8 LPPYYYGMDV 18 | Query Match | 71.7% | Score 43; | DB 2; | Length 23; | |
| Matches | 7 | Conservative | 2; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
| Qy | 1 LATYYFEGLDV 11 | Db | 8 LPPYYYGMDV 18 | Query Match | 71.7% | Score 43; | DB 2; | Length 23; | |
| Matches | 7 | Conservative | 2; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
| Qy | 1 LATYYFEGLDV 11 | Db | 8 LPPYYYGMDV 18 | Query Match | 71.7% | Score 43; | DB 2; | Length 23; | |
| Matches | 7 | Conservative | 2; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
| Qy | 1 LATYYFEGLDV 11 | Db | 8 LPPYYYGMDV 18 | Query Match | 71.7% | Score 43; | DB 2; | Length 23; | |
| Matches | 7 | Conservative | 2; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
| Qy | 1 LATYYFEGLDV 11 | Db | 8 LPPYYYGMDV 18 | Query Match | 71.7% | Score 43; | DB 2; | Length 23; | |
| Matches | 7 | Conservative | 2; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
| Qy | 1 LATYYFEGLDV 11 | Db | 8 LPPYYYGMDV 18 | Query Match | 71.7% | Score 43; | DB 2; | Length 23; | |
| Matches | 7 | Conservative | 2; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
| Qy | 1 LATYYFEGLDV 11 | Db | 8 LPPYYYGMDV 18 | Query Match | 71.7% | Score 43; | DB 2; | Length 23; | |
| Matches | 7 | Conservative | 2; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
| Qy | 1 LATYYFEGLDV 11 | Db | 8 LPPYYYGMDV 18 | Query Match | 71.7% | Score 43; | DB 2; | Length 23; | |
| Matches | 7 | Conservative | 2; | Mismatches | 2; | Indels | 0;</ | | |

RESULT 3
PHI328 Ig heavy chain DJ region (clone C113-148) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PHI328
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A;Reference number: PHI302; MUID:9309476; PMID:1460419
A;Accession: PHI328
A;Molecule type: DNA
A;Residues: 1-29 <WAS>
A;Cross-references: UNIPARC:UPI0000176939
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
Query Match 71.7%; Score 43; DB 2; Length 29;
Best Local Similarity 66.7%; Pred. No. 0.36; Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 3 TYYFGLDV 11
Db 16 SYYYGMDV 24

RESULT 4
D70189 conserves hypothetical integral membrane protein BB0717 - Lyme disease spirochete
C;Species: *Borrelia burgdorferi* (Lyme disease spirochete)
C;Accession: D70189
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.J.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-160 <KLE>
A;Cross-references: UNIPROT:051659; UNIPARC:UPI00000575B2; GB:AE01171; GB:AB000783; NID:
A;Experimental source: strain B31

Query Match 71.7%; Score 43; DB 2; Length 160;
Best Local Similarity 60.0%; Pred. No. 2; Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATYYFGLDV 11
Db 23 ATYVFSIDI 32

RESULT 5
S05271 Ig heavy chain precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
C;Accession: S05271; S04602
R;Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A;Accession: S05271
A;Molecule type: mRNA
A;Residues: 1-160 <KISI>
A;Cross-references: UNIPROT:096BB9; UNIPARC:UPI000176B50; EMBL:X14584
R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
A;Reference number: S05601; MUID:89296497; PMID:2500644
A;Accession: S04602

A;Molecule type: mRNA
A;Residues: 1-144 <KIS>
A;Cross-references: UNIPARC:UPI000176B51; EMBL:X14584
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F1-19;Domain: signal sequence #status predicted <SIG>
F1-160;Product: Ig heavy chain (fragment) #status predicted <MAT>
F1-117;Domain: immunoglobulin homology <IMM>
Query Match 71.7%; Score 43; DB 2; Length 160;
Best Local Similarity 66.7%; Pred. No. 2; Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 3 TYYFGLDV 11
Db 125 SYYYGMDV 133

RESULT 6
B70380 Na+/H+-exchanging protein - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: B70380
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
A;Accession: B70380
A;Reference number: A70300; MUID:9818666; PMID:9531320
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-408 <AOE>
A;Cross-references: UNIPROT:067072; UNIPARC:UPI00000564AB; GB:AB000714; NID:g2983446; PI
A;Experimental source: strain VF5
C;genetics:
A;Gene: napA2
C;Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napA1
C;Species: Aquifex aeolicus Na+/H+-exchanging protein napA1
Query Match 71.7%; Score 43; DB 2; Length 408;
Best Local Similarity 54.5%; Pred. No. 5.2; Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 LATYYFFGIDV 11
Db 116 IVSYIFFGIDL 126

RESULT 7
PHI304 Ig heavy chain DJ region (clone C439-111) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PHI304
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A;Reference number: PHI302; MUID:9309476; PMID:1460419
A;Accession: PHI304
A;Molecule type: DNA
A;Residues: 1-13 <WAS>
A;Cross-references: UNIPARC:UPI000176934
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
Query Match 70.0%; Score 42; DB 2; Length 19;
Best Local Similarity 75.0%; Pred. No. 0.35; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 YYFGLDV 11
Db 7 VYYGMDV 14

A;Residues: 1-74 <MOR>
A;Cross-references: UNIPARC:UPI0000115CFA; EMBL:X61019; NID:932787; PIDN:CAA43353.1; PIC
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 74;

Best Local Similarity 75.0%; Pred. No. 1.4; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YYYFGGLDV 11
Db 56 YYYYGMDV 63

RESULT 14

PH1666 Ig heavy chain V region (clone 6C9) - human (fragment)
C;Species: Homo sapiens (man)

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1666

R;Hillson, J.L.; Katz, N.S.; Oppiger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-335, 1993

A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A

A;Reference number: PH1622; PMID:93301610; PMID:8215383

A;Accession: PH1666

A;Molecule type: mRNA

A;Experimental source: B cell

A;Cross-references: UNIPARC:UPI0000176B57

A;Keywords: heterotetramer; immunoglobulin homology <IMM>

C;Superfamily: immunoglobulin V region; immunoglobulin homology F;7-30/Domain: immunoglobulin homology <IMM>

Query Match 70.0%; Score 42; DB 2; Length 118;

Best Local Similarity 75.0%; Pred. No. 2.2; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YYFGLDV 11
Db 100 YYYGMDV 107

RESULT 15

PH0961 Ig heavy chain V region (G6+ T-133) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996

C;Accession: PH0961

R;Martin, T.; Duffy, S.P.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 982-991, 1992

A;Title: Evidence for somatic selection of natural autoantibodies.

A;Reference number: PH0952; PMID:92202880; PMID:1552291

A;Accession: PH0961

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-119 <MAR>

A;Cross-references: UNIPARC:UPI0000176C85

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-30/Region: framework 1

F;15-98/Domain: immunoglobulin homology <IMM>

F;31-35/Region: complementarity-determining 1

F;36-50/Region: framework 2

F;51-67/Region: complementarity-determining 2

F;68-98/Region: framework 3

F;99-107/Region: complementarity-determining 3

Query Match 70.0%; Score 42; DB 2; Length 119;

Best Local Similarity 75.0%; Pred. No. 2.2; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YYFGLDV 11
Db 101 YYYGMDV 108

Search completed: December 4, 2005, 04:53:32
Job time : 17.583 SECs

GenCore version 5.1.6
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OM protein - protein search, using BW model

Run on: December 4, 2005, 04:31:36 ; Search time 100.375 seconds
(without alignment)
77.318 Million cell updates/sec

Title: US-10-632-706-127
Perfect score: 60
Sequence: 1 LATYYVFFGLDV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80;*
1: uniprot_sprot;*
2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match Length | DB ID | Description |
|------------|-------|-------|--------------|-------|--------------------|
| 1 | 44. | 73.3 | 1348 | 2 | Q4N9V2 THEPA |
| 2 | 44. | 73.3 | 2262 | 2 | Q4UFV8 THELIERIA P |
| 3 | 43. | 71.7 | 160 | 2 | Q51659 PORBJ |
| 4 | 43. | 71.7 | 160 | 2 | Q6F6N6 BORGJ |
| 5 | 43. | 71.7 | 408 | 2 | Q57072 AQUAB |
| 6 | 42. | 70.0 | 364 | 2 | Q7VY71 BORPA |
| 7 | 42. | 70.0 | 364 | 2 | QW926 BORPA |
| 8 | 42. | 70.0 | 364 | 2 | Q7WKHL BORBR |
| 9 | 42. | 70.0 | 378 | 2 | Q9Q10 LEIMA |
| 10 | 42. | 70.0 | 382 | 2 | Q9RNT9 BRAJA |
| 11 | 42. | 70.0 | 594 | 2 | Q74N07 NANED |
| 12 | 42. | 70.0 | 606 | 2 | Q6GMX2 HUMAN |
| 13 | 42. | 70.0 | 1062 | 2 | Q9KX97 SULTO |
| 14 | 42. | 70.0 | 3212 | 2 | Q4FWX4 LEIMA |
| 15 | 41. | 68.3 | 716 | 2 | Q5AQZ1 DESRS |
| 16 | 40. | 66.7 | 288 | 2 | Q5F6N6 ACTRD |
| 17 | 40. | 66.7 | 291 | 2 | Q4ZUBL PSESY |
| 18 | 40. | 66.7 | 293 | 2 | Q6D023 ERWCT |
| 19 | 40. | 66.7 | 447 | 2 | Q8EUT78 OCEBII |
| 20 | 40. | 66.7 | 702 | 2 | Q8C3X8 MOUSE |
| 21 | 40. | 66.7 | 978 | 2 | Q5AVV CANAL |
| 22 | 40. | 66.7 | 1113 | 2 | Q6VEQ5 ARALY |
| 23 | 40. | 66.7 | 3964 | 2 | Q5O8V4 LEIMA |
| 24 | 39. | 65.8 | 651 | 1 | Y637F4 BACHD |
| 25 | 39. | 65.0 | 188 | 2 | Q52C31 MAGGR |
| 26 | 39. | 65.0 | 215 | 2 | Q5YXQ2 NOCFA |
| 27 | 39. | 65.0 | 317 | 2 | Q9TBK3 THEVO |
| 28 | 39. | 65.0 | 375 | 2 | Q9KDV6 BACHD |
| 29 | 39. | 65.0 | 419 | 2 | Q8Z700 MEDTR |
| 30 | 39. | 65.0 | 423 | 2 | Q9SP7A5 MEDTR |
| 31 | 39. | 65.0 | 652 | 2 | Q6ZBX7 ORYSA |

| RESULT | ID | NAME | PRT |
|--------|---------|---|--------------------------------------|
| 1 | Q4N9V2 | THEPAA PRELIMINARY; | 1348 AA. |
| | Q4N9V2; | TREMBREL | Created) |
| | DT | 13-SEP-2005 | (TREMBREL. 31, Last sequence update) |
| | DT | 13-SEP-2005 | (TREMBREL. 31, Hypothetical Protein) |
| | DE | OrfNames=TP01_0021; | |
| | OS | Theileria parva. | |
| | OC | Baculovirus, Alveolata, Apicomplexa, Piroplasmida, Theileriidae; | |
| | OC | Theileria. | |
| | RN | [1] | |
| | RP | NCBI_TAXID=5875; | |
| | RC | NUCLEOTIDE SEQUENCE. | |
| | RA | STRAIN=Muguga; | |
| | RA | Gardner M., Bishop R., Shah T., de Villiers E.P., Carlton J.M., Hall N., Ren Q., Paulsen I.T., Pain A., Berrieman M., Wilson R.J.M., Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.J., Jiang L., Lynn J., Weaver B., Shoebi A., Wasawo D., Crabtree J., Wortman J.R., Haas B., Anguoli S.V., Creasy T.H., Lu C., Sun B., Silva J.C., Utterback T.R., Feldblyum T.V., Pertea M., Allen J., Taracha E.L.N., Salzberg S.L., White O.R., FitzHugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.; | |
| | RT | "Genome sequence of Theileria parva, a bovine pathogen that transforms lymphocytes," | |
| | RL | Science 309:134-137(2005). | |
| | RN | [2] | |
| | RR | NUCLEOTIDE SEQUENCE. | |
| | RC | STRAIN=Muguga; | |
| | RA | Gardner M., Bishop R., Shah T., de Villiers E.P., Carlton J.M., Hall N., Ren Q., Paulsen I.T., Pain A., Berrieman M., Wilson R.J.M., Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.J., Jiang L., Lynn J., Weaver B., Shoebi A., Wasawo D., Crabtree J., Wortman J.R., Haas B., Anguoli S., Creasy T.H., Lu C., Sun B., Silva J.C., Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.N., Salzberg S.L., White O., FitzHugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V., Submitted (JUN 2005) to the EMBL/GenBank/DBJ databases. | |
| | RA | - CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data. | |
| | DR | EMBL: AAGK0100001; EAN33265.1; -; Genomic_DNA. | |
| | KW | Hypothetical protein. | |
| | SQ | SEQUENCE 1348 AA; 155635 MW; 474C3A40C23B8C5F CRC64; | |

Query Match 73.3%; Score 44; DB 2; Length 1348;
Best Local Similarity 87.4%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

ALIGNMENTS

QY 3 TYTFGFD 10
Db 386 SYYVFGD 393

RESULT 2
 Q4UFY8 THEAN PRELIMINARY; PRT; 2262 AA.
 ID Q4UFY8; THEAN PRELIMINARY;
 AC 4
 DT 13-SEP-2005 (TREMBIrel. 31, Created)
 DT 13-SEP-2005 (TREMBIrel. 31, Last annotation update)
 DB Hypothetical protein.
 GN ORFNames-TA19710;
 OS Theileria annulata; Apicomplexa; Piroplasmida; Theileriidae;
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
 OC Theileria;
 OC NCBI_TaxID=5874;
 [1]
 RP NUCLEOTIDE SEQUENCE:
 RC STRAIN=Ankara isolate clone C9;
 RA Hall N., Barrell B.G.;
 RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
 RA Hall N., Barrell B.G.;
 RT "The chromosome 1 sequence of *Theileria annulata*."
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL: CP840347; CAI74001.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 2262 AA; 262068 MW; FD9E8915243BF512 CRC64;

Query Match 73.3%; Score 44; DB 2; Length 2262;
 Best Local Similarity 87.5%; Pred. No. 1e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY :||||| 3 TYYWGLD 10

Db 1244 SYYFGLD 1251

RESULT 3
 O51659_BORBU
 ID O51659_BORBU PRELIMINARY; PRT; 160 AA.
 AC O51659;
 DT 01-JUN-1998 (TREMBIrel. 06, Last sequence update)
 DT 01-JUN-2003 (TREMBIrel. 24, Last annotation update)
 DE Conserved hypothetical integral membrane protein.

GN OrderedLocusNames=BB0717;

OS *Borrelia burgdorferi* (Lyme disease spirochete).
 OC *Borrelia*; Spirochaetes; Spirochaetales; Spirochaetaceae; *Borrelia*;
 OC *Borrelia* burgdorferi group.
 OC NCBI_TaxID=139;
 RN [1]
 RP NUCLEOTIDE SEQUENCE:
 RC STRAIN=ATCC 35210 / B31;
 RX MEDLINE=96065943; PubMed=9403685; DOI=10.1038/37551;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.J., Clayton R.A.,
 RA Lathigra R., White O., Ketchum R.A., Dodson R.J., Hickey E.K.,
 RA Gwin M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
 RA Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J.,
 RA Salzberg S.L., Hanson M., Van Vugt R., Palmer N., Adams M.D., McDonald L.A.,
 RA Gocayne J.D., Weidman J.F., Utterback T.R., Watney L.,
 RA Artlach P., Bowman C., Garland S.A., Fujii C., Cottont M.D., Horst K.,
 RA Roberts K.M., Hatch B., Smith H.O., Venter J.C.,
 RA "Genomic sequence of a Lyme disease spirochete," *Borrelia*
 RT "burgdorferi."

RL Nature 350:580-586(1997).

DR EMBL; AE001171; AAC07057.1; -; Genomic_DNA.

DR PIR; D70189; D70189.

DR TIGR; BB0717; -.

KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 160 AA; 19300 MW; 9DE28A497C0F5737 CRC64;

Query Match 71.7%; Score 43; DB 2; Length 160;
 Best Local Similarity 60.0%; Pred. No. 11;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 23 ATYFFFSIDI 32

RESULT 4
 Q660B6_BORGA
 ID Q660B6_BORGA PRELIMINARY; PRT; 160 AA.
 AC Q660B6;
 DT 25-OCT-2004 (TREMBIrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBIrel. 28, Last annotation update)
 DR Conserved hypothetical integral membrane protein.
 GN OrderidiclusNames=BG0719;

OS *Borrelia garinii*;

OC *Bacillus*; Spirochaetes; Spirochaetales; Spirochaetaceae; *Borrelia*;
 OC *Borrelia* burgdorferi group.
 OC NCBI_TaxID=29519;

RN [1]
 RP NUCLEOTIDE SEQUENCE:
 RC STRAIN=PBI;

RA Glöckner G., Lehmann R., Romualdi A., Pradella S.,
 RA Schulte-Spechtel U., Wilcke B., Suhnel J., Platzer M.,
 RT "Comparative analysis of the *Borrelia garinii* genome.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: CP000013; AU07565.1; -; Genomic_DNA.
 KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 160 AA; B65B15C5197FB89 CRC64;

Query Match 71.7%; Score 43; DB 2; Length 160;
 Best Local Similarity 60.0%; Pred. No. 11;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 23 ATYFFFSIDI 32

RESULT 5
 O67072_AQUAE
 ID O67072_AQUAE PRELIMINARY; PRT; 408 AA.
 AC O67072;
 DT 01-AUG-1998 (TREMBIrel. 07, Created)
 DT 01-JUN-2003 (TREMBIrel. 24, Last annotation update)
 DR Na(+)/H(+) antiporter.

GN Name=napA2; OrderedLocusNames=AQ_929;

OS *Aquifex aeolicus*.

OC *Bacteria*; Aquificae; Aquificales; Aquificaceae; *Aquifex*.
 OC NCBI_TaxID=63363;

RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=VPS;

RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
 RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Snaed M.A., Keller M., Aufay M., Huber R.,
 RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.,
 RT "The complete genome of the hyperthermophilic bacterium *Aquifex*
 aeolicus."

RL Nature 332:353-358(1998).

DR EMBL; AE000714; AAC07034.1; -; Genomic_DNA.

DR PIR; E70380; E70380.

DR GO; GO:0016021; C:integral_to_membrane; IEA.

DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.

DR GO; GO:0006885; P:regulation_of_ph; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR006133; Na_H porter.

DR Pfam; PF00999; Na_H Exchanger; 1.

KW Complete proteome; Transmembrane Transport; CRC64;

SQ SEQUENCE 408 AA; 43582 MW; 7E05B4B38TA6C506

Query Match 71.7%; Score 43; DB 2; Length 408;
 Best Local Similarity 54.5%; Pred. No. 28;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATYYVFGLDY 11
 ID :|||||; PRT; 364 AA.
 Db 116 IVSYFFGLDL 126

RESULT 6
 Q7VY11_BORPE
 ID Q7VY11_BORPE PRELIMINARY; PRT; 364 AA.
 AC Achman M., Atkin R., Baker S., Basham D., Basin N., Chevrevach I.,
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

Putative periplasmic solute-binding protein.

GN Name=simM; Order=locusNames=BBP1487;
 OS Bordetella pertussis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 OC NCBI_TaxID=520;
 RN [1]

NUCLEOTIDE SEQUENCE.
 STRAIN=Tobrama I / ATCC BAA-589 / NCTC 1225I;
 MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
 RA Parkhill J., Seabainia M., Preston A., Murphy L.D., Thomson N.R.,
 RA Harris D.S., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
 RA Achtman M., Atkin R., Baker S., Basham D., Basin N., Chevrevach I.,
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jegel K.,
 RA Leather S., Moulle S., Norbercak H., O'Neil S., Ormond D., Price C.,
 RA Rabbiniowitsch E., Rutter S., Sanders D., Seeger K.,
 RA Sharp S., Simmonds M., Shelton J., Squares R., Squares S., Stevens K.,
 RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,
 RT Bordetella parapertussis and Bordetella bronchiseptica.";
 RL Nat. Genet. 35:32-40(2003);
 DR EMBL; BX640428; CAB37248.1; -; Genomic DNA.
 DR GO; GO:0032088; C:periplasmic space (sensu Gram-negative Bact. . . ; IEA).
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR006311; Tat.
 DR InterPro; IPR004682; TRAP_transprtDctP.
 DR Pfam; PF03480; SBP_bac_7_1.
 DR TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
 DR Complete proteome.
 SQ Sequence 364 AA; 39957 MW; 970BC4608CF1DE8 CRC64;
 KW

Query Match 70.0%; Score 42; DB 2; Length 364;
 Best Local Similarity 77.8%; Pred. No. 38; DB Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATYYVFGLD 10
 ID :|||||; PRT; 364 AA;
 Db 98 ASYYVFGKD 106

RESULT 8
 Q7WKH1_BORBR
 ID Q7WKH1_BORBR PRELIMINARY; PRT; 364 AA.
 AC Q7WKH1;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

Putative periplasmic solute-binding protein.

GN Name=simM; Order=locusNames=BB2116;
 OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 OC NCBI_TaxID=518;
 RN [1]

NUCLEOTIDE SEQUENCE.
 STRAIN=RB50 / ATCC BAA-588;
 MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
 RA Parkhill J., Seabainia M., Preston A., Murphy L.D., Thomson N.R.,
 RA Harris D.S., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
 RA Achtman M., Atkin R., Baker S., Basham D., Basin N., Chevrevach I.,
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jegel K.,
 RA Leather S., Moulle S., Norbercak H., O'Neil S., Ormond D., Price C.,
 RA Rabbiniowitsch E., Rutter S., Sanders D., Seeger K.,
 RA Sharp S., Simmonds M., Shelton J., Squares R., Squares S., Stevens K.,
 RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,
 RT Bordetella parapertussis and Bordetella bronchiseptica.";
 RL Nat. Genet. 35:32-40(2003);
 DR EMBL; BX640443; CAB32632.1; -; Genomic DNA.
 DR GO; GO:0032088; C:periplasmic space (sensu Gram-negative Bact. . . ; IEA).
 DR GO; GO:0008810; P:transport; IEA.
 DR InterPro; IPR006311; Tat.
 DR InterPro; IPR004682; TRAP_transprtDctP.
 DR Pfam; PF03480; SBP_bac_7_1.
 DR TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
 DR Complete proteome.
 SQ Sequence 364 AA; 39997 MW; 8AB6672BA3BF09AD CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;
 Best Local Similarity 77.8%; Pred. No. 38;

| | Matches | 7; Conservative | 1; Mismatches | 1; Indels | 0; Gaps | 0; |
|--|---------------------|-----------------|---------------|-----------|---------|----|
| Qy | 2 ATYYVFGID 10 | | | | | |
| Db | 98 ASYYVFGKD 106 | | | | | |
| RESULT 9 | | | | | | |
| 04QAI0 LEIMA | | | | | | |
| ID 04QAI0 LEIMA PRELIMINARY; | PRT; | 378 AA. | | | | |
| AC 04QAI0; | | | | | | |
| DT 13-SEP-2005 (TREMBLrel. 31; Created) | | | | | | |
| DT 13-SEP-2005 (TREMBLrel. 31; Last sequence update) | | | | | | |
| DE Hypothetical protein. | | | | | | |
| GN ORFNames=ImpF25_0840; | | | | | | |
| OS Leishmania major. | | | | | | |
| OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania. | | | | | | |
| OX NCBI_TAXID=5664; | | | | | | |
| RN [1] | | | | | | |
| RP NUCLEOTIDE SEQUENCE. | | | | | | |
| RC STRAIN=Friedlin; | | | | | | |
| RA Peacock C.S.; Murphy L.; Ivens A.C.; Berriman M.; Blackwell J.'; | | | | | | |
| RA Smith D.; Collins M.; Fosker N.; Harris D.; Oliver K.; O'Neill S.'; | | | | | | |
| RA Saunders D.; Seeger K.; Warren T.; Rajandream M.'; and Barrell B.G.'; | | | | | | |
| RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases. | | | | | | |
| DR EMBL; C1005264; CAJ04989.1; -; Genomic_DNA. | | | | | | |
| KW Hypothetical protein. | | | | | | |
| SQ SEQUENCE 378 AA; 41605 MW; 9E3BEGC7C1F04839 CRC64; | | | | | | |
| Query Match 70.0%; Score 42; DB 2; Length 378; | | | | | | |
| Best Local Similarity 100.0%; Pred. No. 40; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | | |
| Qy 3 TYYVFGL 9 | | | | | | |
| Db | 112 TYYVFGL 118 | | | | | |
| RESULT 10 | | | | | | |
| 089NT9 BRAJA | | | | | | |
| ID 089NT9_BRAJA PRELIMINARY; | PRT; | 382 AA. | | | | |
| AC 089NT9; | | | | | | |
| DT 01-JUN-2003 (TREMBLrel. 24; Created) | | | | | | |
| DT 01-OCT-2003 (TREMBLrel. 25; Last annotation update) | | | | | | |
| DE Periplasmic mannitol-binding protein. | | | | | | |
| GN OrderredLocusName=blr3745; | | | | | | |
| OS Bradyrhizobium japonicum. | | | | | | |
| OC Bacteria; Proteobacteria; Rhizobiales; | | | | | | |
| OC Bradyrhizobiaceae; Bradyrhizobium. | | | | | | |
| DR NCBI_TAXID=375; | | | | | | |
| RN [1] | | | | | | |
| RP NUCLEOTIDE SEQUENCE. | | | | | | |
| RC SIRALM-USDA 110; | | | | | | |
| RX MEDLINE=22434998; PubMed=12597275; | | | | | | |
| RL DNA Res. 9:189-197(2002); | | | | | | |
| RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., | | | | | | |
| RA Sasamoto S., Watanabe A., Idesawa K., Iriuchih M., Kawashima K., | | | | | | |
| RA Kohara M., Matsumoto M., Shimojo S., Tsuruoka H., Wada T., Yamada M., | | | | | | |
| RA Tabata S.; | | | | | | |
| RT Bradyrhizobium japonicum USDA110;" | | | | | | |
| RT Complete genomic sequence of nitrogen-fixing symbiotic bacterium | | | | | | |
| RT SIRALM-USDA 110; | | | | | | |
| Qy 1 LATYYVGLDV 11 | | | | | | |
| Db | 569 LSRYHYFGVDI 579 | | | | | |
| RESULT 12 | | | | | | |
| 06GMY2_HUMAN | | | | | | |
| ID QZGMY2_HUMAN PRELIMINARY; | PRT; | 606 AA. | | | | |
| AC 06GMY2; | | | | | | |
| DT 05-JUL-2004 (TREMBLrel. 27; Created) | | | | | | |
| DT 05-JUL-2004 (TREMBLrel. 27; Last sequence update) | | | | | | |
| DT 05-JUL-2004 (TREMBLrel. 27; Last annotation update) | | | | | | |
| DE tGHM protein. | | | | | | |
| GN Name=tGHM; | | | | | | |
| OS Homo sapiens (Human). | | | | | | |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | | |
| OC Mammalia; Butheria; Euarchontoglires; Primates; Cetartiodactyla; Homino. | | | | | | |
| OC Homo. | | | | | | |
| DR NCBI_TAXID=9606; | | | | | | |
| RN [1] | | | | | | |
| RP NUCLEOTIDE SEQUENCE. | | | | | | |
| RC TISSUE=Primary B-Cell; | | | | | | |
| RX MEDLINE=2248825; PubMed=12477932; DOI=10.1073/pnas.242603899; | | | | | | |
| RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G., | | | | | | |
| RA Klausner R.D., Collins F.S., Wagner L., Shemesh C., Schuler G.D., | | | | | | |
| RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., | | | | | | |
| RA Hopkins R.M., Jordan R.H., Moore T., Max S.I., Wang J.J., Heien F., | | | | | | |
| RA Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., | | | | | | |
| RA Stapleton M., Soares M.B., Ronald M.P., Casavant T.L., Scheetz T.E., | | | | | | |
| RA Brownstein M.J., Usdin T.B., Yoshiyuki S., Carninci P., Prange C., | | | | | | |
| RA Rosa S.S., Loquaiano N.A., Peters G.J., Abramson R.D., Mullaly S.J., | | | | | | |
| RA Bosak S.A., McEvans P.J., McKernan K.J., Malek J.A., Gunaratne P.H., | | | | | | |
| RA SO SEQUENCE 382 AA; 42090 MW; 23C264980A9FB8BD CRC64; | | | | | | |
| Qy 2 ATYYVFGID 10 | | | | | | |
| Db | 117 ASYYVFGKD 125 | | | | | |

RX PubMed:15305914; DOI=10.1111/j.1462-2920.2004.00655.x;
 RA Rabus R., Ruepp A., Frickey T., Rattke T., Farthmann B., Stark M.,
 RA Zibat A., Lombardet T., Rattke T., Becker I., Amann J., Gellner K.,
 RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
 RA Klenk H.-P.;
 RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
 from permanently cold Arctic sediments.";
 RL Environ. Microbiol. 6:887-902 (2004).
 DR EMBL; CR522870; CAG35233.1; -; Genomic_DNA.
 DR GO; GO:0005737; CYTOPLASM; IEA.
 DR GO; GO:001036; DISULFIDE_OXIDOREDUCTASE_ACTIVITY; IEA.
 DR GO; GO:005060; FAD_BINDING; IEA.
 DR GO; GO:0006118; P-electron_transport; IEA.
 DR InterPro; IPR00127; FAD_Pyr_redox.
 DR InterPro; IPR000815; Hg_reductase.
 DR InterPro; IPR006162; Phantme_S.
 DR InterPro; IPR001100; Pyr_redox.
 DR InterPro; IPR004039; Pyr_redox_dim.
 DR Pfam; PF00070; PYR_redox_2.
 DR Pfam; PF0252; PYR_redox_dim; 1.
 DR PRINTS; PR00568; FADPNR.
 DR PRINTS; PR00945; HGRTDSE.
 DR PRINTS; PR00411; PNDDTASEI.
 DR PRODOM; PDD00139; FAD_Pyr_redox; 1.
 DR PROSITE; PS00012; PHOSPHOPANTETHINE; UNKNOWN_1.
 DR PROSITE; PS00076; PYRINE_REDOK_1; 1.
 KW Complete proteome.
 SQ SEQUENCE 716 AA; 78725 MW; 68BFC0600DBE44094 CRC64;

Query Match 68.3%; Score 41; DB 2; Length 716;

Best local similarity 60.0%; Pred. No. 1.e+02; Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

| | | |
|----|---------------|----|
| Qy | 1 LATVYVFGID | 10 |
| Db | 14 VSAYVFFGID | 23 |

Search completed: December 4, 2005, 04:52:20
 Job time : 104.375 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: December 4, 2005, 03:59:51 ; Search time 23.6042 Seconds
Title: US-10-632-706-127
Perfect score: 60
Sequence: 1 IATYYVFLDV 11
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 57260 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 57260

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/pctodata/1/iaa/5_COMB.pep:*
- 2: /cgn2_6/pctodata/1/iaa/H_COMB.pep:*
- 3: /cgn2_6/pctodata/1/iaa/PCTUS_COMB.pep:*
- 4: /cgn2_6/pctodata/1/iaa/RE_COMB.pep:*
- 5: /cgn2_6/pctodata/1/iaa/bacfile1.pep:*
- 6: /cgn2_6/pctodata/1/iaa/bacfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|--|
| 1 | 43 | 71.7 | 33 | 1 US-08-053-131-78 Sequence 78, Appl |
| 2 | 43 | 71.7 | 33 | 1 US-08-645-611-78 Sequence 78, Appl |
| 3 | 43 | 71.7 | 33 | 1 US-07-853-408B-78 Sequence 78, Appl |
| 4 | 43 | 71.7 | 33 | 1 US-08-036-762-78 Sequence 78, Appl |
| 5 | 43 | 71.7 | 33 | 1 US-08-08-855-78 Sequence 78, Appl |
| 6 | 43 | 71.7 | 33 | 2 US-09-042-353-275 Sequence 215, Appl |
| 7 | 43 | 71.7 | 33 | 2 US-08-759-417A-123 Sequence 123, Appl |
| 8 | 43 | 71.7 | 33 | 4 PCT-US-10983-78 Sequence 78, Appl |
| 9 | 43 | 71.7 | 125 | 2 US-09-840-459-84 Sequence 84, Appl |
| 10 | 43 | 71.7 | 125 | 2 US-09-497-625A-84 Sequence 84, Appl |
| 11 | 42 | 70.0 | 29 | 1 US-08-053-131-73 Sequence 73, Appl |
| 12 | 42 | 70.0 | 29 | 1 US-08-643-641-73 Sequence 73, Appl |
| 13 | 42 | 70.0 | 29 | 1 US-07-853-408B-73 Sequence 73, Appl |
| 14 | 42 | 70.0 | 29 | 1 US-08-96-762-73 Sequence 73, Appl |
| 15 | 42 | 70.0 | 29 | 1 US-08-308-865-73 Sequence 73, Appl |
| 16 | 42 | 70.0 | 29 | 2 US-09-042-353-270 Sequence 210, Appl |
| 17 | 42 | 70.0 | 29 | 2 US-08-758-417A-118 Sequence 73, Appl |
| 18 | 42 | 70.0 | 29 | 4 PCT-US-92-10983-73 Sequence 73, Appl |
| 19 | 42 | 70.0 | 31 | 1 US-08-053-131-83 Sequence 83, Appl |
| 20 | 42 | 70.0 | 31 | 1 US-08-645-641-83 Sequence 83, Appl |
| 21 | 42 | 70.0 | 31 | 1 US-07-853-408B-83 Sequence 83, Appl |
| 22 | 42 | 70.0 | 31 | 1 US-08-09-042-353-280 Sequence 83, Appl |
| 23 | 42 | 70.0 | 31 | 2 US-09-042-353-280 Sequence 280, Appl |
| 24 | 42 | 70.0 | 31 | 2 US-08-758-417A-128 Sequence 128, Appl |
| 25 | 42 | 70.0 | 31 | 4 PCT-US-92-10983-83 Sequence 83, Appl |
| 26 | 42 | 70.0 | 36 | 1 US-08-053-131-84 Sequence 84, Appl |
| 27 | 42 | 70.0 | 36 | 1 US-08-053-131-84 Sequence 84, Appl |

ALIGNMENTS

RESULT 1
US-08-053-131-78
Sequence 78, Application US/08053131
Patent No. 5651016

GENERAL INFORMATION:

APPLICANT: Loberg, Nilg
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-H
NUMBER OF SEQUENCES: 197
TITLE OF INVENTION: Producing Heterologous Antigenic Polypeptides
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Bassick
STREET: One Market Plaza, Stewart Tower, San Francisco, CA
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPILER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APR-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30.223
REFERENCE DOCKET NUMBER: 114643-9-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-053-131-78

Query Match 71.7%; Score 43; DB 1; Length 33;
 Best Local Similarity 66.7%; Pred. No. 1.6;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TYTYFGLDV 11
 Db 10 SYYYGMDV 18

RESULT 2 US-08-645-641-78

; Sequence 78, Application US/08645641
 ; Patent No. 5719032
 ; GENERAL INFORMATION:
 ; APPLICANT: Lomberg, Nils
 ; APPLICANT: Kay, Robert M.
 ; TITLE OF INVENTION: Producing Heterologous Antibodies
 ; TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/853,408B
 ; FILING DATE: 19930318
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M.
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 14643-9
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-326-2400
 ; TELEFAX: 415-326-2422
 ; INFORMATION FOR SEQ ID NO: 78:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 33 amino acids
 ; TYPE: AMINO ACID
 ; STRANDEDNESS: single
 ; TOPOLogy: linear
 ; MOLECULAR TYPE: peptide
 ; US-07-853-408B-78

Query Match 71.7%; Score 43; DB 1; Length 33;
 Best Local Similarity 66.7%; Pred. No. 1.6;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TYTYFGLDV 11
 Db 10 SYYYGMDV 18

RESULT 4 US-08-096-762-78

; Sequence 78, Application US/08096762
 ; Patent No. 5814318
 ; GENERAL INFORMATION:
 ; APPLICANT: Lomberg, Nils
 ; APPLICANT: Kay, Robert M.
 ; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
 ; TITLE OF INVENTION: Producing Heterologous Antibodies
 ; NUMBER OF SEQUENCES: 210
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: One Market Plaza, Steuart Tower, Suite 200
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/096,762
 ; FILING DATE: 22-JUL-1993
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/053,131
 ; FILING DATE: 26-APR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/990,860

RESULT 3 US-07-853-408B-78

; Sequence 78, Application US/07853408B
 ; Patent No. 5789650
 ; GENERAL INFORMATION:
 ; APPLICANT: Lomberg, Nils
 ; APPLICANT: Kay, Robert M.
 ; TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
 ; TITLE OF INVENTION: Producing Heterologous Antibodies

PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/904,068
 FILING DATE: 23-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/853,408
 FILING DATE: 18-MAR-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/810,279
 FILING DATE: 17-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 14643-9-4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 78:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-308-865-78
 RESULT 5
 Query Match 71.7%; Score 43; DB 1; Length 33;
 Best Local Similarity 66.7%; Pred. No. 1.6;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TYYFGDV 11
 ::|::|:|||:
 Db 10 SYYYGMDV 18
 US-08-308-865-78
 RESULT 6
 US-09-042-353-275
 Sequence 275, Application US/09042353
 ; Patent No. 5877397
 ; GENERAL INFORMATION:
 ; APPLICANT: Lonberg, Nils
 ; APPLICANT: Kay, Robert M.
 ; TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for Producing Heterologous Antibodies
 ; NUMBER OF SEQUENCES: 150
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/042,353
 ; FILING DATE: 13-MAR-1998
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/810,279
 ; FILING DATE: 17-DEC-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/853,408
 ; FILING DATE: 18-MAR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/904,068
 ; FILING DATE: 23-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/053,131
 ; FILING DATE: 26-APR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/096,762
 ; FILING DATE: 22-JUL-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/155,301
 ; FILING DATE: 18-NOV-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/161,739
 ; FILING DATE: 03-DEC-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/165,699
 ; FILING DATE: 10-DEC-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/209,741
 ;

INFORMATION FOR SEQ ID NO: 78:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-308-865-78
 Query Match 71.7%; Score 43; DB 1; Length 33;
 Best Local Similarity 66.7%; Pred. No. 1.6;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TYYFGDV 11
 ::|::|:|||:
 Db 10 SYYYGMDV 18
 US-08-308-865-78

FILING DATE: 09-MAR-1994
 PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/152,322

FILING DATE: 07-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/544,404

FILING DATE: 10-OCT-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/728,463

FILING DATE: 10-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US96/16433

FILING DATE: 10-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/728,417

FILING DATE: 02-DEC-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US96/21803

FILING DATE: 01-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 014643-009040US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 275:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 123:

US-09-042-353-275

RESULT 7
 US-09-758-417A-123

; Sequence 123, Application US/08758417A

; Patent No. 6300129

GENERAL INFORMATION:

APPLICANT: Lomberg, Nils

Kay, Robert M.

TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for

Producing Heterologous Antibodies

NUMBER OF SEQUENCES: 417

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

ZIP/CITY: USA

ZIP/CITY: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/758,417A

FILING DATE: 02-Dec-1996

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/728,463

FILING DATE: 10-OCT-1996

RESULT 8
 PCT-US92-10983-78

; Sequence 78, Application PC/TUS9210983

; GENERAL INFORMATION:

APPLICANT: Lomberg, Nils

Kay, Robert M.

TITLE OF INVENTION: Transgenic Non-Human Animals for

Producing Heterologous Antibodies

NUMBER OF SEQUENCES: 152

CORRESPONDENCE ADDRESS:

ADDRESSEE: William M. Smith

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP/CITY: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10983

FILING DATE: 19921217

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 14643-9-2

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 78:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US92-10983-78

Query Match 71.7%; Score 43; DB 4; Length 33;
 Best Local Similarity 66.7%; Pred. No. 1.6; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TYYFGGLDV 11
 Db 10 SYYYGMDV 18

RESULT 9
 US-09-840-459-84
 Sequence 84, Application US/09840459
 ; Sequence 84, Application US/09840459
 ; Patent No. 696650
 GENERAL INFORMATION:
 APPLICANT: Harosa, Gregory J.
 APPLICANT: Horvath, Christopher
 APPLICANT: Newman, Walter
 APPLICANT: Jones, S. Tarran
 APPLICANT: O'Keefe, Theresa
 APPLICANT: Sllobohan H.
 TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND METHODS OF USE THEREFOR
 FILE REFERENCE: 1855_1052_012
 CURRENT APPLICATION NUMBER: US/09/840,459
 CURRENT FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: PCT/US01/03537
 PRIOR FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: 09/497,625
 PRIOR FILING DATE: 2000-02-03
 PRIOR APPLICATION NUMBER: 09/359,193
 PRIOR FILING DATE: 1999-07-22
 PRIOR APPLICATION NUMBER: 09/121,781
 PRIOR FILING DATE: 1998-07-23
 NUMBER OF SEQ ID NOS: 107
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 84
 LENGTH: 125
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-840-459-84

Query Match 71.7%; Score 43; DB 2; Length 125;
 Best Local Similarity 66.7%; Pred. No. 6.4; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TYYFGGLDV 11
 Db 106 SYYYGMDV 114

RESULT 10
 US-09-497-625A-84
 Sequence 84, Application US/09497625A
 ; Sequence 84, Application US/09497625A
 ; Patent No. 6721349
 GENERAL INFORMATION:
 APPLICANT: Laroba, Gregory J.
 APPLICANT: Horvath, Christopher
 APPLICANT: Newman, Walter
 APPLICANT: Jones, S. Tarran
 APPLICANT: O'Brien, Siobhan H.
 APPLICANT: O'Keefe, Theresa

RESULT 11
 US-08-053-131-73
 Sequence 73, Application US/08053131
 ; Sequence 73, Application US/08053131
 ; Patent No. 5661016
 GENERAL INFORMATION:
 APPLICANT: Lombberg, Nils
 APPLICANT: Kay, Robert M.
 TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for Producing Heterologous Antibodies
 NUMBER OF SEQUENCES: 197
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: One Market Plaza, Steuart Tower, Suite 200
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIN Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/053,131
 FILING DATE: 26-APR-1993
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/990,860
 FILING DATE: 16-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/810,279
 FILING DATE: 17-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/853,408
 FILING DATE: 18-MAR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 14643-9-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 73:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

? Mon Dec 5 13:14:55 2005

us-10-632-706-127.rai

Page 7

FILING DATE: 26-APR-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/390,860
 FILING DATE: 16-DEC-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/304,068
 FILING DATE: 23-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/353,408
 FILING DATE: 18-MAR-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/810,279
 FILING DATE: 17-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 14643-9-4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-308-865-73

Query Match 70.0%; Score 42; DB 1; Length 29;

Best Local Similarity 75.0%; Pred. No. 2.1; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 73:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acidsATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 14643-9-4

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-308-865-73

Query Match 70.0%; Score 42; DB 1; Length 29;
 Best Local Similarity 75.0%; Pred. No. 2.1; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;Query Match 70.0%; Score 42; DB 1; Length 29;
 Best Local Similarity 75.0%; Pred. No. 2.1; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 73:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acidsATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 14643-9-4

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-308-865-73

Query Match 70.0%; Score 42; DB 1; Length 29;
 Best Local Similarity 75.0%; Pred. No. 2.1; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;Query Match 70.0%; Score 42; DB 1; Length 29;
 Best Local Similarity 75.0%; Pred. No. 2.1; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 73:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acidsATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 14643-9-4

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-308-865-73

US-08-308-865-73

RESULT 15
 US-08-308-865-73
 ; Sequence 73, Application US/08308865
 ; Patent No. 5877397
 GENERAL INFORMATION:
 APPLICANT: Loberg, Nils
 APPLICANT: Kay, Robert M.
 TITLE OF INVENTION: Producing Heterologous Antibodies
 NUMBER OF SEQUENCES: 150
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: William M. Smith
 STREET: One Market Plaza, Steuart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/308,865
 FILING DATE:
 CLASSIFICATION: 800
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/145,707
 FILING DATE:
 APPLICATION NUMBER: US 07/904,068
 FILING DATE: 23 JUN 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 14643-9-1-1

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OM protein - protein search, using sw model

GenCore version 5.1.6

SUMMARIES

569

RESULTS

| Description | Alignment |
|---|-----------------|
| Sequence 126, Application US/10632706 | ALIGMENTS |
| RESULT 1 | |
| US-10-632-706-126 | |
| ; Sequence 126, Application US/10632706 | |
| ; Publication No. US20040175385A1 | |
| ; GENERAL INFORMATION: | |
| ; APPLICANT: MARKS, JAMES D. | |
| ; ATTORNEY/AGENT: AMERSDORFER, PETER | |
| ; TITLE OF INVENTION: THERAPEUTIC MONOClonAL ANTIBODIES THAT NEUTRALIZE BOTULINUM | |
| ; TIME OF INVENTION: NEUROTOXINS | |
| ; FILE REFERENCE: 407T-89512005 | |
| ; CURRENT APPLICATION NUMBER: US/10/632,706 | |
| ; CURRENT FILING DATE: 2003-08-01 | |
| ; PRIOR APPLICATION NUMBER: US 60/400,721 | |
| ; PRIOR FILING DATE: 2002-08-01 | |
| ; PRIOR APPLICATION NUMBER: US 09/144,806 | |
| ; PRIOR FILING DATE: 1998-08-31 | |
| ; NUMBER OF SEQ ID NOS: 278 | |
| ; SOFTWARE: Patentin version 3.2 | |
| ; SEQ ID NO 126 | |
| ; LENGTH: 11 | |
| ; TYPE: PRT | |
| ; ORGANISM: Artificial | |
| ; FEATURE: | |
| ; OTHER INFORMATION: single chain antibody fragment | |
| US-10-632-706-126 | |
| Query Match 100.0%; Score 60; DB 4; Length 11; | |
| Best Local Similarity 100.0%; Pred. No. 0.0027; Mismatches 0; Indels 0; Gaps 0; | |
| Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| Oy | 1 LATYYVGLDV 11 |
| Db | 1 LATYYVGLDV 11 |

RESULT 2

| Sequence | Publication No. | Application No. |
|---|-------------------|-----------------|
| Sequence 127, APP | US-10-632-706-127 | US/10632706 |
| Sequence 3068, APP | US-10-632-706-127 | US20040175385A1 |
| ; GENERAL INFORMATION: | | |
| ; APPLICANT: MARKS, JAMES D. | | |
| ; ATTORNEY/AGENT: AMERSDORFER, PETER | | |
| ; TITLE OF INVENTION: THERAPEUTIC MONOClonAL ANTIBODIES THAT NEUTRALIZE BOTULINUM | | |
| ; TIME OF INVENTION: NEUROTOXINS | | |
| ; FILE REFERENCE: 407T-89512005 | | |
| ; CURRENT APPLICATION NUMBER: US/10/632,706 | | |
| ; CURRENT FILING DATE: 2003-08-01 | | |
| ; PRIOR APPLICATION NUMBER: US 60/400,721 | | |
| ; PRIOR FILING DATE: 2002-08-01 | | |
| ; PRIOR APPLICATION NUMBER: US 09/144,806 | | |

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; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 127
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
; US-10-632-706-127

Query Match      100.0%; Score 60; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0027; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Qy 1 LATYYFGLDV 11
Db 1 LATYYFGLDV 11

RESULT 3
US-11-031-485-116
; Sequence 116, Application US/11031485
; Publication No. US2005023297A1
; GENERAL INFORMATION:
; APPLICANT: FULLER, NICHOLAS
; APPLICANT: MOLLOY, ELIZABETH
; APPLICANT: KELLERMANN, STRID-AIMEE
; APPLICANT: GREEN, LARRY L.
; APPLICANT: HAAK-FRENSCHO, MARY
; TITLE OF INVENTION: ANTIBODIES TO MADCAM
; FILE REFERENCE: ABX-P65
; CURRENT APPLICATION NUMBER: US/11/031,485
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: US 60/535,490
; PRIOR FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO: 116
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-031-485-116

Query Match      80.0%; Score 48; DB 6; Length 122;
Best Local Similarity 63.6%; Pred. No. 2.8%; Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0; Qy 1 LATYYFGLDV 11
Db 100 WVTYYIGMDV 110

RESULT 4
US-10-364-743-101
; Sequence 101, Application US/10364743
; Publication No. US20040009178A1
; GENERAL INFORMATION:
; APPLICANT: BOWDISH, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: Nolan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 98 CIP (1087-73 CIP)
; CURRENT APPLICATION NUMBER: US/10/452,593
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/364,743
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/356,086
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/376,408
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 101
; LENGTH: 129
; TYPE: PRT
; ORGANISM: human
; US-10-452-593-101

Query Match      78.3%; Score 47; DB 5; Length 129;
Best Local Similarity 77.8%; Pred. No. 4.4%; Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0; Qy 3 TYYYFGLDV 11
Db 105 TYYYGMDV 113

RESULT 5
US-10-452-593-101
; Sequence 101, Application US/0452593
; Publication No. US2004025869A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: Nolan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 98 CIP (1087-73 CIP)
; CURRENT APPLICATION NUMBER: US/10/452,593
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/364,743
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/356,086
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/376,408
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 101
; LENGTH: 129
; TYPE: PRT
; ORGANISM: human
; US-10-452-593-101

Query Match      78.3%; Score 47; DB 5; Length 129;
Best Local Similarity 77.8%; Pred. No. 4.4%; Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0; Qy 3 TYYYFGLDV 11
Db 105 TYYYGMDV 113

RESULT 6
US-10-364-743-15
; Sequence 15, Application US/10364743
; Publication No. US20040009178A1
; GENERAL INFORMATION:
; APPLICANT: BOWDISH, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: Nolan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 84 (1087-73)
; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 15
; LENGTH: 134
; TYPE: PRT
; US-10-364-743-15

```

; ORGANISM: human
; US-10-364-743-15
; Query Match 78.3%; Score 47; DB 4; Length 134;
; Best Local Similarity 77.8%; Pred. No. 4.5;
; Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
; Qy 3 TYYFGGLDV 11
; Db 110 TYYYGMDV 118

RESULT 7
US-10-452-593-15
; Sequence 15, Application US/10452593
; Publication No. US20040258699A1
; GENERAL INFORMATION:
; APPLICANT: PULLEN, NICHOLAS
; APPLICANT: Wild, Martha A.
; APPLICANT: Frederickson, Shana
; APPLICANT: Maruama, Toshiaki
; APPLICANT: Nolan, Marty Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 98 CIP (1087-73 CIP)
; CURRENT APPLICATION NUMBER: US/10/452,593
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/364,743
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/356,086
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/376,408
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 134
; TYPE: PRT
; ORGANISM: human
; US-10-452-593-15

Query Match 78.3%; Score 47; DB 5; Length 134;
Best Local Similarity 77.8%; Pred. No. 4.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 110 TYYYGMDV 118

RESULT 8
US-11-031-485-56
; Sequence 56, Application US/11031485
; Publication No. US20050232917A1
; GENERAL INFORMATION:
; APPLICANT: PULLEN, NICHOLAS
; APPLICANT: MOLLOY, ELIZABETH
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: HAAK-FRENDSCHO, MARY
; APPLICANT: GREEN, LARRY L.
; TITLE OF INVENTION: ANTIBODIES TO MADCAM
; FILE REFERENCE: ABX-PFG
; CURRENT APPLICATION NUMBER: US/11/031,485
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 60/535,490
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 18
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-031-485-18

Query Match 78.3%; Score 47; DB 6; Length 469;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 3 TYYFGGLDV 11
Db 123 TYYYGMDV 131

RESULT 9
US-11-031-485-18
; Sequence 18, Application US/11031485
; Publication No. US20050232917A1
; GENERAL INFORMATION:
; APPLICANT: PULLEN, NICHOLAS
; APPLICANT: MOLLOY, ELIZABETH
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: HAAK-FRENDSCHO, MARY
; TITLE OF INVENTION: ANTIBODIES TO MADCAM
; FILE REFERENCE: ABX-PFG
; CURRENT APPLICATION NUMBER: US/11/031,485
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 60/535,490
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 18
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-031-485-18

Query Match 78.3%; Score 47; DB 6; Length 469;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 3 TYYFGGLDV 11
Db 123 TYYYGMDV 131

RESULT 10
US-10-632-706-114
; Sequence 114, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOClonal ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-8512015
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
; US-10-632-706-114

Query Match 76.7%; Score 46; DB 4; Length 13;
Best Local Similarity 70.0%; Pred. No. 0.64;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 3 TYYFGGLDV 11
Db 123 TYYYGMDV 131

RESULT 11
US-10-632-706-114
; Sequence 114, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOClonal ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-8512015
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
; US-10-632-706-114

Query Match 76.7%; Score 46; DB 4; Length 13;
Best Local Similarity 70.0%; Pred. No. 0.64;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATYYYFGLDV 11
 | |||:|||:
 4 ANYYYGMDV 13

RESULT 11
 US-10-783-311-41
 ; Sequence 141, Application US/1073311
 ; Publication No. US20050009136A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nixon, Andrew
 ; TITLE OF INVENTION: PAPP-A LIGANDS
 ; FILE REFERENCE: 10280-059001
 ; CURRENT APPLICATION NUMBER: US/10/783,311
 ; CURRENT FILING DATE: 2004-02-19
 ; PRIOR APPLICATION NUMBER: US 60/448,515
 ; NUMBER OF SEQ ID NOS: 394
 ; SEQ ID NO: 277
 ; LENGTH: 16
 ; SOFTWARE: FastSBQ for Windows Version 4.0
 ; PRIORITY APPLICATION NUMBER: US 60/448,515
 ; PRIORITY FILING DATE: 2003-02-19
 ; NUMBER OF SEQ ID NOS: 394
 ; SEQ ID NO: 141
 ; LENGTH: 21
 ; TYPE: PRT
 ; FEATURE:
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Heavy Chain amino acid sequence
 ; US-10-783-311-41

Query Match 76.7%; Score 46; DB 5; Length 21;
 Best Local Similarity 63.6%; Pred. No. 1;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 LATYYYFGLDV 11
 ; | |||:|||:
 Db 11 LGNYYYGMDV 21

RESULT 12
 US-10-783-311-35
 ; Sequence 135, Application US/1073311
 ; Publication No. US20050009136A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nixon, Andrew
 ; TITLE OF INVENTION: PAPP-A LIGANDS
 ; FILE REFERENCE: 10280-059001
 ; CURRENT APPLICATION NUMBER: US/10/783,311
 ; CURRENT FILING DATE: 2004-02-19
 ; PRIOR APPLICATION NUMBER: US 60/448,515
 ; PRIOR FILING DATE: 2003-02-19
 ; NUMBER OF SEQ ID NOS: 394
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 135
 ; LENGTH: 140
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Heavy Chain amino acid sequence
 ; US-10-783-311-35

Query Match 76.7%; Score 46; DB 5; Length 140;
 Best Local Similarity 63.6%; Pred. No. 6.9%;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 LATYYYFGLDV 11
 ; | |||:|||:
 Db 109 LGNYYYGMDV 119

RESULT 13
 US-10-783-311-277
 ; Sequence 277, Application US/1073311

Publication No. US20050009136A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nixon, Andrew
 ; TITLE OF INVENTION: PAPP-A LIGANDS
 ; FILE REFERENCE: 10280-059001
 ; CURRENT APPLICATION NUMBER: US/10/783,311
 ; CURRENT FILING DATE: 2004-02-19
 ; PRIOR APPLICATION NUMBER: US 60/448,515
 ; NUMBER OF SEQ ID NOS: 394
 ; SEQ ID NO: 277
 ; LENGTH: 16
 ; SOFTWARE: FastSBQ for Windows Version 4.0
 ; PRIORITY APPLICATION NUMBER: US/09/880,748
 ; PRIORITY FILING DATE: 2001-06-15
 ; PRIORITY APPLICATION NUMBER: 60/212,210
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PFS23
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 3068
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-880,748-3068

Query Match 75.0%; Score 45; DB 3; Length 21;
 Best Local Similarity 70.0%; Pred. No. 1.5%;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 ATYYYFGLDV 11
 ; | |||:|||:
 Db 12 APYYYYGMDV 21

RESULT 15
 US-10-293-418-3068
 ; Sequence 3068, Application US/10293418
 ; Publication No. US20030223996A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PFS23P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 3068
LENGTH: 21

TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-3068

Query Match 75.0%; Score 45; DB 4; Length 21;
Best Local Similarity 70.0%; Pred. No. 1,5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

| | | | |
|----|----|-----------|----|
| QY | 2 | ATYYFGIDV | 11 |
| | | | |
| Db | 12 | APYYYGMDV | 21 |

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Job time : 80.8333 secs

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OM protein - protein search, using SW model
Run on: December 4, 2005, 04:08:08 ; Search time 3.20833 Seconds
(without alignments)
16.417 Million cell updates/sec

Title: US-10-632-706-127
Perfect score: 60
Sequence: 1 LATYYFGLDV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_New:+

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3: /cgmn2_6/ptodata/1/pupaa/us07 NEW PUB.PEP:*
4: /cgmn2_6/ptodata/1/pupaa/us08 NEW PUB.PEP:*
5: /cgmn2_6/ptodata/1/pupaa/bct NEW PUB.PEP:*
6: /cgmn2_6/ptodata/1/pupaa/us10 NEW PUB.PEP:*
7: /cgmn2_6/ptodata/1/pupaa/us11 NEW PUB.PEP:*
8: /cgmn2_6/ptodata/1/pupaa/us60 NEW PUB.PEP:*
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'pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.'

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|--|
| 1 | 45 | 75.0 | 21 | US-11-054-515-3068 Sequence 3068, AP |
| 2 | 45 | 75.0 | 256 | 7 US-11-054-515-1600 Sequence 1600, AP |
| 3 | 44 | 73.3 | 16 | 7 US-11-054-515-2129 Sequence 2129, AP |
| 4 | 44 | 73.3 | 17 | 7 US-11-054-515-2876 Sequence 2876, AP |
| 5 | 44 | 73.3 | 252 | 7 US-11-054-515-1431 Sequence 1431, AP |
| 6 | 44 | 73.3 | 254 | 7 US-11-054-515-153 Sequence 3, Appl |
| 7 | 44 | 73.3 | 254 | 7 US-11-054-515-838 Sequence 838, AP |
| 8 | 44 | 73.3 | 254 | 7 US-11-054-515-870 Sequence 870, AP |
| 9 | 44 | 73.3 | 254 | 7 US-11-054-515-1287 Sequence 1287, AP |
| 10 | 44 | 73.3 | 254 | 7 US-11-054-515-1288 Sequence 1288, AP |
| 11 | 43 | 71.7 | 306 | 7 US-11-017-515-47 Sequence 47, Appl |
| 12 | 42 | 70.0 | 13 | 7 US-11-054-515-3091 Sequence 3091, AP |
| 13 | 42 | 70.0 | 17 | 7 US-11-054-515-2817 Sequence 2817, AP |
| 14 | 42 | 70.0 | 19 | 7 US-11-054-515-2735 Sequence 2735, AP |
| 15 | 42 | 70.0 | 19 | 7 US-11-054-515-2899 Sequence 2899, AP |
| 16 | 42 | 70.0 | 19 | 7 US-11-054-515-2935 Sequence 2935, AP |
| 17 | 42 | 70.0 | 19 | 7 US-11-054-515-3038 Sequence 3038, AP |
| 18 | 42 | 70.0 | 19 | 7 US-11-054-515-3052 Sequence 3052, AP |
| 19 | 42 | 70.0 | 19 | 7 US-11-054-515-3067 Sequence 3067, AP |
| 20 | 42 | 70.0 | 19 | 7 US-11-054-515-3087 Sequence 3087, AP |
| 21 | 42 | 70.0 | 19 | 7 US-11-054-515-3145 Sequence 3145, AP |
| 22 | 42 | 70.0 | 20 | 7 US-11-040-159-4 Sequence 4, Appl |
| 23 | 42 | 70.0 | 20 | 7 US-11-054-515-2767 Sequence 2767, AP |
| 24 | 42 | 70.0 | 20 | 7 US-11-054-515-3039 Sequence 3039, AP |
| 25 | 42 | 70.0 | 20 | 7 US-11-054-515-3039 Sequence 3039, AP |

ALIGNMENTS

RESULT 1
US-11-054-515-3068
; Sequence 3068, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS2JP3
; CURRENT APPLICATION NUMBER: US/11/054, 515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543, 296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580, 347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293, 418
; PRIOR APPLICATION NUMBER: 60/331, 469
; PRIOR FILING DATE: 2003-11-16
; PRIOR APPLICATION NUMBER: 60/340, 817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880, 748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293, 499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277, 379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276, 248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240, 816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 3068
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-3068

Query Match 75.0%; Score 45; DB 7; Length 21;
Best Local Similarity 70.0%; Pred. No. 0.017; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 2 ATYYFGLDV 11
Db |||||:||||:||| 12 APYYYFGLDV 21

US-11-054-515-1600
; Sequence 1600, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS
; FILE REFERENCE: PFP23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR APPLICATION NUMBER: 60/531,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1600
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-1600

RESULT 3
Query Match 75.0%; Score 45; DB 7; Length 256;
Best Local Similarity 70.0%; Pred. No. 0.19; 0;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 ATYYYFGLDV 11
Db 110 APYYYGMDV 119

US-11-054-515-2129
Sequence 2129, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS
FILE REFERENCE: PFP23P3
CURRENT APPLICATION NUMBER: US/11/054,515
PRIOR APPLICATION NUMBER: 60/531,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/293,418
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2876
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-2876

RESULT 4
Query Match 73.3%; Score 44; DB 7; Length 17;
Best Local Similarity 63.6%; Pred. No. 0.021; 0;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 LATYYYFGLDV 11
Db 6 LTGYYYGMDV 16

US-11-054-515-2876
Sequence 2876, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS
FILE REFERENCE: PFP23P3
CURRENT APPLICATION NUMBER: US/11/054,515
PRIOR APPLICATION NUMBER: 60/531,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/293,418
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2876
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1431
Sequence 1431, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P3
CURRENT APPLICATION NUMBER: US/11/054, 515
CURRENT FILING DATE: 2005-02-10
PRIORITY APPLICATION NUMBER: 60/543, 296
PRIORITY FILING DATE: 2004-02-11
PRIORITY APPLICATION NUMBER: 60/580, 347
PRIORITY FILING DATE: 2004-06-18
PRIORITY APPLICATION NUMBER: 10/293, 418
PRIORITY FILING DATE: 2002-11-14
PRIORITY APPLICATION NUMBER: 60/331, 469
PRIORITY FILING DATE: 2001-11-16
PRIORITY APPLICATION NUMBER: 60/340, 817
PRIORITY FILING DATE: 2001-12-19
PRIORITY APPLICATION NUMBER: 09/880, 748
PRIORITY FILING DATE: 2001-06-15
PRIORITY APPLICATION NUMBER: 60/293, 499
PRIORITY FILING DATE: 2001-05-25
PRIORITY APPLICATION NUMBER: 60/277, 379
PRIORITY FILING DATE: 2001-03-21
PRIORITY APPLICATION NUMBER: 60/276, 248
PRIORITY FILING DATE: 2001-03-16
PRIORITY APPLICATION NUMBER: 60/240, 816
PRIORITY FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1
; SEQ ID NO 3
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-3
Query Match 73.3%; Score 44; DB 7; Length 254;
Best Local Similarity 63.6%; Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2;
; Indels 0; Gaps 0;
QY 1 LATYYYFGLDV 11
Db 107 LTGYYYGMDV 117
RESULT 7
US-11-054-515-838
; Sequence 838, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054, 515
; CURRENT FILING DATE: 2005-02-10
; PRIORITY APPLICATION NUMBER: 60/543, 296
; PRIORITY FILING DATE: 2004-02-11
; PRIORITY APPLICATION NUMBER: 60/580, 347
; PRIORITY FILING DATE: 2004-06-18
; PRIORITY APPLICATION NUMBER: 10/293, 418
; PRIORITY FILING DATE: 2002-11-14
; PRIORITY APPLICATION NUMBER: 60/331, 469
; PRIORITY FILING DATE: 2001-11-16
; PRIORITY APPLICATION NUMBER: 60/340, 817
; PRIORITY FILING DATE: 2001-12-19
; PRIORITY APPLICATION NUMBER: 09/880, 748
; PRIORITY FILING DATE: 2001-06-15
; PRIORITY APPLICATION NUMBER: 60/293, 499
; PRIORITY FILING DATE: 2001-05-25
; PRIORITY APPLICATION NUMBER: 60/277, 379
; PRIORITY FILING DATE: 2001-03-21
; PRIORITY APPLICATION NUMBER: 60/276, 248
; PRIORITY FILING DATE: 2001-03-16
; PRIORITY APPLICATION NUMBER: 60/331, 469
; PRIORITY FILING DATE: 2001-11-16
; PRIORITY APPLICATION NUMBER: 60/340, 817
; PRIORITY FILING DATE: 2001-12-19
; PRIORITY APPLICATION NUMBER: 09/880, 748
; PRIORITY FILING DATE: 2001-06-15
; PRIORITY APPLICATION NUMBER: 60/293, 499
; PRIORITY FILING DATE: 2001-05-25
; PRIORITY APPLICATION NUMBER: 60/277, 379
; PRIORITY FILING DATE: 2001-03-21
; PRIORITY APPLICATION NUMBER: 60/276, 248
; PRIORITY FILING DATE: 2001-03-16
; PRIORITY APPLICATION NUMBER: 60/240, 816
; PRIORITY FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-838
Query Match 73.3%; Score 44; DB 7; Length 254;
Best Local Similarity 63.6%; Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2;
; Indels 0; Gaps 0;
QY 1 LATYYYFGLDV 11
Db 107 LTGYYYGMDV 117
RESULT 8
US-11-054-515-870
; Sequence 870, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054, 515
; CURRENT FILING DATE: 2005-02-10
; PRIORITY APPLICATION NUMBER: 60/543, 296

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; PRIOR FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/233,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; SEQ ID NO: 870
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: NAME/KEY: Site
; LOCATION: (240)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-11-054-515-870
; Remaining Prior Application data removed - See File Wrapper or PALM.

; Query Match 73.3%; Score 44; DB 7; Length 254;
; Best Local Similarity 63.6%; Pred. No. 0.28;
; Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS2P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/233,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.

; SEQ ID NO: 1287
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-1287
; Query Match 73.3%; Score 44; DB 7; Length 254;
; Best Local Similarity 63.6%; Pred. No. 0.28;
; Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS2P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/233,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-03-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.

; SEQ ID NO: 1287
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-1287
; Query Match 73.3%; Score 44; DB 7; Length 254;
; Best Local Similarity 63.6%; Pred. No. 0.28;
; Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS2P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296

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PRIOR FILING DATE: 2004-03-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1288
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1288

RESULT 11
US-11-017-550-47
Query Match 73.3%; Score 44; DB 7; Length 254;
Best Local Similarity 63.6%; Pred. No. 0.28; Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 LATYYFGLDV 11
Db 107 LIGYYYGMDV 117

US-11-017-550-47 Application US/11017550
; Sequence 47, Application US/11017550
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/343,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/880,347
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 3091
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-3091

RESULT 13
US-11-054-515-2817
Query Match 70.0%; Score 42; DB 7; Length 13;
Best Local Similarity 75.0%; Pred. No. 0.035; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 4 YYYFGLDV 11
Db 6 WYYYGMDV 13

US-11-054-515-2817 Application US/11054515
; Sequence 2817, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817

Query Match 71.7%; Score 43; DB 7; Length 306;
Best Local Similarity 77.8%; Pred. No. 0.5; Length 306;
US-11-017-550-47
TYPE: PRT
ORGANISM: Methanococcus jannaschii

```

; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/275,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO: 2899
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-2817

Query Match          70.0%; Score 42; DB 7; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.046;          0;
Matches      6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Oy           4 YYYFGGLDV 11
Db           10 YYYYGMDV 17

RESULT 14
US-11-054-515-2735
Sequence 2735, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS
FILE REFERENCE: PFS3P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/275,248
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2899
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-2899

Query Match          70.0%; Score 42; DB 7; Length 19;
Best Local Similarity 75.0%; Pred. No. 0.051;          0;
Matches      6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Oy           4 YYYFGGLDV 11
Db           12 YYYYGMDV 19

Search completed: December 4, 2005, 04:37:48
Job time : 3.20833 secs

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Query Match 70.0%; Score 42; DB 7; Length 19;
Best Local Similarity 75.0%; Pred. No. 0.051; 0;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Oy 4 YYYFGGLDV 11
Db 12 YYYYGMDV 19

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GenCore version 5.1.6

OM protein - protein search, using SW model

Run on: December 4, 2005, 04:07:28 ; Search time 78.8333 Seconds
(without alignments)
58.302 Million cell updates/sec

Title: US-10-632-706-128

Perfect score: 66

Sequence: 1 GPMELVGFDS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 41789326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main: *

1: /cggn2_6/ptodata/1/pubpaal/us07_PUBCOMB.pep: *
2: /cggn2_6/ptodata/1/pubpaal/us08_PUBCOMB.pep: *
3: /cggn2_6/ptodata/1/pubpaal/us09_PUBCOMB.pep: *
4: /cggn2_6/ptodata/1/pubpaal/us10_PUBCOMB.pep: *
5: /cggn2_6/ptodata/1/pubpaal/us10B_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|--------|----------------------|
| 1 | 66 | 100.0 | 11 4 | US-10-632-706-128 |
| 2 | 45 | 68.2 | 290 4 | US-10-632-706-128 |
| 3 | 44 | 66.7 | 306 4 | US-10-282-122A-7455 |
| 4 | 44 | 66.7 | 367 4 | US-10-882-122A-74966 |
| 5 | 44 | 66.7 | 367 4 | US-10-282-122A-75801 |
| 6 | 42 | 63.6 | 381 4 | US-10-437-963-19224 |
| 7 | 41 | 62.1 | 125 4 | US-10-425-115-25365 |
| 8 | 41 | 62.1 | 171 4 | US-10-424-599-186345 |
| 9 | 41 | 62.1 | 475 4 | US-10-282-122A-48377 |
| 10 | 41 | 62.1 | 792 5 | US-10-483-032A-252 |
| 11 | 41 | 62.1 | 1352 6 | US-11-097-14-29418 |
| 12 | 40 | 60.6 | 50 4 | US-10-424-599-182764 |
| 13 | 40 | 60.6 | 78 4 | US-10-425-115-319649 |
| 14 | 40 | 60.6 | 146 4 | US-10-477-57-27-21 |
| 15 | 40 | 60.6 | 150 4 | US-10-425-115-333207 |
| 16 | 40 | 60.6 | 477 4 | US-10-425-114-70098 |
| 17 | 40 | 60.6 | 507 4 | US-10-422-99-229226 |
| 18 | 40 | 60.6 | 891 4 | US-10-425-115-229314 |
| 19 | 40 | 60.6 | 931 5 | US-10-732-923-22388 |
| 20 | 40 | 60.6 | 949 5 | US-10-424-599-163986 |
| 21 | 40 | 60.6 | 1355 4 | US-10-437-963-110486 |
| 22 | 40 | 60.6 | 511 4 | US-10-425-114-52508 |
| 23 | 39 | 59.8 | 118 4 | US-10-424-599-197468 |
| 24 | 39 | 59.1 | 207 4 | US-10-424-599-163986 |
| 25 | 39 | 59.1 | 235 5 | US-10-732-923-22418 |
| 26 | 39 | 59.1 | 591 4 | US-10-424-599-224678 |
| 27 | 39 | 59.1 | 650 4 | US-10-424-599-224678 |

ALIGNMENTS

RESULT 1

US-10-632-706-128

; Sequence 128, Application US/10632706

; Publication No. US20040175385A1

; GENERAL INFORMATION:

; APPLICANT: MARKS, JAMES D.

; ATTORNEY: AMERSDORFER, PETER

; TITLE OF INVENTION: THERAPEUTIC MONOClonAL ANTIBODIES THAT NEUTRALIZE BOTULINUM

; TITLE OF INVENTION: NEUROTOXINS

; FILE REFERENCE: 407T-8851205

; CURRENT APPLICATION NUMBER: US/10-632-706

; CURRENT FILING DATE: 2003-08-01

; PRIORITY FILING NUMBER: US 60/400,721

; PRIORITY FILING DATE: 2002-08-01

; PRIORITY FILING NUMBER: US 09/144,806

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 128

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial

; FEATURES:

; OTHER INFORMATION: single chain antibody fragment

US-10-632-706-128

Query Match 100.0%; Score 66; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. 0.00072; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPMELVGFDS 11

Db 1 GPMELVGFDS 11

RESULT 2

US-10-156-761-9341

; Sequence 9341, Application US/10156761

; Publication No. US20030119018A1

; GENERAL INFORMATION:

; APPLICANT: OMURA, SATOSHI

; ATTORNEY: IKEDA, HARUO

; ATTORNEY: ISHIKAWA, JUN

; ATTORNEY: HORIKAWA, HIROSHI

; ATTORNEY: SHIBA, TADAYOSHI

; ATTORNEY: SAKAI, YOSHIOUKI

; ATTORNEY: HATTORI, MASAHIRA

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 219-262

CURRENT APPLICATION NUMBER: US/10/156,761

Sequence 194057, A

Sequence 10546, A

Sequence 121136, A

Sequence 46814, A

Sequence 50763, A

Sequence 22382, A

Sequence 22383, A

Sequence 204079, A

Sequence 121132, A

Sequence 111662, A

Sequence 3713, A

Sequence 277808, A

Sequence 1570254, A

Sequence 141911, A

Sequence 205846, A

Sequence 60011, A

Sequence 230098, A

Sequence 53925, A

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; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9341
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9341

Query Match 68.2%; Score 45; DB 4; Length 290;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 3 WELVGYFDS 111
Db 171 WMLIGYFDS 179

RESULT 3 US-10-282-122A-73455
; Sequence 73455, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA_034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/205,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-3
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74966
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-10-282-122A-74966

Query Match 66.7%; Score 44; DB 4; Length 367;
Best Local Similarity 69.2%; Pred. No. 69;
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
Qy 1 GPWELV---GYF 9
Db 127 GPWELVGGPGYF 139

RESULT 4 US-10-282-122A-74966
; Sequence 74966, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA_034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-3
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74966
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-10-282-122A-75801

Query Match 66.7%; Score 44; DB 4; Length 306;
Best Local Similarity 69.2%; Pred. No. 58;
; TYPE: PRT
; ORGANISM: Salmonella paratyphi A
US-10-282-122A-73455

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QY 1 GPWELVGYFD 10
 ||| : ; |||
 Db 14 GPWDEMKYFD 23

RESULT 9
 US-10-282-122A-48377
 ; Sequence 18747, Application US/10437963
 ; Publication No. US2004029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangbu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Hasebeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xui, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELTRIA-034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 48377

LENGTH: 475
 TYPE: PRT
 ORGANISM: Bacteroides fragilis

US-10-282-122A-48377

Query Match 62.1%; Score 41; DB 4; Length 475;
 Best Local Similarity 70.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

RESULT 11
 US-10-481-032A-252
 ; Sequence 252, Application US/10481032A
 ; Publication No. US20050177901A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhu, Tong
 ; APPLICANT: Cheng, Wanqiong
 ; APPLICANT: Briggs, Steven
 ; APPLICANT: Cooper, Bret
 ; APPLICANT: Goff, Stephen A.
 ; APPLICANT: Moughamer, Todd
 ; APPLICANT: Glazebrook, Jane
 ; APPLICANT: Katagiri, Fumiaki
 ; APPLICANT: Krebs, Joel
 ; APPLICANT: Prohart, Nicolas
 ; APPLICANT: Riche, Darrell

TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES

FILE REFERENCE: 60148USPCT
 CURRENT APPLICATION NUMBER: US/10/481,032A

CURRENT FILING DATE: 2003-12-16

PRIOR APPLICATION NUMBER: US 60/300,112

PRIOR FILING DATE: 2001-06-22

PRIOR APPLICATION NUMBER: US 60/325,277

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: US 60/342,327

PRIOR FILING DATE: 2001-12-20

PRIOR APPLICATION NUMBER: PCT/IB02/02450

PRIOR FILING DATE: 2002-06-21

NUMBER OF SEQ ID NOS: 1201
 SOFTWARE: Patentin Ver. 2.2
 SEQ ID NO: 252

LENGTH: 792
 TYPE: PRT
 ORGANISM: Oryza sativa

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (12)..(14)
 OTHER INFORMATION: Xaa = any naturally occurring amino acid
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (16)..(16)

RESULT 10
 US-10-437-963-487947
 ; Sequence 18747, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei
 APPLICANT: Wu, Wei
 APPLICANT: Boukharov, Andrey A.
 APPLICANT: Barbazuk, Brad
 APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B
 CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO: 167947
 LENGTH: 475
 TYPE: PRT
 ORGANISM: Oryza sativa
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)..(475)
 OTHER INFORMATION: unsure at all Xaa locations
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT4530_845C.1.pep

US-10-437-963-187947
 Query Match 62.1%; Score 41; DB 4; Length 475;
 Best Local Similarity 70.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

QY 1 GPWELVGYFD 10
 ||| : ; |||
 Db 115 GPWEGKGYHD 124

OTHER INFORMATION: Xaa = any naturally occurring amino acid
; FEATURE:
; LOCATION: misc feature
; NAME/KEY: misc feature
; OTHER INFORMATION: Xaa = any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (669)..(669)
; OTHER INFORMATION: Xaa = any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (671)..(671)
; OTHER INFORMATION: Xaa = any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: Xaa = any naturally occurring amino acid
; SEQ ID NO: US-10-481-032A-252

Query Match 62.1%; Score 41; DB 5; Length 792;
Best Local Similarity 66.7%; Pred. No. 4.3e+02; Mismatches 1; Indels 0; Gaps 0;

QY 2 PWLVLGYFD 10
Db 245 PWLVLGYFD 253

RESULT 12
US-11-097-143-23418
; Sequence 29418, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEAR ACID
; TITLES OF INVENTION: ARRAYS FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIORITY NUMBER: 60/157,832
; PRIORITY FILING DATE: 1999-10-05
; PRIORITY NUMBER: 60/160,191
; PRIORITY FILING DATE: 1999-10-19
; PRIORITY NUMBER: 60/161,932
; PRIORITY FILING DATE: 1999-10-28
; PRIORITY NUMBER: 60/164,769
; PRIORITY FILING DATE: 1999-11-12
; PRIORITY NUMBER: 60/173,383
; PRIORITY FILING DATE: 1999-12-28
; PRIORITY NUMBER: 60/175,693
; PRIORITY FILING DATE: 2000-01-12
; PRIORITY NUMBER: 60/184,831
; PRIORITY FILING DATE: 2000-02-24
; PRIORITY NUMBER: 60/191,637
; PRIORITY FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FabSeq for Windows Version 4.0
; SEQ ID NO: 29418
; LENGTH: 1352
; TYPE: PRT
; ORGANISM: DROSOPHILA
; SEQ ID NO: US-11-097-143-29418

RESULT 13
US-10-424-599-182764
; Sequence 182764, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovacic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO: 182764
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURES:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_13604C.1.pep
; SEQ ID NO: US-10-424-599-182764

Query Match 60.6%; Score 40; DB 4; Length 78;
Best Local Similarity 66.7%; Pred. No. 73; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPWELVGF 9
Db 32 GPWELVGF 40

RESULT 14
US-10-425-115-319649
; Sequence 319649, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO: 319649
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURES:
; OTHER INFORMATION: Clone ID: MRT4577_54590C.1.pep
; SEQ ID NO: US-10-425-115-319649

Query Match 60.6%; Score 40; DB 4; Length 78;
Best Local Similarity 66.7%; Pred. No. 73; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPWELVGF 9
Db 21 GPWELVGF 29

RESULT 15
US-10-477-227-221
; Sequence 21, Application US/10477527
; Publication No. US20040171807A1

GENERAL INFORMATION:

APPLICANT: The Trustees of the University of Pennsylvania
APPLICANT: Gao, Guangping
APPLICANT: Wilson, James M.
TITLE OF INVENTION: Method for Rapid Screening of Bacterial Transformants and Novel S
FILE REFERENCE: UPN-N2630PCT
CURRENT APPLICATION NUMBER: US/10/477,527
CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: US 60/300,501
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/385,632
PRIOR FILING DATE: 2002-06-04
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 146
TYPE: PRT
ORGANISM: Chimpanzee C6B adenovirus protein
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (62) - (62)
OTHER INFORMATION: Xaa can be any amino acid
US-10-477-527-21

Query Match 60.6%; Score 40; DB 4; Length 146;

Best Local Similarity 85.7%; Pred. No. 1.3e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPWELVG 7
Db 101 GPWEVVG 107

Search completed: December 4, 2005, 04:37:29
Job time : 79.8333 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 4, 2005, 03:59:51 ; Search time 23.6042 Seconds
(without alignments)
38.528 Million cell updates/sec

Title: US-10-632-706-128
Perfect score: 66
Sequence: 1 GPVELVGFDS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cggn2_6/ptodata/1/iaa/H_COMB.pep: *
4: /cggn2_6/ptodata/1/iaa/PCTUS_COMB.pep: *
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6: /cggn2_6/ptodata/1/iaa/backfilesl.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--|
| 1 | 41 | 62.1 | 12 | 1 | US-08-264-093-17 Sequence 17, Appl |
| 2 | 41 | 62.1 | 121 | 1 | US-08-264-093-3 Sequence 3, Appl |
| 3 | 39 | 59.1 | 274 | 2 | US-09-903-540-14253 Sequence 14253, A |
| 4 | 38 | 57.6 | 332 | 2 | US-09-561-763-5 Sequence 5, Appl |
| 5 | 38 | 57.6 | 332 | 2 | US-09-431-36B-5 Sequence 5, Appl |
| 6 | 38 | 57.6 | 493 | 2 | US-09-941-10836 Sequence 10836, A |
| 7 | 38 | 57.6 | 1207 | 2 | US-09-976-594-4 Sequence 4, Appl |
| 8 | 37 | 56.1 | 427 | 2 | US-09-902-540-15261 Sequence 15261, A |
| 9 | 37 | 56.1 | 484 | 2 | US-09-543-681A-6615 Sequence 6615, Ap |
| 10 | 36 | 54.5 | 132 | 2 | US-09-311-021-162 Sequence 162, App |
| 11 | 36 | 54.5 | 140 | 2 | US-09-690-341-29 Sequence 29, Appl |
| 12 | 36 | 54.5 | 174 | 2 | US-09-901-503-13916 Sequence 13916, A |
| 13 | 36 | 54.5 | 194 | 1 | US-08-260-202A-15 Sequence 15, Appl |
| 14 | 36 | 54.5 | 194 | 1 | US-08-260-202A-24 Sequence 24, Appl |
| 15 | 36 | 54.5 | 194 | 1 | US-08-260-151A-17 Sequence 17, Appl |
| 16 | 36 | 54.5 | 194 | 1 | US-08-017-14-17 Sequence 17, Appl |
| 17 | 36 | 54.5 | 194 | 2 | US-08-505-307-15 Sequence 15, Appl |
| 18 | 36 | 54.5 | 194 | 2 | US-08-503-307-17 Sequence 17, Appl |
| 19 | 36 | 54.5 | 194 | 2 | US-09-603-151A-15 Sequence 15, Appl |
| 20 | 36 | 54.5 | 194 | 2 | US-09-603-151A-17 Sequence 17, Appl |
| 21 | 36 | 54.5 | 194 | 4 | FCT-US94-02034-15 Sequence 17, Appl |
| 22 | 36 | 54.5 | 194 | 4 | PCT-US94-02034-17 Sequence 17, Appl |
| 23 | 36 | 54.5 | 206 | 2 | US-09-902-16467 Sequence 206, A |
| 24 | 36 | 54.5 | 235 | 2 | US-09-252-991A-29814 Sequence 235, A |
| 25 | 36 | 54.5 | 266 | 2 | US-09-252-991A-21116 Sequence 266, A |
| 26 | 36 | 54.5 | 321 | 2 | US-09-134-000-3783 Sequence 321, App |
| 27 | 36 | 54.5 | 500 | 2 | US-09-538-092-831 Sequence 500, App |

ALIGNMENTS

RESULT 1
US-08-264-093-17
Sequence 17, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; STREET: 101 Richmond Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE: CLASSIFICATION: 536
; PRIORITY APPLICATION DATA: No. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R.
; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: not applicable
; TOPOLOGY: linear
US-08-264-093-17

Query Match 62.1%; Score 41; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 0.51; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 2; Misnmatches 2; Indels 0; Gaps 0;

QY 1 GPVELVGFDS 10
Db 2 GWDLINWFD 11

RESULT 2 ; ORGANISM: Myxococcus xanthus
 US-09-902-540-14253
 ; Sequence 3, Application US/08264093
 ; Patent No. 5639863
 GENERAL INFORMATION:
 APPLICANT: Michael D. Dan TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
 TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
 TITLE OF INVENTION: ANTIGEN
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Ridout & Maybee
 STREET: 2300 Richmond Adelaide Centre
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 2J7
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: MS-DOS 6.00
 SOFTWARE: ASCII Editor
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08-264,093
 FILING DATE:
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA: No. 5639863 applicable
 ATTORNEY/AGENT INFORMATION:
 NAME: Lake, James R.
 REGISTRATION NUMBER: 31081
 REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 368-4882
 TELEFAX: (416) 362-0823
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 121 amino acids
 TYPE: amino acid
 STRANDEDNESS: not applicable
 TOPOLOGY: linear
 ; US-08-264-093-3

Query Match 62.1%; Score 41; DB 1; Length 121;
 Best Local Similarity 60.0%; Pred. No. 6.7%;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPWELVGF 10
 Db 100 GVMGLNLYFD 109

RESULT 3 ; ORGANISM: Homo sapiens
 US-09-902-540-14253
 ; Sequence 14233, Application US/09902540
 ; Patent No. 6533447
 GENERAL INFORMATION:
 APPLICANT: Goldman, Barry S.
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Wiegard, Roger C.
 TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 FILE REFERENCE: 38-10(15849)B
 CURRENT APPLICATION NUMBER: US/08-902,540
 CURRENT FILING DATE: 2001-07-10
 PRIORITY FILING DATE: 2000-07-10
 NUMBER OF SEQ ID NOS: 16825
 SEQ ID NO 14253
 LENGTH: 274
 TYPE: PRT

RESULT 4 ; ORGANISM: Myxococcus xanthus
 US-09-902-540-14253
 ; Sequence 5, Application US/09561763
 ; Patent No. 6664373
 GENERAL INFORMATION:
 APPLICANT: Curis, Rory A.J. et al.
 TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
 FILE REFERENCE: MNI-074CP2
 CURRENT APPLICATION NUMBER: US/09/561,763
 CURRENT FILING DATE: 2000-04-29
 PRIOR APPLICATION NUMBER: 09/431,367
 PRIOR FILING DATE: 01-11-1999
 PRIOR APPLICATION NUMBER: US 09/259,951
 PRIOR FILING DATE: 01-03-1999
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 5
 LENGTH: 332
 TYPE: PRT
 ORGANISM: Homo sapiens
 ; US-09-561-763-5

Query Match 57.6%; Score 38; DB 2; Length 332;
 Best Local Similarity 57.6%; Pred. No. 72%;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPWELVGF 9
 Db 99 GRWELVGSP 107

RESULT 5 ; ORGANISM: Homo sapiens
 US-09-431-367B-5
 ; Sequence 5, Application US/09431367B
 ; Patent No. 6670199
 GENERAL INFORMATION:
 APPLICANT: Curtis, Roxy A. J.
 TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
 FILE REFERENCE: MNI-074CP
 CURRENT APPLICATION NUMBER: US/09/431,367B
 CURRENT FILING DATE: 1999-11-01
 PRIOR APPLICATION NUMBER: 09/259,951
 PRIOR FILING DATE: 1999-03-01
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 5
 LENGTH: 332
 TYPE: PRT
 ORGANISM: Homo sapiens
 ; US-09-431-367B-5

Query Match 57.6%; Score 38; DB 2; Length 332;
 Best Local Similarity 57.6%; Pred. No. 72%;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPWELVGF 9
 Db 99 GRWELVGSP 107

RESULT 6

US-09-949-016-10836
; Sequence 10836 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: "WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIORITY APPLICATION NUMBER: 60/1241,755
; PRIORITY FILING DATE: 2000-10-20
; PRIORITY APPLICATION NUMBER: 60/237,768
; PRIORITY FILING DATE: 2000-10-03
; PRIORITY APPLICATION NUMBER: 60/231,498
; PRIORITY FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 10836
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10836

Query Match 57.6%; Score 38; DB 2; Length 493;
Best Local Similarity 60.0%; Pred. No. 1.1e+02; Mismatches 6; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 3;

Qy 2 PWBLVGYFDS 11
Db 69 PWTKVYFDN 78

RESULT 7
US-09-976-594-4
; Sequence 4, Application US/09976594
; GENERAL INFORMATION:
; PATENT NO.: 6673549
; APPLICANT: Furness, Michael
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041-US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIORITY APPLICATION NUMBER: 60/240,409
; PRIORITY FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SEQ ID NO: 4
; LENGTH: 1207
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: mbc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1863336CDD1
; US-09-976-594-4

Query Match 57.6%; Score 38; DB 2; Length 1207;
Best Local Similarity 77.8%; Pred. No. 3.1e+02; Mismatches 7; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPWBLVGYF 9
Db 389 GPTEAVGYF 397

RESULT 8
US-09-902-540-15261
; Sequence 15261, Application US/09902540
; Patent No. 683347
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.

Query Match 56.1%; Score 37; DB 2; Length 427;
Best Local Similarity 66.7%; Pred. No. 1.5e+02; Mismatches 6; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 2;

Qy 1 GPWBLVGYF 9
Db 82 GPFSFVGYF 90

RESULT 9
US-09-543-681A-6615
; Sequence 6615, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709_1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIORITY APPLICATION NUMBER: 1999-04-09
; PRIORITY FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO: 6615
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; US-09-543-681A-6615

Query Match 56.1%; Score 37; DB 2; Length 484;
Best Local Similarity 55.6%; Pred. No. 1.7e+02; Mismatches 5; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WBLVGYFDS 11
Db 155 WALIGYQSQ 163

RESULT 10
US-09-311-021-162
; Sequence 162, Application US/09311021
; Patent No. 6706869
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Rechtein, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6300-11A
; CURRENT APPLICATION NUMBER: US/09/311,021
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 268
; SEQ ID NO: 162
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens

US-03-311-021-162

Query Match 54.5%; Score 36; DB 2; Length 132;

Best Local Similarity 55.6%; Pred. No. 59;

Matches 5; Conservative 2; Mismatches 2;

Qy 1 GPMELVGF 9
Db 121 GPMDOLVYP 129

RESULT 11

Query Match 54.5%; Score 36; DB 2; Length 132;
Sequence 29, Application US/09693341

Patent No. 6746273

GENERAL INFORMATION:

APPLICANT: Sorge, Joseph

APPLICANT: Hurlbut Hogrefe, Holly

APPLICANT: Connie, Hansen

TITLE OF INVENTION: Compositions and Methods Utilizing DNA Polymerases

FILE REFERENCE: 25416-1560

CURRENT APPLICATION NUMBER: US/09/698,341

CURRENT FILING DATE: 2000-10-27

PRIOR APPLICATION NUMBER: 60/162,600

PRIOR FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 29

LENGTH: 140

TYPE: PRT

ORGANISM: Thermococcus sp. JDP-3

FEATURE: NAME/KEY: UNSURE

LOCATION: (92); -(92)

OTHER INFORMATION: X = Unknown

US-09-698-341-29

Query Match 54.5%; Score 36; DB 2; Length 140;
Best Local Similarity 50.0%; Pred. No. 63;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPMELVGF 10
Db 55 GPMDNIVYLD 64

RESULT 12

Query Match 54.5%; Score 36; DB 2; Length 140;
Sequence 13916, Application US/09902540

Patent No. 633347

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10158491B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO: 13916

LENGTH: 174

TYPE: PRT

ORGANISM: Myxococcus xanthus

US-09-902-540-13916

Query Match 54.5%; Score 36; DB 2; Length 174;
Best Local Similarity 85.7%; Pred. No. 81;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LVGYFDS 11
.

Db 6 LIGYFDS 12

RESULT 13

Query Match 54.5%; Score 36; DB 1; Length 194;
Sequence 24, Application US/08260202A

Patent No. 5573910

GENERAL INFORMATION:

APPLICANT: Derevic, Vojo

APPLICANT: Martin, Daniel W.

TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCOIDY IN PSUEDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSE: Arnold, White & Durkee

STREET: P. O. Box 4433

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/260,202A

FILING DATE: 12-FEB-1993

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/260,202

REGISTRATION NUMBER: 31,026

REFERENCE/DOCKET NUMBER: UTSK:221\HOD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-5777

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 194 amino acids

TYPE: amino acid

STRANDEDNESS: TOPOLOGY: linear

US-08-260-202A-15

Query Match 54.5%; Score 36; DB 1; Length 194;

Best Local Similarity 71.4%; Pred. No. 91;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPMELVGF 7
Db 81 GPWRVNG 87

RESULT 14

Query Match 54.5%; Score 36; DB 2; Length 174;

Best Local Similarity 85.7%; Pred. No. 81;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LVGYFDS 11
.

US-08-260-202A-24

Query Match 54.5%; Score 36; DB 2; Length 174;

Best Local Similarity 85.7%; Pred. No. 81;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LVGYFDS 11
.

Page 4

CITY: Houston ;
 STATE: TX ;
 COUNTRY: USA ;
 ZIP: 77210-4433 ;

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/260, 202A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/260, 202
 FILING DATE: 15-JUN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/017, 114
 FILING DATE: 12-FEB-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Hodgins, Daniel S.
 REGISTRATION NUMBER: 31,026
 REFERENCE/DOCKET NUMBER: UTSK:221\HOD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 194 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPeOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-017-114-15

Query Match 54.5%; Score 36; DB 1; Length 194;
 Best Local Similarity 71.4%; Pred. No. 91;
 Matches 5; Conservative 1; Mismatches 1;
 QY 1 GPEHLVGV 7
 Db 81 GPGRMVG 87

Search completed: December 4, 2005, 04:09:43
 Job time : 23.6042 SECs

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/320-7200
 TELEFAX: 512/474-7577
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 194 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: Single
 TOPeOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-017-114-15

Query Match 54.5%; Score 36; DB 1; Length 194;
 Best Local Similarity 71.4%; Pred. No. 91;
 Matches 5; Conservative 1; Mismatches 1;
 QY 1 GPEHLVGV 7
 Db 81 GPGRMVG 87

US-08-260-202A-24

RESULT 15
 US-08-017-114-15
 Sequence 15, Application US/08017114
 Patent No. 5,591,838

GENERAL INFORMATION:
 APPLICANT: Matin, Daniel W.
 TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCOIDY IN
 PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS
 NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P. O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77210

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/017, 114
 FILING DATE: 19930212
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Hodgins, Daniel S.
 REGISTRATION NUMBER: 31,026
 REFERENCE/DOCKET NUMBER: UTSK:205/HOD

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GenCore version 5.1.6
 copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 4, 2005, 04:31:36 ; Search time 100.375 Seconds
 (without alignments)
 77.318 Million cell updates/sec.

Title: US-10-632-706-128
 Perfect score: 66
 Sequence: 1 GRHELVSIVFDS 11

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched:

2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt 05.80;*
 1: uniprot_sprot;*
 2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|----------------|
| 1 | 45 | 68.2 | 279 | 2 | O87858 STRECO |
| 2 | 45 | 68.2 | 290 | 2 | O824M5B STRAW |
| 3 | 45 | 68.2 | 748 | 2 | Q5NQ32_2YMMO |
| 4 | 44 | 66.7 | 367 | 1 | WECA_SALTY |
| 5 | 44 | 66.7 | 367 | 1 | WECA_SALTY |
| 6 | 44 | 66.7 | 367 | 2 | O5PKL1 SALPA |
| 7 | 44 | 66.7 | 449 | 2 | O63N53_BURPS |
| 8 | 43 | 65.2 | 231 | 2 | O4K719_PSEF5 |
| 9 | 43 | 65.2 | 1201 | 2 | O7U7R6_RHOBIA |
| 10 | 43 | 65.2 | 1633 | 1 | YPT4_CABEL |
| 11 | 43 | 65.2 | 2548 | 2 | O5WRUL_CABEL |
| 12 | 42 | 63.6 | 272 | 2 | O7748S8_GEOSEL |
| 13 | 42 | 63.6 | 381 | 2 | O6KL15_ORYSA |
| 14 | 42 | 63.6 | 454 | 2 | O8TUV9_METACV |
| 15 | 42 | 63.6 | 578 | 2 | O8D959_VIBVU |
| 16 | 42 | 63.6 | 2 | O7MLB3_VIBVU | |
| 17 | 42 | 63.6 | 1275 | 2 | O80061_METMMA |
| 18 | 41 | 62.1 | 211 | 2 | O8KHK7_PSEBFN |
| 19 | 41 | 62.1 | 241 | 2 | O82347_ARATH |
| 20 | 41 | 62.1 | 273 | 2 | O7UND8_PHOBA |
| 21 | 41 | 62.1 | 318 | 2 | O4KEFO_PSEBF5 |
| 22 | 41 | 62.1 | 491 | 1 | GNA_ARCTA |
| 23 | 41 | 62.1 | 518 | 2 | O5Hb40_BACFN |
| 24 | 41 | 62.1 | 621 | 2 | O64XZ7_BACFN |
| 25 | 41 | 62.1 | 613 | 2 | O6BT13_DIBBHA |
| 26 | 41 | 62.1 | 619 | 1 | GCKR_XENLA |
| 27 | 41 | 62.1 | 619 | 1 | O8G55_THE8 |
| 28 | 41 | 62.1 | 619 | 2 | O6PAX3_XENLA |
| 29 | 41 | 62.1 | 697 | 1 | Y2126_WYCTU |
| 30 | 41 | 62.1 | 697 | 1 | Y2553_MYCBA |
| 31 | 41 | 62.1 | 1350 | 2 | O9V5J7_DRONE |

Scoring table: Gapop 10.0 , Gapext 0.5

Searched:

2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt 05.80;*
 1: uniprot_sprot;*
 2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|----------------|
| 1 | 45 | 68.2 | 279 | 2 | O87858_STRECO |
| 2 | 45 | 68.2 | 290 | 2 | O824M5B_STRAW |
| 3 | 45 | 68.2 | 748 | 2 | Q5NQ32_2YMMO |
| 4 | 44 | 66.7 | 367 | 1 | WECA_SALTY |
| 5 | 44 | 66.7 | 367 | 1 | WECA_SALTY |
| 6 | 44 | 66.7 | 367 | 2 | O5PKL1_SALPA |
| 7 | 44 | 66.7 | 449 | 2 | O63N53_BURPS |
| 8 | 43 | 65.2 | 231 | 2 | O4K719_PSEF5 |
| 9 | 43 | 65.2 | 1201 | 2 | O7U7R6_RHOBIA |
| 10 | 43 | 65.2 | 1633 | 1 | YPT4_CABEL |
| 11 | 43 | 65.2 | 2548 | 2 | O5WRUL_CABEL |
| 12 | 42 | 63.6 | 272 | 2 | O7748S8_GEOSEL |
| 13 | 42 | 63.6 | 381 | 2 | O6KL15_ORYSA |
| 14 | 42 | 63.6 | 454 | 2 | O8TUV9_METACV |
| 15 | 42 | 63.6 | 578 | 2 | O8D959_VIBVU |
| 16 | 42 | 63.6 | 2 | O7MLB3_VIBVU | |
| 17 | 42 | 63.6 | 1275 | 2 | O80061_METMMA |
| 18 | 41 | 62.1 | 211 | 2 | O8KHK7_PSEBFN |
| 19 | 41 | 62.1 | 241 | 2 | O82347_ARATH |
| 20 | 41 | 62.1 | 273 | 2 | O7UND8_PHOBA |
| 21 | 41 | 62.1 | 318 | 2 | O4KEFO_PSEBF5 |
| 22 | 41 | 62.1 | 491 | 1 | GNA_ARCTA |
| 23 | 41 | 62.1 | 518 | 2 | O5Hb40_BACFN |
| 24 | 41 | 62.1 | 621 | 2 | O64XZ7_BACFN |
| 25 | 41 | 62.1 | 613 | 2 | O6BT13_DIBBHA |
| 26 | 41 | 62.1 | 619 | 1 | GCKR_XENLA |
| 27 | 41 | 62.1 | 619 | 1 | O8G55_THE8 |
| 28 | 41 | 62.1 | 619 | 2 | O6PAX3_XENLA |
| 29 | 41 | 62.1 | 697 | 1 | Y2126_WYCTU |
| 30 | 41 | 62.1 | 697 | 1 | Y2553_MYCBA |
| 31 | 41 | 62.1 | 1350 | 2 | O9V5J7_DRONE |

Scoring table: Gapop 10.0 , Gapext 0.5

Searched:

2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt 05.80;*
 1: uniprot_sprot;*
 2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|----------------|
| 1 | 45 | 68.2 | 279 | 2 | O87858_STRECO |
| 2 | 45 | 68.2 | 290 | 2 | O824M5B_STRAW |
| 3 | 45 | 68.2 | 748 | 2 | Q5NQ32_2YMMO |
| 4 | 44 | 66.7 | 367 | 1 | WECA_SALTY |
| 5 | 44 | 66.7 | 367 | 1 | WECA_SALTY |
| 6 | 44 | 66.7 | 367 | 2 | O5PKL1_SALPA |
| 7 | 44 | 66.7 | 449 | 2 | O63N53_BURPS |
| 8 | 43 | 65.2 | 231 | 2 | O4K719_PSEF5 |
| 9 | 43 | 65.2 | 1201 | 2 | O7U7R6_RHOBIA |
| 10 | 43 | 65.2 | 1633 | 1 | YPT4_CABEL |
| 11 | 43 | 65.2 | 2548 | 2 | O5WRUL_CABEL |
| 12 | 42 | 63.6 | 272 | 2 | O7748S8_GEOSEL |
| 13 | 42 | 63.6 | 381 | 2 | O6KL15_ORYSA |
| 14 | 42 | 63.6 | 454 | 2 | O8TUV9_METACV |
| 15 | 42 | 63.6 | 578 | 2 | O8D959_VIBVU |
| 16 | 42 | 63.6 | 2 | O7MLB3_VIBVU | |
| 17 | 42 | 63.6 | 1275 | 2 | O80061_METMMA |
| 18 | 41 | 62.1 | 211 | 2 | O8KHK7_PSEBFN |
| 19 | 41 | 62.1 | 241 | 2 | O82347_ARATH |
| 20 | 41 | 62.1 | 273 | 2 | O7UND8_PHOBA |
| 21 | 41 | 62.1 | 318 | 2 | O4KEFO_PSEBF5 |
| 22 | 41 | 62.1 | 491 | 1 | GNA_ARCTA |
| 23 | 41 | 62.1 | 518 | 2 | O5Hb40_BACFN |
| 24 | 41 | 62.1 | 621 | 2 | O64XZ7_BACFN |
| 25 | 41 | 62.1 | 613 | 2 | O6BT13_DIBBHA |
| 26 | 41 | 62.1 | 619 | 1 | GCKR_XENLA |
| 27 | 41 | 62.1 | 619 | 1 | O8G55_THE8 |
| 28 | 41 | 62.1 | 619 | 2 | O6PAX3_XENLA |
| 29 | 41 | 62.1 | 697 | 1 | Y2126_WYCTU |
| 30 | 41 | 62.1 | 697 | 1 | Y2553_MYCBA |
| 31 | 41 | 62.1 | 1350 | 2 | O9V5J7_DRONE |

Scoring table: Gapop 10.0 , Gapext 0.5

Searched:

2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt 05.80;*
 1: uniprot_sprot;*
 2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|----------------|
| 1 | 45 | 68.2 | 279 | 2 | O87858_STRECO |
| 2 | 45 | 68.2 | 290 | 2 | O824M5B_STRAW |
| 3 | 45 | 68.2 | 748 | 2 | Q5NQ32_2YMMO |
| 4 | 44 | 66.7 | 367 | 1 | WECA_SALTY |
| 5 | 44 | 66.7 | 367 | 1 | WECA_SALTY |
| 6 | 44 | 66.7 | 367 | 2 | O5PKL1_SALPA |
| 7 | 44 | 66.7 | 449 | 2 | O63N53_BURPS |
| 8 | 43 | 65.2 | 231 | 2 | O4K719_PSEF5 |
| 9 | 43 | 65.2 | 1201 | 2 | O7U7R6_RHOBIA |
| 10 | 43 | 65.2 | 1633 | 1 | YPT4_CABEL |
| 11 | 43 | 65.2 | 2548 | 2 | O5WRUL_CABEL |
| 12 | 42 | 63.6 | 272 | 2 | O7748S8_GEOSEL |
| 13 | 42 | 63.6 | 381 | 2 | O6KL15_ORYSA |
| 14 | 42 | 63.6 | 454 | 2 | O8TUV9_METACV |
| 15 | 42 | 63.6 | 578 | 2 | O8D959_VIBVU |
| 16 | 42 | 63.6 | 2 | O7MLB3_VIBVU | |
| 17 | 42 | 63.6 | 1275 | 2 | O80061_METMMA |
| 18 | 41 | 62.1 | 211 | 2 | O8KHK7_PSEBFN |
| 19 | 41 | 62.1 | 241 | 2 | O82347_ARATH |
| 20 | 41 | 62.1 | 273 | 2 | O7UND8_PHOBA |
| 21 | 41 | 62.1 | 318 | 2 | O4KEFO_PSEBF5 |
| 22 | 41 | 62.1 | 491 | 1 | GNA_ARCTA |
| 23 | 41 | 62.1 | 518 | 2 | O5Hb40_BACFN |
| 24 | 41 | 62.1 | 621 | 2 | O64XZ7_BACFN |
| 25 | 41 | 62.1 | 613 | 2 | O6BT13_DIBBHA |
| 26 | 41 | 62.1 | 619 | 1 | GCKR_XENLA |
| 27 | 41 | 62.1 | 619 | 1 | O8G55_THE8 |
| 28 | 41 | 62.1 | 619 | 2 | O6PAX3_XENLA |
| 29 | 41 | 62.1 | 697 | 1 | Y2126_WYCTU |
| 30 | 41 | 62.1 | 697 | 1 | Y2553_MYCBA |
| 31 | 41 | 62.1 | 1350 | 2 | O9V5J7_DRONE |

Scoring table: Gapop 10.0 , Gapext 0.5

Searched:

2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt 05.80;*
 1: uniprot_sprot;*
 2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|----------------|
| 1 | 45 | 68.2 | 279 | 2 | O87858_STRECO |
| 2 | 45 | 68.2 | 290 | 2 | O824M5B_STRAW |
| 3 | 45 | 68.2 | 748 | 2 | Q5NQ32_2YMMO |
| 4 | 44 | 66.7 | 367 | 1 | WECA_SALTY |
| 5 | 44 | 66.7 | 367 | 1 | WECA_SALTY |
| 6 | 44 | 66.7 | 367 | 2 | O5PKL1_SALPA |
| 7 | 44 | 66.7 | 449 | 2 | O63N53_BURPS |
| 8 | 43 | 65.2 | 231 | 2 | O4K719_PSEF5 |
| 9 | 43 | 65.2 | 1201 | 2 | O7U7R6_RHOBIA |
| 10 | 43 | 65.2 | 1633 | 1 | YPT4_CABEL |
| 11 | 43 | 65.2 | 2548 | 2 | O5WRUL_CABEL |
| 12 | 42 | 63.6 | 272 | 2 | O7748S8_GEOSEL |
| 13 | 42 | 63.6 | 381 | 2 | O6KL15_ORYSA |
| 14 | 42 | 63.6 | 454 | 2 | O8TUV9_METACV |
| 15 | 42 | 63.6 | 578 | 2 | O8D959_VIBVU |
| 16 | 42 | 63.6 | 2 | O7MLB3_VIBVU | |
| 17 | 42 | 63.6 | 1275 | 2 | O80061_METMMA |
| 18 | 41 | 62.1 | 211 | 2 | O8KHK7_PSEBFN |
| 19 | 41 | 62.1 | 241 | 2 | O82347_ARATH |
| 20 | 41 | 62.1 | 273 | 2 | O7UND8_PHOBA |
| 21 | 41 | 62.1 | 318 | 2 | O4KEFO_PSEBF5 |
| 22 | 41 | 62.1 | 491 | 1 | GNA_ARCTA |
| 23 | 41 | 62.1 | 518 | 2 | O5Hb40_BACFN |
| 24 | 41 | 62.1 | 621 | 2 | O64XZ7_BACFN |
| 25 | 41 | 62.1 | 613 | 2 | O6BT13_DIBBHA |
| 26 | 41 | 62.1 | 619 | 1 | GCKR_XENLA |
| 27 | 41 | 62.1 | 619 | 1 | O8G55_THE8 |
| 28 | 41 | 62.1 | 619 | 2 | O6PAX3_XENLA |
| 29 | 41 | 62.1 | 697 | 1 | Y2126_WYCTU |
| 30 | 41 | 62. | | | |

| Db | 160 WMLIGYFDS 168 | OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; OC Sphingomonadaceae; Zymomonas. NCBI_TaxID=542; |
|--|-------------------|--|
| RESULT 2 | | |
| 082M88 STRAW PRELIMINARY; | PRT; 290 AA. | |
| ID 082M88_ | | |
| AC 082M88; | | |
| DT 01-JUN-2003 (TREMBLel. 24, Created) | | |
| DT 01-FEB-2005 (TREMBLel. 24, Last sequence update) | | |
| DT 01-MAR-2004 (TREMBLel. 26, Last annotation update) | | |
| DE Putative sugar ABC transporter permease protein. | | |
| GN OrderedLocusNames=STV1802; | | |
| OS Streptomyces avermitilis. | | |
| OC Bacteria; Actinobacteria; Actinomycetales; Streptomycomycetaceae; Streptomyces. | | |
| OX NCBI_TaxId=33903; | | |
| RN [1] | | |
| RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]. | | |
| RC STRAIN=ATCC 31821 / ZM4 / CP4; | | |
| RX Published=15592456; DOI=10.1038/nbt045; | | |
| RA Seo J.-S., Chong H., Park H.S., Yoon K.-O., Jung C., Kim J.-J., | | |
| RA Hong J.-H., Kim H.-K., Kil J.-I., Park C.J., Oh H.-M., | | |
| RA Lee J.-S., Jin S.-J., Um H.-W., Lee H.-J., Oh S.-J., Kim J.Y., | | |
| RA Kang H.-J., Lee S.Y., Lee K.-J., Kang H.-S.; | | |
| RA "The genome sequence of the ethanologenic bacterium Zymomonas mobilis | | |
| RA ZM4."; | | |
| RL Nat. Biotechnol. 23:63-68 (2005); | | |
| DR EMBL; AR008692; AAU89173; 1; -; Genomic_DNA. | | |
| DR GO; GO:000175; F:3'-5'-exoribonuclease activity; IEA. | | |
| DR GO; GO:0004654; F:polynucleotide nucleotidyltransferase a...; IEA. | | |
| DR GO; GO:0016740; F:transferase activity; IEA. | | |
| DR GO; GO:0006396; P:RNA processing; IEA. | | |
| DR InterPro; IPRO01247; 3_Exoribnase. | | |
| DR InterPro; IPRO04087; KH. | | |
| DR InterPro; IPRO04088; KH type_1. | | |
| DR InterPro; IPRO012162; PNPase. | | |
| DR InterPro; IPRO03029; SI. | | |
| DR Pfam; PF00013; KH_1; 1. | | |
| DR Pfam; PF03726; PNase; 1. | | |
| DR Pfam; PF01138; RNase_PH; 2. | | |
| DR Pfam; PF03725; RNase_PH_C; 2. | | |
| DR PIRP; PIRSP05499; PNPase; 1. | | |
| DR SMART; SM00322; KH; 1. | | |
| DR SMART; SM0316; SI; 1. | | |
| DR PROSITE; PS50084; KH_TYPE_1; 1. | | |
| DR PROSITE; PS50126; SI; 1. | | |
| KW Complete proteome; Transport. | | |
| SEQUENCE 290 AA; 31323 MW; 92650429419A35B9 CRC64; | | |
| Query 2 PWELVGYFDS 11 | | |
| Best Local Similarity 80.0%; Pred. No. 67; Mismatches 2; Indels 0; Gaps 0; | | |
| Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0; | | |
| Db 230 PWELVSYDPS 239 | | |
| RESULT 4 | | |
| WECA_SALTI WECA_SALTI STANDARD; PRT; 367 AA. | | |
| ID WECA_SALTI | | |
| AC 082386; | | |
| DT 28-FEB-2003 (Rel. 41, Created) | | |
| DT 28-FEB-2003 (Rel. 41, Last sequence update) | | |
| DT 10-MAY-2005 (Rel. 47, Last annotation update) | | |
| DE Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate | | |
| DE transferase (EC 2.7.8.-) (UDP-GlcNAc:undecaprenyl-phosphate GlcNAc-1- | | |
| DE phosphatase transferase). | | |
| DE Name=weca; Synonyms=we; OrderedLocusNames=STY3337, t337; | | |
| GN Salmonella typhi | | |
| OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; | | |
| OC Enterobacteriaceae; Salmonella. | | |
| CC Entrobacteriaceae; Salmonella. | | |
| OX NCBI_TaxId=601; | | |
| RN [1] | | |
| RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]. | | |
| RC STRAIN=CT18; | | |
| RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607; | | |
| RA Partill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., | | |
| RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., | | |
| RA Baker S., Baslam D., Brooks K., Chillingworth T., Connerton P., | | |
| RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., | | |
| RA Fellwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., | | |
| RA Krogh A., Larsen T.S., Leatner S., Moile S., O'Gaora P., Parry C., | | |
| RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., | | |
| OS Zymomonas mobilis. | | |

| | | | |
|-------------|--|--|--|
| RN | RA | Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant <i>Salmonella enterica</i> serovar Typhi CT8."; RT | DE Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate |
| [2] | RT | "Comparative genomics of <i>Salmonella enterica</i> serovar Typhi strains Ty2 and CT8"; PMID=22331367; PubMed=12641504; DOI=10.1128/JB.185.7.2330-2337.2003; | DE phosphate transferase (EC 2.7.8.-) (UDP-GlcNAc:undecaprenyl-phosphate GlcNAc-1- |
| RR | RA | Deng W., Liou S., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodeyani V., Schwartz D.C., Blattner F.R.; "Comparative genomics of <i>Salmonella enterica</i> serovar Typhi CT8"; PMID=22331367; PubMed=12641504; DOI=10.1128/JB.185.7.2330-2337.2003; | DE Name=weca; Synonyms=wrf; OrderedLocusNames=STM3918; ORFNames=STM1..72; |
| RR | RA | J. Bacteriol. 185:2330-2337(2003). | GN Salmonella typhimurium. |
| RR | RC | -I- FUNCTION: Catalyzes the synthesis of Und-PGlcNAc (Lipid I), the first lipid-linked intermediate involved in ECA synthesis. This lipid is also an acceptor for the addition of subsequent sugars to complete the biosynthesis of O-antigen (BY similarity). | OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella. |
| RR | RP | -I- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + undecaprenyl phosphate = UMP + N-acetyl-alpha-D-glucosaminylidiphospho-undecaprenol. | OC NCBI_TaxID=602; |
| CC | CC | -I- COFACTOR: Magnesium and manganese (BY similarity). | OC |
| CC | CC | -I- PATHWAY: Synthesis of enterobacterial common antigen (ECA). | OX |
| CC | CC | Synthesis of lipopolysaccharide O-antigen. (BY similarity). | |
| CC | CC | -I- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane (BY similarity). | |
| CC | CC | -I- SIMILARITY: Belongs to the glycosyltransferase 4 family. Weca | |
| CC | CC | This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed. | |
| CC | CC | EMBL; AL627279; CAD09398.1; -; Genomic_DNA. | |
| CC | CC | DR; AE01645; AA07039.1; -; Genomic_DNA. | |
| CC | CC | DR; InterPro; IPR012750; ECA_Weca_rel. | |
| CC | CC | DR; InterPro; IPR000715; Glyco_transf_4. | |
| CC | CC | PFam; PF0053; Glycos_transf_4; 1. | |
| CC | CC | TIGRFAMs; TIGR02380; ECA_weca; 1. | |
| CC | CC | Complete proteome; Glycosyltransferase; Magnesium; Manganese; Membrane; Lipopolysaccharide biosynthesis; Magnesium; Manganese; Membrane; Transferase; Transmembrane. | |
| CC | CC | Potential. | |
| FT | CC | TRANSMEM 3 23 Potential. | |
| FT | CC | TRANSMEM 45 65 Potential. | |
| FT | CC | TRANSMEM 69 89 Potential. | |
| FT | CC | TRANSMEM 106 126 Potential. | |
| FT | CC | TRANSMEM 129 149 Potential. | |
| FT | CC | TRANSMEM 158 178 Potential. | |
| FT | CC | TRANSMEM 187 207 Potential. | |
| FT | CC | TRANSMEM 213 233 Potential. | |
| FT | CC | TRANSMEM 242 262 Potential. | |
| FT | CC | TRANSMEM 294 314 Potential. | |
| FT | CC | TRANSMEM 318 338 Potential. | |
| SQ | CC | SEQUENCE 367 AA; 41086 MW; 28DA31CB1A2D930 CRC64; | |
| Query Match | CC | Best Local Similarity 66.7%; Score 44; DB 1; Length 367; Matches 9; Conservative 69.2%; Pred. No. 49; Mismatches 0; Indels 4; Gaps 1; | |
| QY | 1 | GPMLV---GYF 9 | |
| DB | 127 | GPWELVLGSPFGYF 139 | |
| RESULT 5 | | | |
| ID | WECA_SALTY | WECA_SALTY STANDARD; PRT: 367 AA. | |
| AC | Q916R7; Q93378; | | |
| DT | 28-FEB-2003 (Rel. 41, Created) | | |
| DT | 28-FEB-2003 (Rel. 41, Last Sequence update) | | |
| DT | 10-MAY-2005 (Rel. 47, Last annotation update) | | |
| FT | DE Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate | | |
| FT | DR InterPro; IPR012750; Glyco_transf_4; 1. | | |
| DR | EMBL; AP233324; AAF33469.1; -; Genomic_DNA. | | |
| DR | EMBL; AB00883; AAL22767.1; -; Genomic_DNA. | | |
| DR | EMBL; AJ002275; CAA5287.1; -; Genomic_DNA. | | |
| DR | StyGene; SGTP7; rfe; ECA_Weca_rel. | | |
| DR | InterPro; IPR000715; Glyco_transf_4. | | |
| DR | PFam; PF0053; Glycos_transf_4; 1. | | |
| DR | TIGRFAMs; TIGR02380; ECA_weca; 1. | | |
| DR | Complete proteome; Glycosyltransferase; Inner membrane; Lipopolysaccharide biosynthesis; Magnesium; Manganese; Membrane; Transferase; Transmembrane. | | |
| FT | FT TRANSMEM 3 23 Potential. | | |
| FT | FT TRANSMEM 45 65 Potential. | | |
| FT | FT TRANSMEM 69 89 Potential. | | |
| FT | FT TRANSMEM 106 126 Potential. | | |
| FT | FT TRANSMEM 129 149 Potential. | | |
| FT | FT TRANSMEM 158 178 Potential. | | |
| FT | FT TRANSMEM 187 207 Potential. | | |
| FT | FT TRANSMEM 213 233 Potential. | | |
| FT | FT TRANSMEM 242 262 Potential. | | |
| FT | FT TRANSMEM 294 314 Potential. | | |
| FT | FT TRANSMEM 318 338 Potential. | | |
| FT | FT CONFFLICT 118 120 HLG -> ALS (in Ref. 2). | | |

FT CONFLICT 128 138 PWELVLGPGFV -> ALGVASWPLWH (in Ref. 2).
 FT CONFLICT 148 WAR -> C (in Ref. 2).
 FT CONFLICT 220 S -> C (in Ref. 2).
 SQ SEQUENCE 367 AA; 41087 MW; 1EDA31CBIAE2D38 CRC64;
 RN
 RQ Query Match Best Local Similarity 69.2%; Score 44; DB 1; Length 367;
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 RP NUCLEOTIDE SEQUENCE.
 RESULT 6 OSPKKL_SALPA
 ID O5PKKL_SALPA PRELIMINARY; PRT; 367 AA.
 AC OSPKKL; SALPA
 DT 01-FEB-2005 (TREMBLrel. 29, Created)
 DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
 DE Putative undecarrenyl-phosphate alpha-N-
 DE Acetylglucosaminyltransferase.
 GN Name=fe; OrderedLocusNames=SP3758;
 OS Salmonella paratyphi-a.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonellae.
 NCBI_TAXID=54388;
 [1]
 RN
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 9150;
 RX PMID=1551882; DOI=10.1038/ng1470;
 RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
 RA Porwollik S., Sabo A., Meyer R., Bieri T., Oparsky P., McClelland M.,
 RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
 RA Kohlberg S., Strong C., Du F., Carter J., Kremlizki C., Layman D.,
 RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P., Florea L.,
 RA Delhaunty K., Pronick C., Magrini V., Nhan M., Warren W., Florea L.,
 RA Spieh J., Wilson R.K.;
 RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
 RT restricted serovars of *Salmonella enterica* that cause typhoid.";
 RL Nat. Genet. 36:1268-1274 (2004).
 DR EMBL; CP00026; AAVP9540.1; -; Genomic_DNA.
 DR GO; GO:0019866; C:inner membrane; IEA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016279; F:transferase activity; transferring glycosyl. . .; IEA.
 DR GO; GO:0010103; P:lipopolysaccharide biosynthesis; IEA.
 DR InterPro; IPR008715; Glyco_trans_4.
 DR InterPro; IPR001865; Ribosomal_S2.
 DR Pfam; PF0053; Glycos_transf_1.
 DR PROSITE; PS00962; RIBOSOMAL_S2.1; UNKNOWN 1.
 SQ Complete proteome; GLYCOSYLTRANSFERASE; Transferase.
 SEQUENCE 367 AA; 41086 MW; 1EDA31CBIAE2D38 CRC64;

Query Match Best Local Similarity 66.7%; Score 44; DB 2; Length 367;
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 RQ 1 PWELV---GYF 9
 DB 127 GPWELVIGPPGYF 139

RESULT 7 Q63N53_BURPS
 ID Q63N53_BURPS PRELIMINARY; PRT; 449 AA.
 AC Q63N53;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=BPS30443;

OS Burkholderia pseudomallei (Pseudomonas pseudomallei)
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia; pseudomallei group.
 NCBI_TAXID=28450;
 [1]
 RN
 RQ Query Match Best Local Similarity 69.2%; Score 44; DB 1; Length 367;
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 RP NUCLEOTIDE SEQUENCE.
 RESULT 8 Q4K719_PSEBF5
 ID Q4K719_PSEBF5 PRELIMINARY; PRT; 231 AA.
 AC Q4K719;
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DR Phosphoserine phosphotransferase, putative.
 GN ORFNAME=PF_4883;
 OS Pseudomonas fluorescens (strain pf-5).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 NCBI_TAXID=220664;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RESULT 9 Q7UVR6_RHOBA
 ID Q7UVR6_RHOBA
 AC Q7UVR6;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=BPS30443;

ID OTUYR6_RHOBIA PRELIMINARY; PRT; 1201 AA.
AC O7YVR7; PRT; 1201 AA.
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusName=RB126;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomyctaceae; Pirellulida.
OX NCBI_TaxID=117;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Goeckner F.T.O., Kube M., Bauer M., Teeling H., Lombardot T.,
ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.;
Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
RL EMBL; BX294133; CAD71575.1; -; Genomic_DNA.
DR GO; GO:000037; F:heme binding; IEA.
DR GO; GO:006118; P:electron transport; IEA.
DR InterPro; IPR01282; Cytochrome_C_R.
DR InterPro; IPR01144; DUF1549.
DR Pfam; PF07635; PSCyt1; 1.
DR Pfam; PF07583; PSCyt2; 1.
DR Pfam; PF07587; PSD1; 1.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 1201 AA; 13482 MW; 7286B2773513001 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 1201;
Best Local Similarity 72.7%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GPWELVGFDS 11
Db 1029 GLWEAVGTYDS 1039

RESULT 10
YP74_CAEEL STANDARD; PRT; 1633 AA.
ID YP74_CAEEL STANDARD; PRT; 1633 AA.
AC 009221; O10908; PRT; 1633 AA.
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DR Hypothetical protein B0228_4 in chromosome II.
GS ORFNames=B0228_4; B0228_2;
GS Cenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabdidae; Peioderinae; Caenorhabditis.
OC NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=Bristol N2; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode *C. elegans*: a platform for
investigating biology";
RL Science 283:2012-2018 (1998);
DR EMBL; U23168; AMU87832.1; -; Genomic_DNA.
DR Ensembl; B0228_4; Cenorhabditis elegans.
DR WormBase; WBGene0015051; B0228_4.
DR WormPep; B0228_4C; CB37470.
DR InterPro; IPR010734; Copine.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF07002; Copine; 1.
DR SMART; SM00327; WWA; 1.
DR SMART; SM00327; WWA; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 7548 AA; 840564 MW; 88E3CC03D12C1C8 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 7548;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 GPWELVGFDS 10
Db 7482 GPWNMMGRFD 7491

RESULT 12
Q748S8_GEOSL ID Q748S8_GEOSL PRELIMINARY; PRT; 272 AA.
AC 0748S8; PRT; 272 AA.
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Glutamate racemase (EC 5.1.1.3);
GN Name=muri; OrderedLocusName=GSU2923;

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

| | Matches | 6; | Conservative | 1; | Mismatches | 1; | Indels | 0; | Gaps | 0; |
|---|---------|----------------|--------------|-------------|------------|----|--------|----|------|----|
| OC | | | | | | | | | | |
| Gaobacter | | | | | | | | | | |
| Bullfurreducens | | | | | | | | | | |
| Deltaproteobacteria | | | | | | | | | | |
| Desulfurimonadales | | | | | | | | | | |
| Geobacteraceae; | | | | | | | | | | |
| Geobacter | | | | | | | | | | |
| [NCBI_TaxID=35554; | | | | | | | | | | |
| RN | | | | | | | | | | |
| RP | | | | | | | | | | |
| RC | | | | | | | | | | |
| STRAIN=CA / ATCC 51573; | | | | | | | | | | |
| RX | | | | | | | | | | |
| PubMed-146714; DOI:10.1126/science.1089727; | | | | | | | | | | |
| RA | | | | | | | | | | |
| Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C., | | | | | | | | | | |
| Heidelberg J.P., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J., | | | | | | | | | | |
| Medupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., | | | | | | | | | | |
| Grinn M.L., Kolonay J.F., Sullivan S.A., Haff D.H., Selengut J., | | | | | | | | | | |
| Davidson T.M., Zafar N., White O., Tran B., Romero C., Borberger H.A., | | | | | | | | | | |
| Reidman J.F., Khouri H.M., Feldblum T.V., Utterback T.R., | | | | | | | | | | |
| Van Aken S.E., Lorley D.R., Fraser C.M., | | | | | | | | | | |
| RT | | | | | | | | | | |
| "Genome of Geobacter sulfurreducens: metal reduction in subsurface | | | | | | | | | | |
| environments". | | | | | | | | | | |
| Science 302:1967-1969(2003). | | | | | | | | | | |
| RL | | | | | | | | | | |
| EMBL; AB017180; AAC36315.1; -; Genomic_DNA. | | | | | | | | | | |
| DR | | | | | | | | | | |
| HSPB; P56868; 1B74. | | | | | | | | | | |
| DR | | | | | | | | | | |
| TIGR; GSU923; -. | | | | | | | | | | |
| DR | | | | | | | | | | |
| GO; GO_0008891; F-glutamate racemase activity; IEA. | | | | | | | | | | |
| DR | | | | | | | | | | |
| GO; GO_0008152; P-metabolism; IEA. | | | | | | | | | | |
| DR | | | | | | | | | | |
| InterPro; IPR01930; Asp_Glu_Race. | | | | | | | | | | |
| DR | | | | | | | | | | |
| IPR01777; Asp_Glu_race; 1. | | | | | | | | | | |
| DR | | | | | | | | | | |
| TIGRFAM; TIGR00067; Glut_race; 1. | | | | | | | | | | |
| DR | | | | | | | | | | |
| PROSITE; PS00923; ASP_GLU_RACEMASE_1; 1. | | | | | | | | | | |
| DR | | | | | | | | | | |
| PROSITE; PS00924; ASP_GLU_RACEMASE_2; 1. | | | | | | | | | | |
| KW | | | | | | | | | | |
| Complete proteome; Isoenzyme; 272 AA; 29512 MM; 674BA01437EC4163 CRC64; | | | | | | | | | | |
| SQ | | | | | | | | | | |
| RESULT 13 | | | | | | | | | | |
| QKLT5_ORYSA | | | | | | | | | | |
| ID | | | | | | | | | | |
| QKLT5_ORYSA_PRELIMINARY; PRT; 381 AA. | | | | | | | | | | |
| AC | | | | | | | | | | |
| QKLT5; PRT; 381 AA. | | | | | | | | | | |
| DT | | | | | | | | | | |
| 05-JUL-2004 (Tremblel. 27, Created) | | | | | | | | | | |
| DT | | | | | | | | | | |
| 05-JUL-2004 (Tremblel. 27, Last sequence update) | | | | | | | | | | |
| DE | | | | | | | | | | |
| Hypothetical protein OSJNBA0038P01..38. | | | | | | | | | | |
| GN | | | | | | | | | | |
| Name=OSJNBA0038P01..38; | | | | | | | | | | |
| OS | | | | | | | | | | |
| Oryza sativa (Japonica cultivar-group). | | | | | | | | | | |
| OC | | | | | | | | | | |
| Spermatophyta; Magnoliopsida; Streptophyta; Embryophyta; Tracheophyta; | | | | | | | | | | |
| OC | | | | | | | | | | |
| Zihartoidea; Oryzeae; Oryza. | | | | | | | | | | |
| OC | | | | | | | | | | |
| NCBI_TaxID=39947; | | | | | | | | | | |
| RN | | | | | | | | | | |
| NUCLEOTIDE SEQUENCE. | | | | | | | | | | |
| RA | | | | | | | | | | |
| Sasaki T., Matsumoto T., Katayose Y.; | | | | | | | | | | |
| "Oryza sativa nippobare" (GA3) genomic DNA, chromosome 2, BAC | | | | | | | | | | |
| RT | | | | | | | | | | |
| Submitted; OSJNBA0038P01..38; to the EMBL/GenBank/DBJ databases. | | | | | | | | | | |
| DR | | | | | | | | | | |
| EMBL; AP006457; BAD22515.1; -; Genomic_C_DNA. | | | | | | | | | | |
| DR | | | | | | | | | | |
| Gramene; Q6K1T5; -. | | | | | | | | | | |
| DR | | | | | | | | | | |
| GO; GO_0006512; P Ubiquitin cycle; IEA. | | | | | | | | | | |
| DR | | | | | | | | | | |
| InterPro; IPR001810; P_box. | | | | | | | | | | |
| DR | | | | | | | | | | |
| Pfam; PF00649; P_box; 1. | | | | | | | | | | |
| KW | | | | | | | | | | |
| Hypothetical protein. | | | | | | | | | | |
| SEQUENCE 381 AA; 42714 MN; A50564C2F7224FC4 CRC64; | | | | | | | | | | |
| SQ | | | | | | | | | | |
| Query Match | 63.6% | Score 42; | DB 2; | Length 381; | | | | | | |
| Best Local Similarity | 75.0% | Score 1.1e+02; | DB 2; | Length 381; | | | | | | |

DR EMBL; AE016806; AA011091.1; -; Genomic_DNA.
DR HSSP; P02142; IQU7.
DR GO; GO:0019866; C:inner membrane; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0014871; F:signal transducer activity; IEA.
DR GO; GO:0009357; P:chemotaxis; IEA.
DR GO; GO:007165; P:signal transduction; IEA.
DR InterPro; IPR004089; Chmtnaxis_transd.
DR InterPro; IPR0366; His_kin_HAMP.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF00015; MCPsSignal; 1.
DR SMART; SM0034; HAMP; 1.
DR SMART; SM00283; MA; 1.
DR PROSITE; PS50111; CHEMOTAXIS_TRANSUDC_2; 1.
DR PROSITE; PS50085; HAMP; 1.
KW Complete proteome.
SQ SEQUENCE 578 AA; 63178 MW; 55004ADC7356DA18 CRC64;

Query Match 63.6%; Score 42; DB 2; Length 578;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

| | | |
|----|-----|--------------|
| Qy | 3 | WELVGYFD 10 |
| Db | 204 | WELVGYFD 211 |

Search completed: December 4, 2005, 04:52:22
Job time : 102.375 secs

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GenCore version 5.1.6
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:45 ; Search time 15.5833 Seconds
 (without alignments)
 67.918 Million cell updates/sec

Title: US-10-632-706-128
 Perfect score: 66
 Sequence: 1 GPWBLVGYRDS 11

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR 80.**

1: pir1:**
 2: pir2:**
 3: pir3:**
 4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description | |
|------------|-------|-------------|--------|--------|--|--|
| 1 | 45 | 68.2 | 279 | 2 | T35791 | |
| 2 | 44 | 66.7 | 2 | AD0222 | probable transmembrane sugar transport protein - Streptomyces coelicolor | |
| 3 | 43 | 65.2 | 1788 | 2 | T29043 | C;Species: Streptomyces coelicolor |
| 4 | 41 | 62.1 | 491 | 2 | EG9368 | C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004 |
| 5 | 41 | 62.1 | 550 | 2 | B84900 | CIAccesion: T35791 |
| 6 | 41 | 62.1 | 619 | 1 | S48729 | R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. |
| 7 | 41 | 62.1 | 697 | 2 | G70704 | submitted to the EMBL Data Library, July 1998 |
| 8 | 40 | 60.6 | 724 | 2 | T87015 | A;Reference number: 221570 |
| 9 | 40 | 60.6 | 726 | 2 | T49095 | A;Accession: T35791 |
| 10 | 40 | 60.6 | 888 | 2 | D84824 | A;Status: preliminary; translated from GB/EMBL/DDJB |
| 11 | 40 | 60.6 | 931 | 2 | D71051 | A;Molecule type: DNA |
| 12 | 39 | 59.1 | 299 | 2 | T33303 | A;Residues: 1-279 <SBE> |
| 13 | 39 | 59.1 | 320 | 2 | T17907 | A;Experimental source: strain A3(2) |
| 14 | 39 | 59.1 | 459 | 2 | S17907 | C;Genetics: |
| 15 | 39 | 59.1 | 471 | 2 | S28476 | A;Gene: SCOPDB:SC8A6_24 |
| 16 | 39 | 59.1 | 578 | 2 | B882204 | C;Superfamily: maltose transport protein malG |
| 17 | 39 | 59.1 | 949 | 1 | FXWMP1 | RESULT 1 |
| 18 | 38 | 57.6 | 173 | 2 | S44403 | T35791 |
| 19 | 38 | 57.6 | 274 | 2 | C75335 | Probable undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase STY3637 [imported] |
| 20 | 38 | 57.6 | 409 | 2 | S63614 | C;Species: Salmonella enterica subsp. enterica serovar Typhi |
| 21 | 38 | 57.6 | 432 | 2 | T17829 | A;Note: This species has also been called <i>Salmonella typhi</i> |
| 22 | 38 | 57.6 | 465 | 2 | T26146 | A;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 03-Feb-2003 |
| 23 | 38 | 57.6 | 495 | 2 | G71693 | C;Accession: AD0922 |
| 24 | 38 | 57.6 | 499 | 2 | G97761 | R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, S.H.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulé, S.; O'Gorman, P. |
| 25 | 38 | 57.6 | 532 | 2 | AF3498 | Nature 413, 848-852, 2001 |
| 26 | 38 | 57.6 | 1091 | 2 | T34247 | A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A;Title: Complete genome sequence of a multiple drug resistant <i>Salmonella enterica</i> serovar |
| 27 | 38 | 57.6 | 1107 | 2 | T34246 | A;Reference number: AB0502; MUID:21534947; PMID:1677608 |
| 28 | 38 | 57.6 | 2100 | 2 | T03223 | A;Accession: AD0922 |
| 29 | 37 | 56.1 | 2100 | 2 | C64041 | A;Status: preliminary |
| 30 | 37 | 56.1 | 217 | 2 | A82491 | A;Molecule type: DNA |
| 31 | 37 | 56.1 | 226 | 2 | A87664 | A;Residues: 1-367 |
| 32 | 37 | 56.1 | 235 | 2 | T44679 | A;Cross-references: UNIPARC:UPI000005A58F; GB:AL513382; PIDN:CAD09398.1; PID:g16504516; |
| 33 | 37 | 56.1 | 241 | 2 | T39330 | C;Genetics: |
| 34 | 37 | 56.1 | 276 | 2 | A95309 | A;Gene: STY3637 |
| 35 | 37 | 56.1 | 277 | 2 | AR3216 | ABC transporter, m |
| 36 | 37 | 56.1 | 349 | 2 | T31856 | hypothetical prote |
| 37 | 37 | 56.1 | 365 | 2 | S61636 | spnU protein homolog |
| 38 | 37 | 56.1 | 400 | 2 | AR0291 | probable 60S acidic |
| 39 | 37 | 56.1 | 413 | 2 | G95965 | probable ABC trans |
| 40 | 37 | 56.1 | 426 | 2 | T08550 | choline monooxygen |
| 41 | 37 | 56.1 | 462 | 2 | T158179 | SH3 receptor subunit |
| 42 | 37 | 56.1 | 468 | 2 | T48615 | hypothetical prote |
| 43 | 37 | 56.1 | 502 | 2 | S50519 | hypothetical prote |
| 44 | 37 | 56.1 | 601 | 1 | A64222 | heat shock protein |
| 45 | 37 | 56.1 | 642 | 2 | G69371 | acetyl-CoA synthet |

ALIGNMENTS

frnE protein VCA01
 hypothetical prote
 spnU protein homolog
 probable 60S acidic
 probable ABC trans
 ABC transporter, m
 hypothetical prote
 hypothetical prote
 probable drug resis
 conserved hypothet
 choline monooxygen
 SH3 receptor subu
 hypothetical prote
 hypothetical prote
 heat shock protein
 acetyl-CoA synthet

Query Match

Best Local Similarity 68.2%; Score 45; DB 2; Length 279;
 Matches 7; Similarity 77.8%; Pred. No. 2.8; Indels 1; Mismatches 0; Gaps 0;

Qy 3 WELVGYRDS 11
 | : ||| | | | |
 Db 160 WMLIGYRDS 168

RESULT 2

AD0922

probable undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase STY3637 [imported]
 C;Species: *Salmonella enterica* subsp. *enterica* serovar *Typhi*
 C;Note: This species has also been called *Salmonella typhi*

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 03-Feb-2003

C;Accession: AD0922

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

R.;T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moulé, S.; O'Gorman, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.,

A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar

A;Reference number: AB0502; MUID:21534947; PMID:1677608

A;Accession: AD0922

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-367

A;Cross-references: UNIPARC:UPI000005A58F; GB:AL513382; PIDN:CAD09398.1; PID:g16504516;

C;Genetics:

A;Gene: STY3637

Query Match 66.7%; Score 44; DB 2; Length 367;
 Best Local Similarity 69.2%; Pred. No. 5.6;

Matches 9; **Conservative** 0; **Mismatches** 0; **Indels** 4; **Gaps** 1;
Qy 1 GPWELV---GPFY 9
Db 127 GPWELVLGPGFCSYF 139

RESULT 3

T29033 hypothetical protein B0228.2 - *Caenorhabditis elegans*
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29033
R;Leimbach, D. submitted to the EMBL Data Library, March 1995
*A;Description: The sequence of *C. elegans* cosmid B0228.*
A;Reference number: Z18324
A;Accession: T29043

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-550 <STO>

A;Cross-references: UNIPROT:082347; UNIPARC:UPI000017A71B; GB:AE002093; NID:93702327; PIRN:

C;Genetics: At2g46220

A;Gene: At2g46220

A;Map Position: 2

A;Molecule type: DNA

A;Residues: 1-550 <STO>

A;Cross-references: UNIPROT:082347; UNIPARC:UPI000017A71B; GB:AE002093; NID:93702327; PIRN:

C;Genetics: At2g46220

A;Gene: At2g46220

A;Map Position: 2

A;Molecule type: DNA

A;Residues: 1-550 <STO>

A;Cross-references: UNIPROT:082347; UNIPARC:UPI000017A71B; GB:AE002093; NID:93702327; PIRN:

C;Genetics: At2g46220

A;Gene: At2g46220

A;Map Position: 2

A;Molecule type: DNA

A;Residues: 1-550 <STO>

A;Cross-references: UNIPROT:082347; UNIPARC:UPI000017A71B; GB:AE002093; NID:93702327; PIRN:

C;Genetics: At2g46220

A;Gene: At2g46220

A;Map Position: 2

A;Molecule type: DNA

A;Residues: 1-550 <STO>

A;Cross-references: UNIPROT:082347; UNIPARC:UPI000017A71B; GB:AE002093; NID:93702327; PIRN:

C;Genetics: At2g46220

A;Gene: At2g46220

A;Map Position: 2

A;Molecule type: DNA

A;Residues: 1-550 <STO>

A;Cross-references: UNIPROT:082347; UNIPARC:UPI000017A71B; GB:AE002093; NID:93702327; PIRN:

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A;Molecule type: DNA

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C;Genetics: At2g46220

A;Gene: At2g46220

A;Map Position: 2

A;Molecule type: DNA

A;Residues: 1-550 <STO>

A;Cross-references: UNIPROT:082347; UNIPARC:UPI000017A71B; GB:AE002093; NID:93702327; PIRN:

C;Genetics: At2g46220

A;Gene: At2g46220

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shan, M.; Vanken, S.E.; Umeyam, L.; Tallon, L.; Neuss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: B84900

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-550 <STO>

A;Cross-references: UNIPROT:082347; UNIPARC:UPI000017A71B; GB:AE002093; NID:93702327; PIRN:

C;Genetics: At2g46220

A;Gene: At2g46220

A;Map Position: 2

A;Molecule type: DNA

A;Residues: 1-550 <STO>

A;Cross-references: UNIPROT:082347; UNIPARC:UPI000017A71B; GB:AE002093; NID:93702327; PIRN:

C;Genetics: At2g46220

A;Gene: At2g46220

A;Map Position: 2

A;Molecule type: DNA

A;Residues: 1-550 <STO>

A;Cross-references: UNIPROT:082347; UNIPARC:UPI000017A71B; GB:AE002093; NID:93702327; PIRN:

C;Genetics: At2g46220

A;Gene: At2g46220

A;Map Position: 2

A;Molecule type: DNA

A;Residues: 1-550 <STO>

A;Cross-references: UNIPROT:082347; UNIPARC:UPI000017A71B; GB:AE002093; NID:93702327; PIRN:

C;Genetics: At2g46220

A;Gene: At2g46220

A;Map Position: 2

A;Molecule type: DNA

A;Residues: 1-550 <STO>

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A;Gene: At2g46220

A;Map Position: 2

A;Molecule type: DNA

A;Residues: 1-550 <STO>

A;Cross-references: UNIPROT:082347; UNIPARC:UPI000017A71B; GB:AE002093; NID:93702327; PIRN:

C;Genetics: At2g46220

A;Gene: At2g46220

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A;Molecule type: DNA

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A;Gene: At2g46220

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A;Residues: 1-550 <STO>

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C;Genetics: At2g46220

A;Gene: At2g46220

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A;Residues: 1-550 <STO>

A;Cross-references: UNIPROT:082347; UNIPARC:UPI000017A71B; GB:AE002093; NID:93702327; PIRN:

C;Genetics: At2g46220

A;Gene: At2g46220

NID:93702327

PIRN:

PID:

PMID:

NID:9556677

GB:

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 PWEVLGVYFD 10
 Db 196 PWVLLGVFN 204

RESULT 8
 B87015
 ABC transporter ML0848 [imported] - *Mycobacterium leprae*
 C;Species: *Mycobacterium leprae*
 C;Accession: B87015
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 R;Cole, S.T.; Elgimelier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
 R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
 Nature 409, 1007-1011, 2001
 A;Authors: Rutitter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
 A;Title: Massive gene decay in the leprosy bacillus.
 A;Reference number: A86909; MUID:21128732; PMID:11234002
 A;Accession: B87015
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-774 <STO>
 A;Cross-references: UNIPROT:Q9CCF9; UNIPARC:UPI00000C6B27; GB:AL450380; NID:gi1092926; E
 C;Genetics:
 A;Gene: ML0848

Query Match 60.6%; Score 40; DB 2; Length 88;
 Best Local Similarity 63.6%; Pred No. 70; Mismatches 7; Conservative 2; Indels 0; Gaps 0;
 Matches 7; N mismatches 2; N conservative 2; N indels 0; N gaps 0;

Qy 2 PWEVLGVYFD 10
 Db 224 PWMLLGPF 231

RESULT 9
 T44905
 ABC-type transporter homolog [imported] - *Mycobacterium leprae*
 C;Species: *Mycobacterium leprae*
 C;Accession: T44905
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, August 1997
 A;Reference number: 222864
 A;Accession: T44905
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-726 <PAR>
 A;Cross-references: UNIPROT:O32971; UNIPARC:UPI00000BEDDE; EMBL:298741; PIDN:CAB11403.1
 A;Experimental source: cosmid B22
 C;Genetics:
 A;Note: MLCB22.38C

Query Match 60.6%; Score 40; DB 2; Length 726;
 Best Local Similarity 75.0%; Pred No. 57; Mismatches 6; Conservative 1; Indels 0; Gaps 0;
 Matches 6; N mismatches 1; N conservative 1; N indels 0; N gaps 0;

Qy 2 PWEVLGVYFD 10
 Db 226 PWMLLGPF 233

RESULT 10
 D71051
 Hypothetical protein PH1107 - *Pyrococcus horikoshii*
 C;Species: *Pyrococcus horikoshii*
 C;Accession: D71051
 C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 31-Dec-2004
 R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
 M.; Ohfuki, Y.; Punahabli, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
 DNA Res. 5, 55-76, 1998
 A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A;Reference number: A71000; MUID:98344137; PMID:9679194
 A;Accession: D71051
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-399 <KWW>
 A;Cross-references: UNIPROT:O58834; UNIPARC:UPI0000062FB7; GB:AP000005; NID:g3236132; PI
 A;Experimental source: strain OT3
 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C;Genetics:
 A;Gene: PH1107
 C;Superfamily: glycosidase, PH1107 type

Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: D84824
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-888 <STO>
 A;Cross-references: UNIPROT:O04205; UNIPARC:UPI00000A517F; GB:AE002093; NID:g2088656; PI
 C;Genetics:
 A;Map position: 2
 Query Match 60.6%; Score 40; DB 2; Length 88;
 Best Local Similarity 63.6%; Pred No. 70; Mismatches 7; Conservative 2; Indels 0; Gaps 0;
 Matches 7; N mismatches 2; N conservative 2; N indels 0; N gaps 0;

Qy 1 GPWEVLGVYFD 11
 Db 544 GPKETLGFDF 554

RESULT 11
 F84637
 Probable plasma membrane proton ATPase [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Accession: F84637
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nieman, W.C.; White, O.; Elsner, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: F84637
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-931 <STO>
 A;Cross-references: UNIPARC:UPI000016237B; GB:AE002093; NID:g457267B; PIDN:AAD23893.1; G
 C;Genetics:
 A;Gene: At2g24220
 A;Map position: 2
 C;Superfamily: Na(+)/K(+) -transporting ATPase alpha chain; ATPase nucleotide-binding dom
 Query Match 60.6%; Score 40; DB 2; Length 931;
 Best Local Similarity 85.7%; Pred No. 74; Mismatches 6; Conservative 1; Indels 0; Gaps 0;
 Matches 6; N mismatches 1; N conservative 1; N indels 0; N gaps 0;

Qy 1 GPWEVLGVYFD 11
 Db 457 GPWQLVG 463

RESULT 12
 D71051
 Hypothetical protein PH1107 - *Pyrococcus horikoshii*
 C;Species: *Pyrococcus horikoshii*
 C;Accession: D71051
 C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 31-Dec-2004
 R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
 M.; Ohfuki, Y.; Punahabli, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
 DNA Res. 5, 55-76, 1998
 A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A;Reference number: A71000; MUID:98344137; PMID:9679194
 A;Accession: D71051
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-399 <KWW>
 A;Cross-references: UNIPROT:O58834; UNIPARC:UPI0000062FB7; GB:AP000005; NID:g3236132; PI
 A;Experimental source: strain OT3
 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C;Genetics:
 A;Gene: PH1107
 C;Superfamily: glycosidase, PH1107 type

Query Match 59.1%; Score 39; DB 2; Length 299;
 Best Local Similarity 60.0%; Pred. No. 33;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PWELVGYFDS 11
 Db 247 PWELEGHVDN 256

RESULT 13

hypothetical protein R01B10.4 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T33303
 R;Langston, Y.; Beck, C.
 submitted to the EMBL Data Library, May 1998

A;Description: The sequence of *C. elegans* cosmid R01B10.

A;Reference number: 221318
 A;Accession: T33303

A;Status: preliminary; translated from GB/EMBL/DBBJ

A;Molecule type: DNA
 A;Residues: 1-471 <MAN>

A;Cross-references: UNIPROT:O61975; UNIPARC:UPI0000080228; EMBL:AF068718; PIDN: AAC17768.

A;Experimental source: Strain Bristol N2; clone R01B10
 A;Genetics:

A;Gene: CESP:R01B10.4
 A;Map position: 5
 A;Introns: 25/2; 73/2; 211/3; 241/2

Query Match 59.1%; Score 39; DB 2; Length 320;
 Best Local Similarity 55.6%; Pred. No. 36;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PWLVGYFDS 11
 Db 65 WDTIGHFDS 73

RESULT 14

517907 glutamate dehydrogenase (NADP) (EC 1.4.1.4) - yeast (*Schwannomyces occidentalis* var. *occidentalis*)

C;Species: *Schwannomyces occidentalis* var. *occidentalis*
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Oct-2004

C;Accession: S17907
 R;de Zoyba, P.A.; Connerton, I.F.; Watson, D.C.; Johnston, J.R.

Curr. Genet. 20, 213-224, 1991
 A;Title: Cloning, sequencing and expression of the *Schwannomyces occidentalis* NADP-dep-

A;Reference number: S17907; MUID:92035089; PMID:1934128
 A;Accession: S17907

A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-159 <DBZ>

A;Cross-references: UNIPROT:PA9507; UNIPARC:UPI00001292F9
 C;Keywords: NADP; oxidoreductase

Query Match 59.1%; Score 39; DB 2; Length 459;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PWBLVGYFDF 10
 Db 308 PWAKVGHFD 316

RESULT 15

S28476 rfbL protein VC0249 [similarity] - *Vibrio cholerae* (strain N16961 serogroup O1)

C;Species: *Vibrio cholerae*
 C;Accession: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
 C;Accession: S28476; H82346

R;Manning, P.A.
 submitted to the EMBL Data Library, May 1991.

A;Reference number: S28467
 A;Accession: S28476

A;Molecule type: DNA
 A;Residues: 1-471 <MAN>

A;Cross-references: UNIPROT:Q06959; UNIPARC:UPI00000470B; EMBL:X59554; NID:g48381; PIDN:

A;Experimental source: strain 017
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

Chadson, D.; Brzuska, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.

L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Status: preliminary

A;Molecule type: DNA
 A;Residues: 1-471 <HEI>

A;Cross-references: UNIPARC:UPI00000470B; GB:AB004113; GB:AB003852; NID:g9654648; PIDN:

A;Experimental source: Serogroup O1; strain N16961; biotype El Tor

A;Gene: rfbL; VC0249

A;Map position: 1

C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology

F;47-468/Domain: acetate-CoA ligase homology <ACI>

Query Match 59.1%; Score 39; DB 2; Length 471;

Best Local Similarity 60.0%; Pred. No. 54;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PWELVGYFDS 11
 Db 329 PWMLDGFEN 338

Search completed: December 4, 2005, 04:53:34

Job time : 17.5833 sec

| GenCore version 5.1.6 | | | | | | | | | |
|--|-------|--------------|-------|-------------|-----------|------------|-----------|----|------------------------------------|
| Copyright (C) 1993 - 2005 Compugen Ltd. | | | | | | | | | |
| Run on: December 4, 2005, 04:09:54 ; Search time 95.5625 seconds | | | | | | | | | |
| Title: OM protein - protein search, using sw model | | | | | | | | | |
| Scoring table: BL05Hm62 | | | | | | | | | |
| Sequence: Gapop 10.0 , Gapext 0.5 | | | | | | | | | |
| Searched: 2443163 seqs, 439378781 residues | | | | | | | | | |
| Total number of hits satisfying chosen parameters: 2443163 | | | | | | | | | |
| Minimum DB seq length: 0 | | | | | | | | | |
| Maximum DB seq length: 200000000 | | | | | | | | | |
| Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries | | | | | | | | | |
| Database : A_Geneseq_21;*: 1:_geneseqp1990s;*: 2:_geneseqp1990B;*: 3:_geneseqp2_001s;*: 4:_geneseqp2_002B;*: 5:_geneseqp2_003as;*: 6:_geneseqp2_004B;*: 7:_geneseqp2_005s;*: 8:_geneseqp2_005s;* | | | | | | | | | |
| Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | | | | | | | | | |
| SUMMARIES | | | | | | | | | |
| Result No. | Score | Query Length | DB ID | Description | | ALIGNMENTS | | | |
| 1 | 66 | 100.0 | 11 | 8 | ADRI8726 | RESULT 1 | ADR38726 | ID | ADR38726 standard; peptide; 11 AA. |
| 2 | 44 | 66.7 | 306 | 6 | ABU4531 | XX | ADR38726; | XX | |
| 3 | 44 | 66.7 | 367 | 6 | ABU17042 | XX | | XX | |
| 4 | 44 | 66.7 | 367 | 6 | ADHU7877 | XX | | XX | |
| 5 | 43 | 65.2 | 207 | 8 | ADHU2894 | XX | | XX | |
| 6 | 42 | 63.6 | 415 | 7 | ABM09126 | XX | | XX | |
| 7 | 41 | 62.1 | 114 | 4 | AAC008773 | XX | | XX | |
| 8 | 41 | 62.1 | 121 | 2 | AAR88504 | XX | | XX | |
| 9 | 41 | 62.1 | 475 | 6 | ABU20453 | XX | | XX | |
| 10 | 41 | 62.1 | 7 | ADC07986 | XX | | XX | | |
| 11 | 41 | 1352 | 4 | ABB67542 | XX | | XX | | |
| 12 | 40 | 60.6 | 146 | 6 | ABP56656 | XX | | XX | |
| 13 | 40 | 60.6 | 283 | 6 | ADM0292 | XX | | XX | |
| 14 | 40 | 60.6 | 477 | 8 | ADY22314 | XX | | XX | |
| 15 | 40 | 60.6 | 885 | 3 | AAG32050 | XX | | XX | |
| 16 | 40 | 60.6 | 931 | 3 | AAG32049 | XX | | XX | |
| 17 | 40 | 60.6 | 956 | 3 | AAG32048 | XX | | XX | |
| 18 | 39.5 | 59.8 | 511 | 8 | ADK68844 | XX | | XX | |
| 19 | 39 | 59.1 | 79 | 3 | AAG13553 | CC | | CC | |
| 20 | 39 | 59.1 | 103 | 3 | AAG13552 | CC | | CC | |
| 21 | 39 | 59.1 | 112 | 3 | AAG13551 | CC | | CC | |
| 22 | 39 | 59.1 | 166 | 4 | AAM06860 | CC | | CC | |
| 23 | 39 | 59.1 | 211 | 8 | ADM07065 | CC | | CC | |
| 24 | 39 | 59.1 | 233 | 3 | AAG05440 | CC | | CC | |

CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BotA antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain variable region complementarity determining
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.
 XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 66; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Mismatches 11; Conservatve 0; Indels 0; Gaps 0;
 Matches 11; QY 1 GPWELVGYFDS 11

Db 1 GPWELVGYFDS 11

RESULT 2

ID ABU45531
 ID ABU45531 standard; protein; 306 AA.

AC ABU45531;
 AC
 DT 19-JUN-2003 (first entry)

DB XX
 DB Protein encoded by Prokaryotic essential gene #31058.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Salmonella paratyphi.

XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.

XX
 PR 21-MAR-2002; 2002WO-US009107.

XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELTRA PHARM INC.

XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029326/02.
 DR N-PSDB; ACA49401.

XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 73455; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than S. aureus S. typhimurium,
 CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 306 AA;

Query Match 66.7%; Score 44; DB 6; Length 306;
 Best Local Similarity 69.2%; Pred. No. 40; Mismatches 9; Conservatve 0; Indels 4; Gaps 1;
 Matches 9; QY 1 GPWELV---GYF 9

Db 66 GPWELVVLGPFGYF 78

RESULT 3

ID ABU47042
 ID ABU47042 standard; protein; 367 AA.

AC ABU47042;
 AC
 DT 19-JUN-2003 (first entry)

DB XX
 DB Protein encoded by Prokaryotic essential gene #32569.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Salmonella typhimurium.

XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.

XX
 PR 21-MAR-2002; 2002WO-US009107.

XX
 PR 06-SEP-2001; 2001US-00948933.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELTRA PHARM INC.

XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029326/02.
 DR N-PSDB; ACA0912.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 74966; 176pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide;(5) the producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences

XX Sequence 367 AA;

Query Match Score 44; DB 6; Length 367;
 Best Local Similarity 69.2%; Pred. No. 48;
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 GPWELV---GYF 9
 Db 127 GPWELVLGPFGFY 139

RESULT 4

ID ABU47877 standard; protein; 367 AA.

XX AC ABU47877;

AC DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #33404.

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS *Salmonella typhi*.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00348993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX PA (BLIT-) ELTRA PHARM INC.

XX DR N-PSDB; ACH51747.

XX PI Wang L, Zamudio C, Malone C, Haselebeck R, Ohlsen KL, Yamamoto R, Forsyth RA, Xu HH;

XX Wall D, Trawick JD, Carr GJ, DR

XX PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 75801; 176pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide;(5) the producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences

XX Sequence 367 AA;

Query Match Score 44; DB 6; Length 357;
 Best Local Similarity 69.2%; Pred. No. 48;
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 GPWELV---GYF 9
 Db 127 GPWELVLGPFGFY 139

RESULT 5

ID ADH12894 standard; protein; 207 AA.

XX AC ADH12894;

AC DT 25-MAR-2004 (first entry)

DE *Francisella tularensis* immunogenic protein 75, SEQ ID NO:75.

XX KW Immunogenic protein; protective immune response; vaccine;

XX KW Genetic vaccine; antibacterial.

OS *Francisella tularensis*.

XX
 PN WO2004003009-A2.
 XX
 XX
 PD 08-JAN-2004.
 XX
 KK PT 26-JUN-2003; 2003WO-GB002718.
 XX
 PR PT 28-JUN-2002; 2002GB-00014942.
 XX
 PA (MINA) UK SEC FOR DEFENCE.
 XX
 PT Titball RW, Mayers CN, Duffield ML, Miller J, Rowe SC;
 XX
 DR WPI; 2004-083016/08.
 DR N-PSDB; ADH12994.
 XX
 PT New protein, useful as a vaccine for producing a protective immune response in a mammal against infection by *Francisella tularensis*, or preventing or treating *Francisella tularensis* infection in a mammal.
 PS Claim 1; SEQ ID NO 75; 217pp; English.
 XX
 CC The invention relates to 100 potentially immunogenic proteins from *Francisella tularensis* (ADH12820-ADH12919) and nucleic acids encoding them (ADH12920-ADH13019) which may be used in vaccines. The nucleic acids may be contained within a vaccine, bacterial or plasmid vector. The invention also relates to a pharmaceutical composition comprising the protein or the nucleic acid in combination with a pharmaceutical carrier or excipient. The proteins and nucleic acids are useful in vaccine compositions for producing a protective immune response against *Francisella tularensis* infection in a mammal, or for preventing or treating *Francisella tularensis* infection in a mammal. The present sequence represents a *Francisella tularensis* protein of the invention.
 CC
 CC Sequence 207 AA;
 CC
 CC Query Match 65.2%; Score 43; DB 8; Length 207;
 CC Best Local Similarity 100.0%; Pred. No. 39; Mismatches 7; Conservative 0; Indels 0; Gaps 0;
 CC
 CC QY 1 GPWBLVG ?
 CC Db 120 GPWELVG 126
 CC
 RESULT 6
 ABM89126 ABM89126 standard; protein; 415 AA.
 AC ABM89126;
 XX DT 02-JUN-2005 (first entry)
 XX DE Rice abiotic stress responsive polypeptide SEQ ID NO:7372.
 XX KW abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
 XX OS *Oryza sativa*.
 XX PN WO2003008540-A2.
 XX PD 30-JAN-2003.
 XX PR 21-JUN-2002; 2002WO-US019668.
 XX PR 22-JUN-2001; 2001US-0300112P.
 XX PR 24-AUG-2001; 2001US-0314662P.
 XX PR 26-SEP-2001; 2001US-0325277P.
 XX PR 21-NOV-2001; 2001US-0332132P.
 XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX PI Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
 XX
 PI Moughamer T, Provart N, Rieke D, Zhu T;
 XX
 DR WPI; 2003-248011/24.
 XX
 PT New stress-responsive nucleic acid, useful for altering the responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold stress, salt stress or osmotic stress.
 XX
 PR Claim 1; SEQ ID NO 7372; 89pp; English.
 XX
 CC The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of plant to an abiotic stress, such as cold stress, salt stress, osmotic stress or any of their combinations. The present sequence is used in the exemplification of the invention.
 CC
 CC Sequence 415 AA;
 CC
 CC Query Match 63.6%; Score 42; DB 7; Length 415;
 CC Best Local Similarity 75.0%; Pred. No. 1.2e+02; Mismatches 6; Conservative 1; Indels 0; Gaps 0;
 CC Matches 1; Minmatches 1; Maxmatches 1;
 CC
 CC QY 1 GPWELVG ?
 CC Db 176 GPWELVG 183
 CC
 RESULT 7
 AAQ08773 AAQ08773 standard; protein; 114 AA.
 XX
 AC AAQ08773;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human polypeptide SEQ ID NO 22665.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy; KW vaccine; peptide therapy; stem cell; growth factor; haemopoiesis; KW tissue growth factor; immunomodulatory; cancer; leukaemia; KW nervous system disorders; arthritis; inflammation.
 XX OS Homo sapiens.
 PN WO200164835-A2.
 XX PD 07-SEP-2001.
 XX PR 26-FEB-2001; 2001WO-US004927.
 XX PR 28-FEB-2000; 2000US-00515126.
 XX PR 18-MAY-2000; 2000US-00577409.
 XX PR (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX DR WPI; 2001-514836/56.
 XX N-PSDB; AA188704.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
 XX
 PS Claim 20; SEQ ID NO 22665; 1399pp + Sequence listing; English.

XX
 CC The invention relates to human polynucleotides (Al179941-AA193841) and
 CC the encoded proteins (AA00010-AA013910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haemopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 treatment of cancer, leukemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](ftp://wipo.int/pub/published_pct_sequences)
 XX

SQ Sequence 114 AA;
 Query Match 62.1%; Score 41; DB 4; Length 114;
 Best Local Similarity 55.6%; Pred. No. 46;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GPWELVGF 9
 Db 76 GPWKFLGFR 84

RESULT 8
 AAR88504 standard; protein: 121 AA.
 ID AAR88504;
 XX
 AC AAR88504;
 DT 31-JUL-1996 (first entry)
 DE VHmu for antibody BT34/A5.
 KW antibody; variable heavy chain; VHmu; human; monoclonal; MAb; BT34/A5;
 KW BT32/A6; cell cycle independent; tumour specific; glioma; therapy;
 KW detection; complementarity determining region; CDR.
 XX
 OS Homo sapiens.

PH Location/Qualifiers
 FT Region 31..35 /note= "complementarity determining region (specifically
 claimed)"
 FT Region 50..66 /note= "complementarity determining region (specifically
 claimed)"
 FT Region 99..110 /note= "complementarity determining region (specifically
 claimed)"

XX
 PN WO9535374-A1.
 XX
 PD 28-DEC-1995.
 XX
 PF 16-JUN-1995; 95WO-CA000361.
 XX
 PR 21-JUN-1994; 94US-00264093.
 XX
 PA (DANM/) DAN M D.
 PI Dan MD;
 XX
 DR WPI; 1996-058411/06.
 XX
 N-PSDB; AT10938.

XX
 Novel monoclonal antibodies, BT34/A5 and BT32/A6 - used to characterise
 CC glioma specific cell surface antigens, and in the treatment of glioma.
 XX
 Claim 8; Page 33; 53pp; English.

CC AAR88504-R88510 represent regions of the human monoclonal antibodies
 CC (Mab's) BT34/A5 and BT32/A6. This sequence represents the variable region
 CC of the heavy chain, subgroup mu, (VHmu) of BT34/A5. The complementarity
 CC determining regions (CDR's) of this sequence are specifically claimed.
 CC This sequence preferably has an N-terminal extension comprising the
 CC signal sequence represented in AAR88505. The BT34/A5 and BT32/A6 Mab's
 CC recognise a cell cycle independent tumour specific antigen. They also
 CC bind equally well to tumour cell in vitro regardless of their culture
 CC viability, growth characteristics, or culture density. The antibodies present
 CC effectively label the tumour cells by binding to the antigen present on
 CC the cell surface. The Mab's are useful in the detection and the treatment
 CC of glioma. These Mab's are specific for glioma and show none of the cross
 CC -reactivity seen with previous antibodies
 XX

SQ Sequence 121 AA;
 Query Match 62.1%; Score 41; DB 2; Length 121;
 Best Local Similarity 60.0%; Pred. No. 49;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GPWELVGF 10
 Db 100 GWDLILNIFD 109

RESULT 9
 ABU20453 standard; protein: 475 AA.
 ID ABU20453
 XX
 AC ABU20453;
 DT 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #5980.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 KW Bacteroides fragilis.
 OS
 PN WO20027183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PR 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-0094893.
 PR 25-OCT-2001; 2001US-0342933P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Hasselbeck R, Ohlsen KL, Zyskind JW,
 PT Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029925/02.
 XX
 N-PSDB; ACA24323.

PT New antisense nucleic acid, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation or an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a sample or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

SQ Sequence 475 AA;

| Query Match | Score | DB | Length |
|-----------------------|------------|---------------------|------------|
| Best Local Similarity | 54.5% | No. | 2.1e+02 |
| Matches | 6; | Mismatches | 2; |
| QY | 1 | GPWSIIVGIFDS | 11 |
| DB | 404 | GDMKLIIVYVDS | 414 |

XX

RESULT 10

| ID | Accession | Length |
|---|-------------------------------------|--------|
| ADC07986 | ADC07986 standard; protein; 792 AA. | 792 |
| XX | | |
| AC | | |
| XX | | |
| DT | | |
| XX | | |
| DE | | |
| Rice protein sequence Seq ID252 related to grain filling. | | |
| XX | | |
| KW plant biotechnology; carbohydrate synthesis; carbohydrate metabolism; | | |
| KW carbohydrate degradation; carbohydrate; plant; grain; grain filling; corn; | | |
| KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet; sugar beet; wheat; rice; protein; oil; starch; fibre; moisture content; cereal; grain; gene; ds; plant. | | |
| KW | | |
| OS Oryza sativa. | | |
| XX | | |
| PN WO2003000905-A2. | | |
| XX | | |
| PD 03-JAN-2003. | | |
| XX | | |
| PF 21-JUN-2002; 2002WO-1B002450. | | |
| XX | | |
| PR 22-JUN-2001; 2001US-0300112P. | | |
| PR 26-SEP-2001; 2001US-032277P. | | |
| PR 20-DEC-2001; 2001US-0342327P. | | |
| XX | | |
| PA (SYNN) SYNTENIA PARTICIPATIONS AG. | | |
| XX | | |
| PI Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T; | | |
| PI Glazebrook J, Katagiri F, Kreps J, Provart N, Rieke D; | | |
| XX DR WPI; 2003-229341/22. | | |
| XX DR N-P5DB; ADC07985. | | |

PT New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates

PT in the plant grain useful in generating plants having improved
PT nutritional properties.
XX
PS

Claim 23, SEQ ID NO 252; 130pp; English.

This invention, in the area of plant biotechnology, relates to novel
CC polynucleotides comprising a nucleotide sequence encoding a protein which
CC is involved in or associated with the synthesis, metabolism or
CC degradation of carbohydrates in the plant grain and the expression of
CC which is up-regulated during grain filling. The plant is selected from
CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
CC sugarbeet, wheat, and rice. The invention may be useful for the
CC improvement of protein, oil, starch, fibre and moisture content of the
CC cereal grains. In addition, carbohydrate levels may be modified to a more
CC desirable level using the present invention. The present sequence is the
CC amino acid sequence of a rice protein of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp://wipo.int/pub/publishedpat_sequence.

SQ
XX

Sequence 792 AA;

Query Match Similarity 62.1%; **Score** 41; **DB** 7; **Length** 792;
Best Local Similarity 65.7%; **Pred.** No. 3.6e+02; **Mismatches** 1; **Indels** 0; **Gaps** 0;
Matches 6; **Conservative** 2; **Mismatches** 1; **Indels** 0; **Gaps** 0;

| Qy | 2 PWELVGYFD 10 |
|----|-------------------|
| Db | 245 PWQLQGYGD 253 |

RESULT 11

ABB67542
ABB67542 standard; protein; 1352 AA.

ID XX

AC ABB67542;

XX XX

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 29418.

XX KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PP 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE) PE CORP NY.

XX PI Venter JC, Adams M, Li PW, Myers EW;

XX DR WPI; 2001-655860/75.

DR N-PDB; ABL11645.

XX PS Disclosure; SEQ ID NO 29418; 21PP + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention is new isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.

CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL1675) and the encoded protein (AB557737-
 CC ABL72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at fip.wipo.int/pub/published_pct_sequences

SQ Sequence 1352 AA;

| | | | | |
|-------------|-----------------------|-------|------------|----------|
| Query Match | Best Local Similarity | Score | DB | Length |
| Qy | 3 WELWGVYFDS | 62.1% | 4 | 1352 |
| Matches | 7; Conservative | 77.8% | Pred. No. | 6.3e+02; |
| Db | 161 WRLNVGVYFDS | 0 | Mismatches | 2; |
| | | 0; | Indels | 0; |
| | | 0; | Gaps | 0; |

RESULT 12

| | | |
|----|----------------------------|--|
| ID | ABP5656 | standard; protein; 146 AA. |
| XX | ABP5656; | |
| XX | DT | 25-MAR-2003 (first entry) |
| XX | DE | Chimpanzee C68 adenovirus E3 16 kDa protein SEQ ID NO:21. |
| XX | KW | simian adenovirus; cytosatic; antipsoriatic; antimicrobial; vaccine; adenoviral; capsid protein; hexon; penton; fibre protein; cancer; hyperproliferative condition; psoriasis; infection. |
| XX | OS | Mastadenovirus. |
| XX | FH | |
| FT | KEY | Location/qualifiers |
| FT | MISC-difference | 62 /note= "any amino acid" |
| XX | PT | 20-JUN-2002; 2002WO-US019735. |
| PN | WO200300851-A2. | |
| XX | PD | 03-JAN-2003. |
| XX | PP | 22-JUN-2001; 2001US0300501P. |
| PR | PR | 04-JUN-2002; 2002US0385632P. |
| XX | (UYPE-) UNIV PENNSYLVANIA. | |
| PA | XX | |
| PA | PT | Gao G, Wilson JM; |
| XX | PT | WPI: 2003-184043/18. |
| DR | DR | N-PSDB; AB222473. |
| XX | XX | |
| PT | PT | New C68 chimpanzee adenoviral capsid protein, useful for preparing a composition for treating hyperproliferative conditions e.g. cancer or psoriasis and as a vaccine against bacterial, fungal, viral or parasitic infection. |
| PT | PT | Disclosure: Page 88; 124pp; English. |

The present invention describes a chimpanzee C68 adenoviral capsid protein, which is substantially free of other viral proteins with which it is naturally associated, comprising: (a) a hexon protein comprising 513-amino acid sequence (see ABP5652); (b) a penton protein comprising 534-amino acid sequence (see ABP5667); (c) a fibre protein comprising 425-amino acid sequence (see ABP5662); or (d) a unique fragment of any of (A)-(C) comprising 8-amino acid residues in length. Also described: (1) a novel adenovirus serotype comprising a unique fragment of the C68 hexon protein fused to a heterologous adenovirus hexon peptide; (2) a recombinant or pseudodiploid adenovirus comprising a capsid of the novel adenovirus serotype encapsidating a molecule for delivery to a target cell; (3) an adenoviral capsid; (4) a pharmaceutical composition; (5)

CC rapid screening of recombinant constructs; and (6) a host cell. The
 CC chimpanzee C68 adenoviral capsid protein has cytostatic, antipsoriatic
 CC and antimicrobial activities, and can be used in vaccines. The chimpanzee
 CC C68 adenoviral capsid protein is useful for preparing a composition for
 CC treating hyperproliferative conditions e.g. cancer or psoriasis and as a
 CC present sequence represents a chimpanzee C68 adenovirus E3 16 kDa
 CC protein, which is given in the exemplification of the present invention

SQ Sequence 146 AA;

| | | | | |
|-------------|-----------------------|-------|------------|--------|
| Query Match | Best Local Similarity | Score | DB | Length |
| Qy | 1 GPWELVG | 60.6% | 40 | 146 |
| Matches | 6; Conservative | 85.7% | Pred. No. | 89; |
| Db | 101 GPWEVVG | 0 | Mismatches | 1; |
| | | 0; | Indels | 0; |
| | | 0; | Gaps | 0; |

RESULT 13

| | | |
|----|---------------------------------|---|
| ID | ABM70292 | standard; protein; 283 AA. |
| XX | AC | ABM70292; |
| XX | DT | 20-NOV-2003 (first entry) |
| XX | DE | Photorhabdus luminescens protein sequence #3389. |
| XX | KW | Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague; whooping cough. |
| XX | OS | Photorhabdus luminescens. |
| XX | PN | WO200294867-A2. |
| XX | PD | 28-NOV-2002. |
| XX | PP | 07-FEB-2002; 2002WO-1B003040. |
| XX | PR | 07-FEB-2001; 2001FR-00001659. |
| XX | PA | (INSP) INST PASTEUR. |
| PA | (CNRS) CNRS CENT NAT RECH SCI. | |
| XX | PT | Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A; |
| PT | PT | Buchrieser C; |
| XX | PT | WPI: 2003-148459/14. |
| XX | PT | Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides. |
| XX | PT | Claim 2; SEQ ID NO 3389; 1205pp; French. |
| PT | XX | |
| CC | CC | The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of <i>P. luminescens</i> and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of <i>P. luminescens</i> , e.g. in foods. The genes/proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than <i>P. luminescens</i> and are able to alter response or sensitivity to toxins and antibiotics produced by <i>P. luminescens</i> . Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibiotics useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful |

CC therapeutically (to treat microbial infection by bacteria or fungi that
 CC are sensitive to *P. luminescens*-encoded toxins or antibiotics) and as
 CC bipesticides. Other uses of the genes and the proteins as virulence
 CC factors and for identifying targets of human diseases for which *P.
 luminescens* is a model (particularly plague and whooping cough). This
 CC sequence represents one of the isolated *P. luminescens* proteins
 XX SQ Sequence 283 AA:

Query Match 60.6%; Score 40; DB 6; Length 283;
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WELVGVFDS 11
 Db 238 WLIVGVFDA 246

RESULT 14

ADY22314
 ID ADY22314 standard; protein: 477 AA.
 XX
 AC ADY22314;
 XX

DT 21-APR-2005 (first entry)
 XX
 DB Plant full length insert polypeptide seqid 70098.

XX plant protectant; plant growth regulator; gene therapy; plant;

KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen resistance; pest tolerance;

KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;

KW protein content.
 XX OS Unidentified.
 XX
 PN US2004034888-A1.
 XX
 PD 19-FEB-2004.
 XX
 PR 28-APR-2003; 2003US-00425114.

XX
 PR 06-MAY-1999; 99US-0030517.
 PR 05-NOV-2001; 2001US-00985678.

XX PA (LIUJ) LIU J.
 PA (ZHOU) ZHOU Y.
 PA (KOVALIC) KOVALIC D K.
 PA (SCREEN) SCREEN S E.
 PA (TABASKA) TABASKA J E.
 PA (CAOY) CAO Y.

XX PI Liu J, Zhou Y, Kovacic DK, Screen SE, Tabaska JE, Cao Y;
 XX DR WPI: 2004-180133/17.

XX PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.

XX PS Claim 1; SEQ ID NO 70098; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp://seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 improving plant tolerance to cold, heat, drought, herbicides, extreme

CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.

SQ Sequence 477 AA;

Query Match 60.6%; Score 40; DB 8; Length 477;
 Best Local Similarity 60.0%; Pred. No. 3.1e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPWELVGVFD 10
 Db 307 GPWEMMRFFD 316

RESULT 15

ARG32050
 ID AAG32050 standard; protein: 885 AA.
 XX
 AC AAG32050;

XX DT 17-OCT-2000 (first entry)
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 38593.

XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX OS Arabidopsis thaliana.
 XX PN EP1033405-A2.
 XX
 PD 06-SBP-2000.
 XX
 PR 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.
 PR 05-MAR-1999; 99US-0123180P.
 PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-012578P.
 PR 25-MAR-1999; 99US-0126264P.
 PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.
 PR 06-APR-1999; 99US-0128234P.
 PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.
 PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.
 PR 23-APR-1999; 99US-0130510P.

PR 23-APR-1999; 99US-0130891P.
 PR 28-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.
 PR 30-APR-1999; 99US-0132407P.

PR 04-MAY-1999; 99US-0132484P.
 PR 05-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.
 PR 06-MAY-1999; 99US-0132487P.

PR 07-MAY-1999; 99US-0132863P.
 PR 11-MAY-1999; 99US-0134265P.

PR 14-MAY-1999; 99US-0134218P.
 PR 14-MAY-1999; 99US-0134219P.
 PR 14-MAY-1999; 99US-0134221P.
 PR 14-MAY-1999; 99US-0134370P.

PR 18-MAY-1999; 99US-0134768P.

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| PR | 19-MAY-1999; | 99US-0134941P. | PR | 28-JUL-1999; | 99US-0145951P. |
| PR | 20-MAY-1999; | 99US-0135124P. | PR | 02-AUG-1999; | 99US-0146386P. |
| PR | 21-MAY-1999; | 99US-013533P. | PR | 02-AUG-1999; | 99US-0146389P. |
| PR | 24-MAY-1999; | 99US-0135629P. | PR | 02-AUG-1999; | 99US-0147038P. |
| PR | 25-MAY-1999; | 99US-0136021P. | PR | 03-AUG-1999; | 99US-0147204P. |
| PR | 27-MAY-1999; | 99US-0136322P. | PR | 04-AUG-1999; | 99US-0147302P. |
| PR | 28-MAY-1999; | 99US-0136782P. | PR | 04-AUG-1999; | 99US-0147335P. |
| PR | 01-JUN-1999; | 99US-0137222P. | PR | 05-AUG-1999; | 99US-0147192P. |
| PR | 03-JUN-1999; | 99US-0137588P. | PR | 05-AUG-1999; | 99US-0147260P. |
| PR | 04-JUN-1999; | 99US-0137502P. | PR | 06-AUG-1999; | 99US-0147303P. |
| PR | 07-JUN-1999; | 99US-0137724P. | PR | 06-AUG-1999; | 99US-0147416P. |
| PR | 08-JUN-1999; | 99US-0138054P. | PR | 09-AUG-1999; | 99US-0147493P. |
| PR | 10-JUN-1999; | 99US-0138847P. | PR | 09-AUG-1999; | 99US-0147335P. |
| PR | 14-JUN-1999; | 99US-0139119P. | PR | 10-AUG-1999; | 99US-0148171P. |
| PR | 16-JUN-1999; | 99US-0139422P. | PR | 11-AUG-1999; | 99US-0148319P. |
| PR | 17-JUN-1999; | 99US-0139453P. | PR | 12-AUG-1999; | 99US-0148341P. |
| PR | 18-JUN-1999; | 99US-0139458P. | PR | 13-AUG-1999; | 99US-0148565P. |
| PR | 18-JUN-1999; | 99US-0139459P. | PR | 13-AUG-1999; | 99US-0148684P. |
| PR | 18-JUN-1999; | 99US-0139460P. | PR | 16-AUG-1999; | 99US-0149368P. |
| PR | 18-JUN-1999; | 99US-0139465P. | PR | 17-AUG-1999; | 99US-0149175P. |
| PR | 18-JUN-1999; | 99US-0139466P. | PR | 18-AUG-1999; | 99US-0149465P. |
| PR | 18-JUN-1999; | 99US-0139463P. | PR | 20-AUG-1999; | 99US-0149722P. |
| PR | 18-JUN-1999; | 99US-0139750P. | PR | 20-AUG-1999; | 99US-0149723P. |
| PR | 18-JUN-1999; | 99US-0139817P. | PR | 20-AUG-1999; | 99US-0149929P. |
| PR | 18-JUN-1999; | 99US-0138999P. | PR | 23-AUG-1999; | 99US-0149902P. |
| PR | 22-JUN-1999; | 99US-0141842P. | PR | 23-AUG-1999; | 99US-0149330P. |
| PR | 23-JUN-1999; | 99US-0140333P. | PR | 31-AUG-1999; | 99US-0151438P. |
| PR | 23-JUN-1999; | 99US-0140334P. | PR | 25-AUG-1999; | 99US-0150566P. |
| PR | 24-JUN-1999; | 99US-0140655P. | PR | 26-AUG-1999; | 99US-0150884P. |
| PR | 28-JUN-1999; | 99US-0140823P. | PR | 20-AUG-1999; | 99US-0149723P. |
| PR | 29-JUN-1999; | 99US-0140991P. | PR | 23-AUG-1999; | 99US-0150990P. |
| PR | 30-JUN-1999; | 99US-0141287P. | PR | 27-AUG-1999; | 99US-0151303P. |
| PR | 01-JUL-1999; | 99US-0141842P. | PR | 30-AUG-1999; | 99US-0151330P. |
| PR | 01-JUL-1999; | 99US-0142154P. | PR | 31-AUG-1999; | 99US-0151438P. |
| PR | 02-JUL-1999; | 99US-0142055P. | PR | 01-SEP-1999; | 99US-0151930P. |
| PR | 06-JUL-1999; | 99US-0142390P. | PR | 01-SEP-1999; | 99US-0151065P. |
| PR | 08-JUL-1999; | 99US-0142803P. | PR | 27-AUG-1999; | 99US-0151066P. |
| PR | 09-JUL-1999; | 99US-0142920P. | PR | 30-AUG-1999; | 99US-0151303P. |
| PR | 12-JUL-1999; | 99US-0142977P. | PR | 31-AUG-1999; | 99US-0151438P. |
| PR | 13-JUL-1999; | 99US-0143542P. | PR | 01-SEP-1999; | 99US-0151930P. |
| PR | 14-JUL-1999; | 99US-0143624P. | PR | 07-SEP-1999; | 99US-0152163P. |
| PR | 15-JUL-1999; | 99US-0144005P. | PR | 10-SEP-1999; | 99US-0153070P. |
| PR | 16-JUL-1999; | 99US-0144086P. | PR | 13-SEP-1999; | 99US-0153588P. |
| PR | 19-JUL-1999; | 99US-0144325P. | PR | 15-SEP-1999; | 99US-0154018P. |
| PR | 19-JUL-1999; | 99US-0144331P. | PR | 16-SEP-1999; | 99US-0154033P. |
| PR | 19-JUL-1999; | 99US-0144332P. | PR | 20-SEP-1999; | 99US-0154779P. |
| PR | 19-JUL-1999; | 99US-0144334P. | PR | 22-SEP-1999; | 99US-0155139P. |
| PR | 19-JUL-1999; | 99US-0144335P. | PR | 23-SEP-1999; | 99US-0155686P. |
| PR | 19-JUL-1999; | 99US-0144336P. | PR | 24-SEP-1999; | 99US-0155698P. |
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| PR | 20-JUL-1999; | 99US-0144633P. | PR | 29-SEP-1999; | 99US-0156596P. |
| PR | 20-JUL-1999; | 99US-0145087P. | PR | 04-OCT-1999; | 99US-0157117P. |
| PR | 22-JUL-1999; | 99US-0145089P. | PR | 05-OCT-1999; | 99US-0157753P. |
| PR | 22-JUL-1999; | 99US-0145124P. | PR | 06-OCT-1999; | 99US-0157865P. |
| PR | 22-JUL-1999; | 99US-0145145P. | PR | 07-OCT-1999; | 99US-0158059P. |
| PR | 22-JUL-1999; | 99US-0145218P. | PR | 08-OCT-1999; | 99US-0158232P. |
| PR | 23-JUL-1999; | 99US-0145224P. | PR | 12-OCT-1999; | 99US-0158366P. |
| PR | 23-JUL-1999; | 99US-0145276P. | PR | 13-OCT-1999; | 99US-0159233P. |
| PR | 27-JUL-1999; | 99US-0145913P. | PR | 13-OCT-1999; | 99US-0159349P. |
| PR | 27-JUL-1999; | 99US-0145918P. | PR | 13-OCT-1999; | 99US-0159359P. |
| PR | 27-JUL-1999; | 99US-0145919P. | PR | 14-OCT-1999; | 99US-0159359P. |
| PR | 27-JUL-1999; | 99US-0145919P. | PR | 21-OCT-1999; | 99US-0160900P. |
| PR | 27-JUL-1999; | 99US-0145919P. | PR | 22-OCT-1999; | 99US-0160911P. |
| PR | 27-JUL-1999; | 99US-0145919P. | PR | 21-OCT-1999; | 99US-0160911P. |
| PR | 27-JUL-1999; | 99US-0145919P. | PR | 21-OCT-1999; | 99US-0160911P. |
| PR | 27-JUL-1999; | 99US-0145919P. | PR | 25-OCT-1999; | 99US-0161465P. |
| PR | 27-JUL-1999; | 99US-0145919P. | PR | 26-OCT-1999; | 99US-0161399P. |

Mon Dec 5 13:14:57 2005

usb-10-632-706-128.rag

Page 10

PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match Similarity 60.6%; Score 40; DB 3; Length 885;
Best Local Similarity 85.7%; Pred. No. 6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPWELVG 7
Db ||||:||| 411 GPWOLVG 417

Search completed: December 4, 2005, 04:44:57
Job time : 98.5625 secs

Page 1

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 4, 2005, 04:08:08 ; Search time 3.20833 Seconds

Maximum DB seq length: 0 (without alignment)

Maximum DB seq length: 200000000 (with alignment)

16.417 Million cell updates/sec

Title: US-10-632-706-128

Perfect score: 66

Sequence: 1 GPWELVGFDS 11

Scoring table: BioSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA New:*

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6: /cgm2_6/ptodata/1/pupba/us10_NEW_PUB.pep:*

7: /cgm2_6/ptodata/1/pupba/us11_NEW_PUB.pep:*

8: /cgm2_6/ptodata/1/pupba/us60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|--------------------|
| 1 | 36 | 54.5 | 792 | US-10-467-657-6026 |
| 2 | 36 | 54.5 | 792 | US-10-467-657-7528 |
| 3 | 35 | 53.0 | 620 | US-10-467-657-1210 |
| 4 | 34 | 51.5 | 322 | US-11-074-176-36 |
| 5 | 34 | 51.5 | 723 | US-10-677-657-1916 |
| 6 | 34 | 51.5 | 926 | US-10-841-129-2 |
| 7 | 33.5 | 50.8 | 478 | US-11-037-822A-4 |
| 8 | 33 | 50.0 | 198 | US-11-082-389-302 |
| 9 | 33 | 50.0 | 281 | US-11-082-389-304 |
| 10 | 33 | 50.0 | 431 | US-11-055-822-76 |
| 11 | 33 | 50.0 | 724 | US-10-131-826A-60 |
| 12 | 33 | 50.0 | 1510 | US-10-153-822-72 |
| 13 | 33 | 50.0 | 2725 | US-11-113-424-52 |
| 14 | 32 | 48.5 | 456 | US-10-667-657-4150 |
| 15 | 32 | 53.3 | 7 | US-11-147-047-43 |
| 16 | 32 | 48.5 | 771 | US-11-147-047-34 |
| 17 | 31.5 | 47.7 | 532 | US-11-184-380-6 |
| 18 | 31.5 | 47.7 | 544 | US-10-719-311-18 |
| 19 | 31.5 | 47.7 | 588 | US-11-184-380-5 |
| 20 | 31.5 | 47.7 | 598 | US-10-719-311-16 |
| 21 | 31.5 | 47.7 | 724 | US-11-184-380-4 |
| 22 | 31.5 | 47.7 | 734 | US-10-719-311-4 |
| 23 | 31.5 | 47.7 | 735 | US-11-184-380-24 |
| 24 | 47.0 | 142 | 6 | US-21-821-330-1030 |
| 25 | 47.0 | 229 | 6 | US-10-510-386-228 |

ALIGNMENTS

RESULT 1

; Sequence 6026, Ap

; Publication No. US20050260581A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON SPA

; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASTIGNANI Vega

; APPLICANT: MONACI Elisa

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACID

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467-657

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12

; SOFTWARE: Seqwin99, version 1.04

; SEQ ID NO 6026

; LENGTH: 792

; TYPE: PRT

; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-6026

Query Match Score 54.5%; DB 6; Length 54.5%

Best Local Similarity 55.0%; Pred. No. 27; Matches 6; Conservative 2; Mismatches 0; Ind

OY 4 ELVGYFDS 11

Db 390 ELLGYFDN 397

RESULT 2

; Sequence 7558, Application US/10467657

; Publication No. US20050260581A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON Spa

; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASTIGNANI Vega

; APPLICANT: MONACI Elisa

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACID

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467-657

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR FILING DATE: 2001-02-12
 NUMBER OF SEQ ID NOS: 9218
 SOFTWARE: SeqWin99, version 1.04
 SEQ ID NO: 7528
 LENGTH: 792
 ORGANISM: *Neisseria gonorrhoeae*
 US-10-467-657-7528

| Query Match | Score | DB | Length |
|-----------------------|-------|----|------------|
| Best Local Similarity | 54.5% | 6 | 792 |
| Pred. | 75.0% | 27 | |
| Matches | 6 | 2 | Mismatches |
| Conservative | | | 0 |
| Indels | 0 | | |
| Gaps | 0 | | |

Qy 4 BLVGYFDS 11
 Db 390 BLVGYFDN 397

RESULT 3
 US-10-467-657-1210
 Sequence 1210, Application US/10467657
 Publication No. US20050260581A1

GENERAL INFORMATION:
 APPLICANT: CHIRON SPA
 APPLICANT: FONTANA Maria Rita
 APPLICANT: PIZZA Mariagrazia
 APPLICANT: MASIGNANI Vega

APPLICANT: MONACI Elisabetta
 TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/10/467,657
 CURRENT FILING DATE: 2003-08-11
 PRIOR APPLICATION NUMBER: GB-0103424.8
 PRIOR FILING DATE: 2001-02-12
 NUMBER OF SEQ ID NOS: 9218
 SOFTWARE: SeqWin99, version 1.04
 SEQ ID NO: 1210
 LENGTH: 356
 TYPE: PRT
 ORGANISM: *Neisseria gonorrhoeae*
 US-10-467-657-1210

Query Match 53.0%; Score 35; DB 6; Length 356;
 Best Local Similarity 62.5%; Pred. No. 19;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPWELVGY 8
 Db 45 GIWEMEGLY 52

RESULT 4
 US-11-074-176-36
 Sequence 36, Application US/11074176
 Publication No. US20050250135A1

GENERAL INFORMATION:
 APPLICANT: Klaenhammer, Todd R.
 APPLICANT: Russell, William M.
 APPLICANT: Altermann, Eric
 APPLICANT: McAluliffe, Olivia
 APPLICANT: Peril, Andrea Arcarate
 TITLE OF INVENTION: Nucleic Acid Sequences Encoding Proteins and Uses Therefore
 TITLE OF INVENTION: Stress-Related Proteins and Uses Therefor
 FILE REFERENCE: 5051-94
 CURRENT APPLICATION NUMBER: US/11/074,176
 CURRENT FILING DATE: 2005-03-07
 PRIOR APPLICATION NUMBER: 60/551,161
 PRIOR FILING DATE: 2004-03-08
 NUMBER OF SEQ ID NOS: 381
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 36
 LENGTH: 322
 TYPE: PRT

Qy 4 BLVGYFD 10
 Db 43 BLTGYFD 49

RESULT 5
 US-10-467-657-1916
 Sequence 1916, Application US/10467657
 Publication No. US20050260581A1

GENERAL INFORMATION:
 APPLICANT: CHIRON SPA
 APPLICANT: FONTANA Maria Rita
 APPLICANT: PIZZA Mariagrazia
 APPLICANT: MASIGNANI Vega

APPLICANT: MONACI Elisabetta
 TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/10/467,657
 CURRENT FILING DATE: 2003-08-11
 PRIOR APPLICATION NUMBER: GB-0103424.8
 PRIOR FILING DATE: 2001-02-12
 NUMBER OF SEQ ID NOS: 9218
 SOFTWARE: SeqWin99, version 1.04
 SEQ ID NO: 1916
 LENGTH: 723
 TYPE: PRT
 ORGANISM: *Neisseria gonorrhoeae*
 US-10-467-657-1916

Query Match 51.5%; Score 34; DB 6; Length 723;
 Best Local Similarity 53.3%; Pred. No. 55;
 Matches 8; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

Qy 1 GPWELVJ----GYF 9
 Db 260 GNWELVJKSAPGYF 274

RESULT 6
 US-10-841-129-2
 Sequence 2, Application US/10841129
 Publication No. US20050250113A1

GENERAL INFORMATION:
 APPLICANT: Erlenbach, Isolde
 APPLICANT: Zuker, Charles S.
 APPLICANT: Hoon, Mark A.
 APPLICANT: Ryba, Nicholas J. P.
 APPLICANT: Zhang, Yifeng
 APPLICANT: The Regents of the University of California
 APPLICANT: The Government of the United States of America
 APPLICANT: as represented by The Secretary of the
 APPLICANT: Department of Health and Human Services
 TITLE OF INVENTION: A Mammalian Magnesium/Manganese Sensing G Protein
 TITLE OF INVENTION: Coupled Receptor
 FILE REFERENCE: 02078-14540US
 CURRENT APPLICATION NUMBER: US/10/841,129
 CURRENT FILING DATE: 2004-05-07
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 2
 LENGTH: 926
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURES:
 OTHER INFORMATION: coupled receptor (GPCR) R5.24, Mg receptor, Mn

US-10-841-129-2 ; OTHER INFORMATION: receptor

Query Match 51.5%; Score 34; DB 6; Length 926;
 Best Local Similarity 83.3%; Pred. No. 70; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PWELVG 7
 Db 443 PWELVG 448

RESULT 7
 US-11-037-829A-4
 Sequence 4, Application US/11037829A
 Publication No. US20050255551A1
 GENERAL INFORMATION:
 APPLICANT: Targacept, Inc
 APPLICANT: Targacept, Inc Healthcare West
 APPLICANT: Benchirif, Merouane
 APPLICANT: Lukas, Ronald J.
 TITLE OF INVENTION: Methods and Compositions Relating to Chimeric Nicotinic Receptor Subunits

FILE REFERENCE: ST03_1520.PCT
 CURRENT APPLICATION NUMBER: US/11/037.829A
 CURRENT FILING DATE: 2005-01-18
 PRIOR APPLICATION NUMBER: US 60/397,380
 PRIOR FILING DATE: 2002-07-19
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 4

LENGTH: 478
 TYPE: PRT
 ORGANISM: Homo sapien

Query Match 50.8%; Score 33.5; DB 7; Length 478;
 Best Local Similarity 58.3%; Pred. No. 45; Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

Oy 1 PWELVG---YF 9
 Db 207 GWELLVGTYVYPF 218

RESULT 8
 US-11-082-389-302
 Sequence 302, Application US/11082389
 Publication No. US20050244935A1
 GENERAL INFORMATION:
 APPLICANT: Pompejus, Markus
 APPLICANT: Kroger, Burkhard
 APPLICANT: Schroder, Hartwig
 APPLICANT: Zelder, Oskar
 APPLICANT: Haberhauer, Gregor
 TITLE OF INVENTION: CORNYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE TRANSPORT

FILE REFERENCE: BGI-131CPCN
 CURRENT APPLICATION NUMBER: US/11/082,389
 CURRENT FILING DATE: 2005-03-16
 PRIOR APPLICATION NUMBER: US 09/603024
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: US 60/141031
 PRIOR FILING DATE: 1999-06-25
 PRIOR APPLICATION NUMBER: US 60/43262
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: US 60/151281
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: DE 19930487.4
 PRIOR FILING DATE: 1999-07-01
 PRIOR APPLICATION NUMBER: DE 19930489.0
 PRIOR FILING DATE: 1999-07-01
 PRIOR APPLICATION NUMBER: DE 19931549.3
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931550.7
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19932134.5
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19941379.7
 PRIOR FILING DATE: 1999-08-31
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 446

SEQ ID NO 304
 LENGTH: 281
 TYPE: PRT
 ORGANISM: Corynebacterium glutamicum

US-11-082-389-302
 LENGTH: 198
 TYPE: PRT
 ORGANISM: Corynebacterium glutamicum
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: 4
 OTHER INFORMATION: Xaa = Phe, Ser, Tyr, or Cys

US-11-082-389-302
 Query Match 50.0%; Score 33; DB 7; Length 198;
 Best Local Similarity 66.7%; Pred. No. 24; Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 3 WEIYG 8
 Db 99 WQDIGY 104

RESULT 9
 US-11-082-389-304
 Sequence 304, Application US/11082389
 Publication No. US20050244935A1
 GENERAL INFORMATION:
 APPLICANT: Pompejus, Markus
 APPLICANT: Kroger, Burkhard
 APPLICANT: Schroder, Hartwig
 APPLICANT: Zelder, Oskar
 APPLICANT: Haberhauer, Gregor
 TITLE OF INVENTION: CORNYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE TRANSPORT

FILE REFERENCE: BGI-131CPCN
 CURRENT APPLICATION NUMBER: US/11/082,389
 CURRENT FILING DATE: 2005-03-16
 PRIOR APPLICATION NUMBER: US 09/603024
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: US 60/141031
 PRIOR FILING DATE: 1999-06-25
 PRIOR APPLICATION NUMBER: US 60/43262
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: US 60/151281
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: DE 19930487.4
 PRIOR FILING DATE: 1999-07-01
 PRIOR APPLICATION NUMBER: DE 19930489.0
 PRIOR FILING DATE: 1999-07-01
 PRIOR APPLICATION NUMBER: DE 19931549.3
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931550.7
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19932134.5
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19941379.7
 PRIOR FILING DATE: 1999-08-31
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 446

SEQ ID NO 304
 LENGTH: 281
 TYPE: PRT
 ORGANISM: Corynebacterium glutamicum

Query Match 50.0%; Score 33; DB 7; Length 281;
 Best Local Similarity 66.7%; Pred. No. 33;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WELVGYY 8
 Db 153 WOLIGY 158

RESULT 10
 US-10-055-822-76
 ; Sequence 76, Application US/11055822
 ; Publication No. US2005050260707A1
 GENERAL INFORMATION:
 ; APPLICANT: Pompejus, Markus
 ; APPLICANT: Kroger, Burkhard
 ; APPLICANT: Schroder, Hartwig
 ; APPLICANT: Zelzer, Oskar
 ; APPLICANT: Haberhauer, Gregor
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
 ; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
 FILE REFERENCE: BGI-121CPCN
 CURRENT APPLICATION NUMBER: US/11/055, 822
 CURRENT FILING DATE: 2005-02-11
 PRIOR APPLICATION NUMBER: 09/606, 740
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: 60/141, 031
 PRIOR FILING DATE: 1999-06-25
 PRIOR APPLICATION NUMBER: 60/142, 101
 PRIOR FILING DATE: 1999-07-02
 PRIOR APPLICATION NUMBER: 60/148, 613
 PRIOR FILING DATE: 1999-08-12
 PRIOR APPLICATION NUMBER: 60/187, 970
 PRIOR FILING DATE: 2000-03-09
 PRIOR APPLICATION NUMBER: DE 19930476. 9
 PRIOR FILING DATE: 1993-07-01
 PRIOR APPLICATION NUMBER: DE 19931415. 2
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931418. 7
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931419. 5
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931420. 9
 PRIOR FILING DATE: 1999-07-08
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1158
 SEQ ID NO 76
 LENGTH: 431
 TYPE: PRT
 ORGANISM: Corynebacterium glutamicum
 US-11-055-822-76

Query Match 50.0%; Score 33; DB 7; Length 431;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFWEL 5
 Db 284 GFWEL 288

RESULT 11
 US-10-131-826A-60
 ; Sequence 60, Application US/10131826A
 ; Publication No. US20050245730A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filatoff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.

Query Match 50.0%; Score 33; DB 6; Length 724;
 Best Local Similarity 50.0%; Pred. No. 82;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WELVGYYD 10
 Db 83 WDIMSYFD 90

RESULT 12
 US-11-055-822-72
 ; Sequence 72, Application US/11055822
 ; Publication No. US20050260707A1
 GENERAL INFORMATION:
 ; APPLICANT: Pompejus, Markus
 ; APPLICANT: Kroger, Burkhard
 ; APPLICANT: Schroder, Hartwig
 ; APPLICANT: Zelzer, Oskar
 ; APPLICANT: Haberhauer, Gregor
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
 ; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
 FILE REFERENCE: BGI-121CPCN
 CURRENT APPLICATION NUMBER: US/11/055, 822
 CURRENT FILING DATE: 2005-02-11
 PRIOR APPLICATION NUMBER: 09/606, 740
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: 60/141, 031
 PRIOR FILING DATE: 1999-06-25
 PRIOR APPLICATION NUMBER: 60/142, 101
 PRIOR FILING DATE: 1999-07-02
 PRIOR APPLICATION NUMBER: 60/148, 613
 PRIOR FILING DATE: 1999-08-12
 PRIOR APPLICATION NUMBER: 60/187, 970
 PRIOR FILING DATE: 2000-03-09
 PRIOR APPLICATION NUMBER: DE 19930476. 9
 PRIOR FILING DATE: 1993-07-01
 PRIOR APPLICATION NUMBER: DE 19931415. 2
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931418. 7
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931419. 5
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931420. 9
 PRIOR FILING DATE: 1999-07-08
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO 60
 LENGTH: 724
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-131-826A-60

Query Match 50.0%; Score 33; DB 6; Length 724;
 Best Local Similarity 50.0%; Pred. No. 82;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WELVGYYD 10
 Db 83 WDIMSYFD 90

Db 503 GPWYLAFYND 512

RESULT 14
US-10-467-657-4150
; Sequence 4150, Application US/10467657
; Publication No. US20050260581A1

GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Ritta
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO: 4150
LENGTH: 456
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae

US-10-467-657-4150

RESULT 13
US-11-113-424-52
Query Match 50.0%; Score 33; DB 7; Length 1510;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWEL 5
Db 1063 GYWEL 1067

GENERAL INFORMATION:
; APPLICANT: Gangolfi et al.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-225

CURRENT APPLICATION NUMBER: US/11/113,424

CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 2725
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-113-424-52

Query Match 50.0%; Score 33; DB 7; Length 2725;
Best Local Similarity 60.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GPMWLGVYED 10
||| 1 |

RESULT 15
US-11-147-047-33
Query Match 48.5%; Score 32; DB 6; Length 456;
Best Local Similarity 57.1%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PWEIAYV 8
Db 154 PWEIAYV 160

GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Saffia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying

TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GB50015
CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2005-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 33
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-147-047-33

Query Match 48.5%; Score 32; DB 7; Length 533;
Best Local Similarity 83.3%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Mon Dec 5 13:14:57 2005

usb-10-632-706-128.rapbn

Page 6

QY 2 PMELVG 7
|||
Db 178 PMEAVG 183

Search completed: December 4, 2005, 04:37:49
Job time : 4.20833 SECs

OM protein - protein search, using sw model
Run on: December 4, 2005, 04:09:54 (without alignments)
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SUMMARIES

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Maximum DB seq length: 2000000000

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameter

Gapop 10.0 , Gapext 0.5

Scoring table: BLOSUM63
Sequence: 1 EFDWLLWDGDRGAEDV 13

30.370 million wells updated/ per

Run on: December 4, 2005, 04:09:54 ; Search time 130.312 Seconds
(without alignments)
50 572 million reads/sec

OM protein - protein search, using SW model

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ALIGNMENT

| | |
|-----------|-----------|
| AbrG65491 | Bacterial |
| AbrG65591 | Novel hum |
| Ary38595 | Neisseria |
| AbrG9036 | N. gonorr |
| Ary38596 | Neisseria |
| Abp7536 | N. gonorr |
| Abp49038 | N. gonorr |
| Raw26164 | KP-1 |
| Aau30396 | Novel hum |
| Abz20416 | Crab-eati |
| Raw26163 | Milk KP- |
| Adz20410 | Novel apo |
| Aew26165 | Human KP- |
| Adz07645 | Cyclin-de |
| Adz04207 | Novel apo |
| AbrH94428 | M. xanthu |
| Amb88218 | Rice abio |
| Abbo9181 | Pseudomon |
| Abd01564 | Protein e |
| Abd06555 | Pseudomon |
| Aau65794 | Propionib |

CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (II), and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I), and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulinum
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain variable region complementarity determining
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.
 XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPPDWLWGDRGALDV 15
 Db 1 EPPDWLWGDRGALDV 15

RESULT 2

ADR38728

ID ADR38728 standard; peptide; 15 AA.

AC ADR38728;

XX DT 02-DEC-2004 (first entry)

DE Mouse heavy chain variable region CDR3 seqid 130.

XX KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;

KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;

KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;

KW heavy chain variable region; complementarity determining region; CDR3.

OS Mus sp.

XX PN US2004175385-A1.

XX PD 09-SEP-2004.

XX PP 01-AUG-2003; 2003US-00632706.

XX PR 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.

(RGBC) UNIV CALIFORNIA.

XX PI Marks JD, Amerbodtfer P;

XX DR WPI, 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.

XX Example 3; SEQ ID NO 130; 110pp; English.

The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,

CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
 CC comprising BONT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (II); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (II); and a kit comprising (II). (II) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (II) in surplus, where each of (II) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (II) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (II) exhibits specificity and affinity towards BONT/A. (II)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain variable region complementarity determining
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.
 XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPPDWLWGDRGALDV 15
 Db 1 EPPDWLWGDRGALDV 15

RESULT 3

ADR38792

ID ADR38792 standard; peptide; 15 AA.

AC ADR38792;

XX DT 02-DEC-2004 (first entry)

DE Mouse heavy chain anti-BONT-antibody CD3 seqid 194.

XX KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;

KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;

KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;

KW CDR3; complementarity determining region 1.

OS Mus sp.

XX PN US2004175385-A1.

XX PD 09-SEP-2004.

XX PR 01-AUG-2003; 2003US-00632706.

XX XX 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.

(RGBC) UNIV CALIFORNIA.

XX PI Marks JD, Amerbodtfer P;

XX DR WPI, 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.

XX Example 4; SEQ ID NO 194; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,

(BONT/A) An isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone C25, C25, C39, IC6, 3D12, B4, 1F3, huC5, Ar1, Ar2, WRL17, WRL17), 3-1, 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum neurotoxin type A (BONT/A). Also described are: a polypeptide (II) comprising BONT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I); producing (I); and a composition (III) comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising (I); and a kit comprising (I). (I) is useful for neutralising BONT/A antibody and for neutralising a botulinum neurotoxin which involves contacting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. (I) is useful for diagnosing the botulism or for treating pathologies associated with botulinum neurotoxin poisoning. (I) exhibits specificity and affinity towards BONT/A. (I) enables rapid detection or diagnosis of botulism. This is the amino acid sequence of mouse heavy chain anti-BONT-antibody CDR3.

to an epitope specifically bound by an antibody expressed by a specific clone where (I) binds to and neutralises botulinum neurotoxin type A (BoNT/A). An isolated antibody (II) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone S25, C25, C39, 1C6, 3B12, B4, 1F3, huC25, Ar1, Ar2, MR1(V), WRL1(T), 3-1, 3-8, 3-10 and ING1, where (II) binds to and neutralizes botulinum neurotoxin type A (BoNT/A). Also described are: a polypeptide (III) comprising BoNT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I); producing (I); and a composition (III') comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising (I); and a kit comprising (I). (I) is useful for neutralising BoNT/A antibody and for neutralising a botulinum neurotoxin which involves contacting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. (I) is useful for diagnosing the botulism or for treating pathologies associated with botulinum neurotoxin poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I) enables rapid detection or diagnosis of botulism. This is the amino acid

ID ADR38798 standard; peptide; 15 AA.
 XX
 AC
 XX
 ADR38798;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Mouse heavy chain anti-BONT-antibody CD3 seqid 200.
 XX
 KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
 KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
 KW CDR3; complementarity determining region 1.
 XX
 OS Mus sp.
 XX
 PN US2004175385-A1.
 XX
 PD 09-SEP-2004.
 XX
 PR 01-AUG-2003; 2003US-00632706.
 XX
 PR 31-AUG-1998; 98US-00144886.
 PR 01-AUG-2002; 2002US-0400721P.
 XX
 PA (REBC) UNIV CALIFORNIA.
 XX
 PI Marks JD, Amersdorfer P;
 XX
 DR WPI; 2004-652009/63.
 XX
 PT New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.
 XX
 PS Example 4; SEQ ID NO 200; 110P; English.

XX
CC to an epitope specifically bound by an antibody expressed by a specific clone where (I) binds to and neutralises botulinum neurotoxin type A (BONT/A). An isolated antibody (II) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone S25, C25, C39, IC6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WRI(V), WRI(T), 3-1, 3-8, 3-10 and INGL, where (II) binds to and neutralizes botulinum neurotoxin type A (BONT/A). Also described are: a polypeptide (III) comprising BONT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I) producing (II); and a composition (III) comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising (I); and a kit comprising (II). (II) is useful for neutralising BONT/A antibody and for neutralising a botulinum neurotoxin which involves contacting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies in surplus. (I) is useful for diagnosing the botulism or for treating pathologies associated with botulinum neurotoxin poisoning. (I) exhibits specificity and affinity towards BONT/A. (I) enables rapid detection or diagnosis of botulism. This is the amino acid sequence of mouse heavy chain anti-BONT-antibody CDR3.

XX
CC Sequence 15 AA;
XX
CC Best Local Similarity 100.0%; Score 89; DB 8; Length 15;
CC Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
Qy 1 EPDWLWGDGRGALDV 15
CC
Db 1 EPDWLWGDGRGALDV 15
XX
RESULT 6
XX
ID ADR38729
XX
AC ADR38729;
XX
DT 02-DEC-2004 (first entry)
XX
DE Mouse heavy chain variable region CDR3 seqid 131.
XX
KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW heavy chain variable region; complementarity determining region; CDR3.
OS Mus sp.
XX
PN US2004175385-A1.
XX
XX
PD 09-SBP-2004.
XX
PP 01-AUG-2003; 2003US-00632706.
XX
PR 31-AUG-1998; 98US-00144886.
PR 01-AUG-2002; 2002US-0400721P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Marks JD, Amerstorfer P;
XX
DR WPI; 2004-652009/63.
XX
PT New isolated antibody that neutralizes botulinum neurotoxin type A, useful for diagnosing botulism or for treating pathologies associated with botulinum neurotoxin poisoning.

XX
RS Example 3; SEQ ID NO 131; 110P; English.

XX
CC The invention describes an isolated antibody (II) that specifically binds to an epitope specifically bound by an antibody expressed by a specific clone where (II) binds to and neutralises botulinum neurotoxin type A (BONT/A). An isolated antibody (II) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone S25, C25, C39, IC6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WRI(V), WRI(T), 3-1, 3-8, 3-10 and INGL, where (II) binds to and neutralizes botulinum neurotoxin type A (BONT/A). Also described are: a polypeptide (III) comprising BONT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I) producing (II); and a composition (III) comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising (I); and a kit comprising (II). (II) is useful for neutralising BONT/A antibody and for neutralising a botulinum neurotoxin which involves contacting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies in surplus. (I) exhibits specificity and affinity towards BONT/A. (I) enables rapid detection or diagnosis of botulism. This is the amino acid sequence of mouse heavy chain variable region complementarity determining region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

XX
SQ Sequence 15 AA;

XX
CC Best Local Similarity 100.0%; Score 89; DB 8; Length 15;
CC Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
Qy 1 EPDWLWGDGRGALDV 15
CC
Db 1 EPDWLWGDGRGALDV 15
XX
RESULT 7
XX
ID ADR38801
XX
AC ADR38801;
XX
DT 02-DEC-2004 (first entry)
XX
DB Mouse heavy chain anti-BONT-antibody CD3 seqid 203.
XX
KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
KW CDR3; complementarity determining region 1.
OS Mus sp.
XX
PN US2004175385-A1.
XX
XX
PD 09-SBP-2004.
XX
PP 01-AUG-2003; 2003US-00632706.
XX
PR 31-AUG-1998; 98US-00144886.
PR 01-AUG-2002; 2002US-0400721P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Marks JD, Amerstorfer P;
XX
DR WPI; 2004-652009/63.

PT New isolated antibody that neutralizes botulinum neurotoxin type A'
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.

PS Example 4; SEQ ID NO 203; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A'
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, IC6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WRI(V), WRI(T), 3-1,
 CC 3-10, and INGI, where (I) binds to and neutralises botulinum
 CC neurotoxin type A' (BONT/A). Also described are: a polypeptide (II)
 comprising BONT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 XX sequence of mouse heavy chain anti-BONT-antibody CDR3.
 SQ Sequence 15 AA;

Query Match 84.3%; Score 75; DB 8; Length 15;
 Best Local Similarity 93.3%; Pred. No. 0; Mismatches 0;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPDWLWKGDRGALDV 15
 DB 1 EDPWLWKGDRGALDV 15

RESULT 8
 ABG2031
 ID ABG2031 standard; protein; 334 AA.

XX AC ABG2031;

XX DT 13-FEB-2002 (first entry)

DB Novel human diagnostic protein #20322.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PP 30-MAR-2001; 2001WO-US0008631.

PP 31-MAY-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

XX DR WI; 2001-639362/73.
 DR N-PSDB; AAS84518.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 20; SEQ ID NO 50690; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 in diagnostics as expressed sequence tags for identifying expressed
 genes. (I) is useful in gene therapy techniques to restore normal
 activity of (II) or to treat disease states involving (II). (II) is
 useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 supplement. (II) and its partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG3037 represent novel human diagnostic
 CC amino acid sequences. ABG0010-ABG3037 represent novel human diagnostic
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 334 AA;

Query Match 57.3%; Score 51; DB 4; Length 334;

Best Local Similarity 53.3%; Pred. No. 23;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPDWLWKGDRGALDV 15
 DB 263 KPDWSSWGPQGWIDV 277

RESULT 9
 ADJ98189

XX ADJ98189 standard; protein; 201 AA.

XX AC ADJ98189;

XX DT 06-MAY-2004 (first entry)

XX DE Prochlorococcus marinus str MIT 9313 phytol kinase protein.

XX KW phytol kinase; tocopherol biosynthesis; plant; drought resistance;
 KW enzyme.

XX OS Prochlorococcus marinus str. MIT 9313.
 XX PN WO2004013312-A2.

XX PD 12-FEB-2004.

XX PP 05-AUG-2003; 2003WO-US025276.

XX PR 05-AUG-2002; 2002US-0400689P.

PR 05-AUG-2003; 2003US-00634548.

XX (MONS) MONSANTO TECHNOLOGY LLC.

XX Norris SR, Lincoln K, Abad MS, Eilers R, Hartauyker KK,
 PI Hirschberg J, Karunandana B, Moshiri F, Stein JC, Valentin HB;

PI Venkatesh TV;

XX DR WPI; 2004-157125/15.

PT New phytol kinase polynucleotides, useful in mediating tocopherol biosynthesis and in producing plants with increased drought resistance.

PT

XX

PS Claim 1; SEQ ID NO 27; 189pp; English.

XX

CC The invention relates to a novel substantially purified nucleic acid molecule encoding a phytol kinase. The nucleic acid molecules and polypeptides of the invention may be useful in mediating tocopherol biosynthesis and in producing plants with increased drought resistance. The current sequence is that of a phytol kinase protein of the invention.

XX

SQ Sequence 201 AA:

| | | | | | | | |
|-----------------------|-------|--------------|-----|------------|-----|------------|-------|
| Query Match | 53.9% | Score | 48; | DB | 8; | Length | 201; |
| Best Local Similarity | 50.0% | Pred. | No. | 39; | | | |
| Matches | 6; | Conservative | 4; | Mismatches | 2; | Indels | 0; |
| Qy | 2 | PDWLWGDGRAL | 13 | Db | 123 | PNWLGQORKS | I 134 |

RESULT 10

ID ABO6015

ID ABO6015 standard; protein; 229 AA.

XX

AC ABO6015;

XX

DT 29-JUL-2004 (first entry)

XX

DE Klebsiella pneumoniae polypeptide seqid 12532.

XX

KW Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; vaccine.

XX

OS Klebsiella pneumoniae.

XX

DE Klebsiella pneumoniae polypeptide seqid 12532.

XX

KW Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; vaccine.

XX

OS Klebsiella pneumoniae.

XX

PN US6610836-B1.

XX

PD 26-AUG-2003.

XX

PP 27-JAN-2000; 2000US-00489039.

XX

PR 29-JAN-1999; 99US-0117747P.

XX

PA (GENO-) GRNOME THERAPEUTICS CORP.

XX

PI Bretton GL, Osborne M;

XX

DR WPI; 2003-895346/82.

DR N-PSDB; ACRH99566.

XX

PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.

XX

PS Disclosure; SEQ ID NO 12532; 932pp; English.

XX

The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention.

XX

SQ Sequence 229 AA:

| | | | | | | | |
|-----------------------|-------|--------------|-----|------------|-----|---------------|-------|
| Query Match | 53.9% | Score | 48; | DB | 7; | Length | 229; |
| Best Local Similarity | 57.1% | Pred. | No. | 44; | | | |
| Matches | 8; | Conservative | 1; | Mismatches | 5; | Indels | 0; |
| Qy | 1 | PDWLWGDGRALD | 14 | Db | 195 | PDWQIWAQSRGLD | I 207 |

RESULT 12

ID AAY48365

ID AAY48365 standard; protein; 59 AA.

XX

AC AAY48365;

XX

DT 08-DBCC-1999 (first entry)

XX

DE Human prostate cancer-associated protein 62.

XX

KW Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy; cancer; tissue specificity; human.

XX

OS Homo sapiens.

PI Drmanac RT, Liu C, Tang YT,
 XX
 PN DE19811194-A1.
 XX
 XX DR WPI; 2001-639362/73.
 PD N-PSDB; AAS86711.
 XX
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PR diagnostics, forensics, gene mapping, identification of mutations
 XX PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
 XX
 PI Speccht T, Hinmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
 XX DR WPI; 1999-519629/44.
 DR N-PSDB; AA233505.
 XX
 PT New nucleic acid expressed at high level in normal prostatic tissue and
 PT encoded polypeptides, used to treat cancer and screen for therapeutic
 agents.
 PT
 PS Claim 22; 148; 194pp; German.
 XX
 CC This invention describes novel nucleic acid sequences (A) that are
 CC expressed at high level in normal prostatic tissue. Polypeptides (I)
 CC encoded by (A) are used: (a) for identifying agents for treatment of
 CC prostatic cancer and (b) for therapy of prostate cancer, optionally where
 CC expressed by gene therapy methods. (A) is also used to isolate full-
 length genes (for gene therapy) and for recombinant production of (I),
 CC which can be used to raise specific antibodies. (A) are identified by
 CC assembly of ESTs (expressed sequence tags) before these are analyzed for
 CC expression pattern (tissue specificity). This approach eliminates many of
 CC the false results, as regards tissue specificity associated with known
 CC methods that use single (usually short) ESTs. AA48304-Y48456 represent
 CC peptides encoded by the expressed sequence tags described in the method
 CC of the invention
 XX
 SQ Sequence 59 AA;
 Query Match 52.8%; Score 47; DB 2; Length 59;
 Best Local Similarity 87.5%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QV 4 WLLWGDRG 11
 ||||| |
 Db 44 WLLWGSRG 51
 RESULT 13
 ABG2224 ID ABG22524 standard; protein; 455 AA.
 XX AC ABG22524;
 XX DT 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #22515.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSEB-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 PN ADS23387 standard; protein; 904 AA.
 XX AC ADS23387;
 XX DT 02-DEC-2004 (first entry)
 DE Bacterial polypeptide #12420.
 XX Recombinant DNA construct; transformed Plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 OS Bacteria.
 XX
 PN US200233675-A1.
 XX
 PD 18-DEC-2003.
 XX
 PF 20-FEB-2003; 2003US-00369493.
 XX
 PR 21-FEB-2002; 2002US-0360039P.
 XX

PA (CAOY/) CAO Y.
 PA (HINK/) Hinkle G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 PI Cao Y., Hinkle GJ, Slater SC, Chen X, Goldman BS;
 DR
 XX
 WPI; 2004-061375/06.

PT New recombinant DNA construct comprising a promoter positioned to provide
 for expression of a polynucleotide encoding a polypeptide from a
 microbial source, useful for producing plants with improved properties.
 XX
 PS Claim 1; SEQ ID NO 12420; 122pp; English.
 XX
 CC The invention relates to a recombinant DNA construct comprising a
 promoter functional in a plant cell, where the promoter is positioned to
 provide for expression of a polynucleotide encoding a polypeptide from a
 microbial source. The invention also relates to a transformed plant
 comprising the recombinant DNA construct and a method of producing a
 transformed plant having an improved property. The plant is a crop plant
 such as maize or soybean. The method of producing a transformed plant
 having an improved property comprises transforming a plant with the
 recombinant DNA construct and growing the transformed plant, where the
 polynucleotide or polypeptide is useful for improving plant properties.
 The recombinant DNA construct is useful for producing plants with
 improved plant properties, e.g. improved cold, heat or drought tolerance,
 tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 increased resistance to plant disease, better growth rate by modification
 of the cell cycle pathway with plant growth regulators, increased rate of
 homologous recombination, modified seed oil or protein yield and/or
 content, improved yield by modification of carbohydrate, nitrogen or
 phosphorus use and/or uptake, by modification of photosynthesis or by
 providing improved plant growth and development under at least one stress
 condition, improved lignin production or improved galactomannan
 production. This sequence represents a bacterial polypeptide used in the
 scope of the invention. Note: The sequence data for this patent did not
 form part of the printed specification but was obtained in electronic
 format from USPRO at seqdata.uspto.gov/sequence.html.

SQ Sequence 904 AA:

Query Match 52.8%; Score 47; DB 8; Length 904;
 Best Local Similarity 70.0%; Pred. No. 2.6e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY |||||: : :
 DB 460 WLMWGRLAL 13

RESULT 15
 AAM2399
 ID AAM2399 standard; protein; 186 AA.
 XX
 AC AAM2399;
 XX
 DT 12-OCT-2001 (first entry)
 XX
 DB Human EST encoded protein SEQ ID NO: 1924.
 XX
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
 KW gene therapy; nutrition.
 XX
 OS Homo sapiens.
 XX
 PN WO200154477-A2.
 PD 02-AUG-2001.
 XX

PF 25-JAN-2001; 2001WO-US02687.
 XX
 PR 25-JAN-2000; 2000US-00491404.
 PR 17-JUL-2000; 2000US-00517746.
 PR 03-AUG-2000; 2000US-00611451.
 PR 15-SEP-2000; 2000US-0063870.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 XX
 DR N-PSDB; AH99058.
 XX
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use.
 XX
 PS Claim 20; Page 125, 1275pp; English.
 XX
 CC The present invention provides the protein and coding sequences of novel
 proteins from a variety of organisms, including human, dog, cat, horse,
 cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 urchin and tomato. These were derived from expressed sequence tags (ESTs)
 from the organism of interest. They can be used in diagnostics,
 forensics, gene mapping, identification of mutations, to assess
 biodiversity and for nutritional purposes. The present sequence is a
 protein of the invention
 XX
 SQ Sequence 186 AA;
 Query Match 51.7%; Score 46; DB 4; Length 186;
 Best Local Similarity 53.3%; Pred. No. 71;
 Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;
 QY ||||: : :|||:
 DB 168 PGWLWGG--DRGALD 14
 182

Search completed: December 4, 2005, 04:44:59
 Job time : 132.312 secs

A;Genome: plasmid
C;Superfamily: regulatory protein ampr

Query Match 51.1%; Score 45.5%; DB 2; Length 298;

Best Local Similarity 56.3%; Pred. No. 18; Matches 9; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 1 EPDWLWIM-GDGRGALDV 15
Db 199 EPDWLRWCAQAGVADV 214

RESULT 3

G70555 probable entD protein - *Mycobacterium tuberculosis* (strain H37Rv)

C;Species: *Mycobacterium tuberculosis*

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C;Accession: G70555

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

R;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentle, S.; Hamlin, N.; Holroyd, S.

R;Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 531-544, 1998

A;Authors: Squires, R.; Stinson, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome

A;Reference number: A70500; PMID:98295987; PMID:9634220

A;Accession: G70595

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-203 <COL>

A;Cross-references: UNIPROT:005852; UNIPARC:UPI000016534B; GB:Z955120; GB:AU123456; NID:9

A;Experimental source: Strain H37Rv

A;Genes: entD

C;Superfamily: cofactor-dependent phosphoglycerate mutase; phosphoglycerate mutase homolog

Query Match 50.6%; Score 45; DB 2; Length 203;
Best Local Similarity 85.7%; Pred. No. 15; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPDWLW 7
Db 103 EPDWLW 109

RESULT 4

AG0056 probable AMP-binding enzyme-family protein YPO0537 [imported] - *Yersinia pestis* (strain

C;Species: *Yersinia pestis*

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C;Accession: AG0056

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

R;deno-Tarrega, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

R;Il, M.; Rutherford, K.; Simmonds, M.; Shelton, J.; Stevens, K.; Whitehead, S.; Barrell, G.

Nature 413, 522-527, 2001

A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AG0056

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-237 <SIM>

A;Cross-references: UNIPROT:Q9PF4; UNIPARC:UPI0000024F4; GB:AE003916; GB:AB003849; NID:

A;Experimental source: Strain 9aSC

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Accencio, M.; Alvarenga, R.; Alves, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrasco, D.M.; Carter, H.; de Neto, R.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

R;submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme,

A;J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Kurnama, E.B.E.; Laigre, D.;

A;Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Matrino, C.L.; Marques, M.V.; Martins, B.

A;Authors: Martins, E.M.F.; Matsumura, A.Y.; Manck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

A;F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeiro, D.A.

A;Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki,

A;Authors: da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zebedee, A.

A;Residues: 1-601 <UR>

A;Cross-references: UNIPROT:Q821G5; UNIPARC:UPI00000DCD42; GB:AL590842; PIDN:CAC89394.1;

A;Genes: YPO0537

C;Superfamily: Synechocystis long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homolog

Query Match 50.6%; Score 45; DB 2; Length 601;

Best Local Similarity 64.3%; Pred. No. 42; Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EPDWLWIGDGRALD 14
Db 440 EDGLWLKIGDAGALD 453

RESULT 5

T30842 Serine-repeat antigen 3 - *Plasmodium vivax*

C;Species: *Plasmodium vivax*

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C;Accession: T30842

R;Kleter, M.C.; Crawford, K.A.; Boley, L.J.; Landsberg, K.B.; Gibson, H.L.; Kaslow, D.C.

Mol. Biochem. Parasitol. 78, 55-55, 1996

A;Title: Identification and cloning of a locus of serine repeat antigen (sera)-related g-

A;Reference number: Z20898; MUID:96408670; PMID:8813677

A;Accession: T30842

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residue: 1-1076 <KIE>

A;Cross-references: UNIPROT:Q26154; UNIPARC:UPI0000809B3; EMBL:U51723; NID:91381087; PIR:

C;Genetics:

A;Introns: 12/1; 253/1; 302/1

A;Note: V-SERA 3

C;superfamily: Plasmodium vivax serine-repeat antigen

Query Match 50.0%; Score 44.5; DB 2; Length 1076;

Best Local Similarity 40.9%; Pred. No. 87; Matches 9; Conservative 2; Mismatches 4; Indels 7; Gaps 1;

Qy 1 EPDWL-----MDGRGALDV 15
Db 743 KPYWLQLQNWSKGHDKGPKV 764

RESULT 6

G82768 Virulence Protein XPO754 [imported] - *Xylella fastidiosa* (strain 9aSc)

C;Species: *Xylella fastidiosa*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: G82768

R;anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequenc-

A;Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: For a complete list of authors see reference number A59328 below

A;Accession: G82768

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-237 <SIM>

A;Cross-references: UNIPROT:Q9PFC4; UNIPARC:UPI0000024F4; GB:AE003916; GB:AB003849; NID:

A;Experimental source: Strain 9aSC

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Accencio, M.; Alvarenga, R.; Alves, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrasco, D.M.; Carter, H.; de Neto, R.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

R;submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme,

A;J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Kurnama, E.B.E.; Laigre, D.;

A;Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Matrino, C.L.; Marques, M.V.; Martins, B.

A;Authors: Martins, E.M.F.; Matsumura, A.Y.; Manck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

A;F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeiro, D.A.

A;Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki,

A;Authors: da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zebedee, A.

A;Residues: 1-601 <UR>

A;Cross-references: UNIPROT:Q821G5; UNIPARC:UPI00000DCD42; GB:AL590842; PIDN:CAC89394.1;

A;Genes: YPO0537

C;Superfamily: type IV secretory pathway, VirJ component

C;Genetics:

A;Contents: annotation

A;Gene: XP0754

C;Contents: annotation

A;Gene: XP0754

C;Superfamily: Synechocystis long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homolog

Query Match 49.4%; Score 44; DB 2; Length 237;

Best Local Similarity 58.3%; Pred. No. 24; Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 WLWLGEGHGRDV 15
Db 151 WLWLGEGHGRDV 162

RESULT 7
 R;Galibert, F.; Finn, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federer, N.A.; Fisher, R.F.; B75010 L.; Hyman, R.W.; Jones, T.
 hypothetical protein PAB1063 - *Pyrococcus abyssi* (strain Orsay)
 C;Species: *Pyrococcus abyssi*
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C;Accession: B75010
 R;Anonymous, Genoscope submitted to the EMBL Data Library, July 1999
 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
 A;Reference number: A75001
 A;Accession: B75010
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1409 <KAW>
 A;Cross-references: UNIPROT:Q9UY92; UNIPARC:UPI0000034560; GB:AJ248288; GB:AL096836; NID:
 A;Experimental source: strain Orsay
 C;Genetics:
 A;Gene: PAB1063

RESULT 8
 Query Match 49.4%; Score 44; DB 2; Length 409;
 Best Local Similarity 39.1%; Pred. No. 41;
 Matches 9; Conservative 2; Mismatches 2; Indels 10; Gaps 1;
 Qy 2 PDWLW-----GDRGA 14
 | :| :| :| :| :| :| :| :|
 Db 354 PGWILWGLLILMGRVGNPGALD 376

RESULT 9
 Query Match 49.4%; Score 44; DB 2; Length 491;
 Best Local Similarity 61.5%; Pred. No. 49;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 DWLWLGDAALDV 15
 ::| :| :| :| :| :| :| :| :|
 Db 413 BFWLHGDRGALDL 425

RESULT 10
 Query Match 49.4%; Score 44; DB 2; Length 601;
 Best Local Similarity 85.7%; Pred. No. 59;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 PDWLWAG 8
 | :| :| :| :| :| :| :| :|
 Db 169 PDWLWAG 175

RESULT 10
 S77614 phosphoribosylformylglycinamide synthase (EC 6.3.5.3) component II - *Synechococcus* sp.
 N;Alternate Names: FGAM synthetase
 C;Species: *Synechococcus* sp.
 C;Accession: T10330
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C;Accession: T10330
 R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 A;Reference number: Z17215
 A;Accession: T10330
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-491 <PAR>
 A;Cross-references: UNIPROT:O86654; UNIPARC:UPI00000DAD67; EMBL:AL031231; NID:e1315070;
 A;Experimental source: strain A3(2)
 C;Genetics:
 A;Gene: 3C3.21

RESULT 11
 Query Match 49.4%; Score 44; DB 2; Length 491;
 Best Local Similarity 61.5%; Pred. No. 49;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 DWLWLGDAALDV 15
 ::| :| :| :| :| :| :| :| :|
 Db 413 BFWLHGDRGALDL 425

RESULT 9
 E85296 probable ABC-type iron transport system protein SMA0525 [imported] - *Sinorhizobium meliloti*
 C;Species: *Sinorhizobium meliloti*
 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C;Accession: E85296
 R;Barman, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.B.; Barloy-Hubler, F.; Bowe ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9889, 2001
 A;Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti* A;131; reference number: A95262; MUID:21396509; PMID:11481432
 A;Accession: E85296
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-601 <KUR>
 A;Cross-references: UNIPROT:Q93001; UNIPARC:UPI00000BE03E; GB:AB006469; PIDN:AAK64935.1;
 A;Experimental source: strain 1021, megaplasmid psymA

RESULT 11
 T50422 homolog to yeast orf Yor166c. [imported] - fission yeast (*Schizosaccharomyces pombe*)
 C;Species: *Schizosaccharomyces pombe*
 C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
 C;Accession: T50422

R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

Submitted to the EMBL Data Library, February 2000

A;Reference number: Z25039

A;Accession: T50422

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Residues: 1-462 <SEE>

A;Cross-references: UNIPROT:Q8P7J1; UNIPARC:UPI000006AAB; EMBL:AL157991; PIDN:CAB76224.

C;Genetics:

A;Gene: SPDB:SPCC24B10.15

A;Molecule position: 3

Query Match 48.3%; Score 43; DB 2; Length 462;

Best Local Similarity 55.6%; Pred. No. 65; Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DWLWMDRG 11

Db 394 EPWMLWAERG 402

RESULT 12

JC5393 zinc finger protein KF-1 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 01-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004

R;Yabojima, K.; Tsujimura, A.; Mizuno, T.; Shigeyoshi, Y.; Inazawa, J.; Kikuno, R.; Kuma

Biochem. Biophys. Res. Commun. 231: 481-487, 1997

A;Title: Cloning of human and mouse cDNAs encoding novel zinc finger proteins expressed

A;Reference number: JC5392; MUID:97223484; PMID:9070305

A;Accession: JC5393

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Cross-references: UNIPROT:008883; UNIPARC:UPI0000086061; DDBJ:D76445; NID:92058262; PI

C;Comment: This protein is involved in membranous protein-sorting apparatus similarly to

C;Genetics: A;Gene: kf-1

C;Superfamily: zinc finger protein KF-1 precursor - mouse

C;Keywords: zinc finger protein KF-1 precursor; zinc finger homology

C;Domain: signal sequence #status predicted <SIG>

F;1-19/Domain: transmembrane #status predicted <TM1>

F;32-34/Domain: transmembrane #status predicted <TM2>

F;617-668/Domain: RING finger homology <RNG>

Query Match 48.3%; Score 43; DB 2; Length 685;

Best Local Similarity 85.7%; Pred. No. 95; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPDWMLW 7

Db 605 EPDWMLW 611

RESULT 14

AS2593 hypothetical protein XF2169 [imported] - Xylella fastidiosa (strain 945c)

C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: AS2593

R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A;Reference number: AS2515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number AS9328 below

A;Accession: AS2593

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-698 <SIM>

A;Cross-references: UNIPROT:Q9PBH5; UNIPARC:UPI000002968; GB:AB004030; GB:AE003849; NID

A;Experimental source: strain 945c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Accencio, M.; Alvaranga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.B.A.; Carraro, D.M.; Caxier, H

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

Submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurmaev, E.E.; Laige-

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, B

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Maracca, E.C.; Miyaki, C.Y.I.

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.

Rodrigues, V.; Rosa, A.J.de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Swanson

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silveira, M.H.; Vaihala, H.; Van Sluys, M.A.; Vettore, A.L.; Z

A;Reference number: AS9328

A;Comments: annotation

C;Genetics:

A;Gene: XF2169

RESULT 15

H83276 probable lipase PA2949 [imported] - *Pseudomonas aeruginosa* (strain PAO1)

C;Species: *Pseudomonas aeruginosa*

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 12-Jul-2004

C;Accession: H83276

R;Stover, C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

RESULT 13

Query Match 48.3%; Score 43; DB 2; Length 698;

Best Local Similarity 63.6%; Pred. No. 97; Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DWLWMDRGAL 13

Db 554 DWLWMDNSLL 564

RESULT 14

Query Match 48.3%; Score 43; DB 2; Length 685;

Best Local Similarity 85.7%; Pred. No. 95; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPDWMLW 7

Db 605 EPDWMLW 611

RESULT 15

Query Match 48.3%; Score 43; DB 2; Length 698;

Best Local Similarity 63.6%; Pred. No. 97; Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DWLWMDRGAL 13

Db 554 DWLWMDNSLL 564

RESULT 16

Query Match 48.3%; Score 43; DB 2; Length 698;

Best Local Similarity 63.6%; Pred. No. 97; Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DWLWMDRGAL 13

Db 554 DWLWMDNSLL 564

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 955-964, 2000
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A;Reference number: A82930; MURID:28437337; PMID:10984033
A;Accession: R33276
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-115 <STO>
A;Cross-references: UNIPROT:Q9KQG6; UNIPARC:UPI00000C4BC6; GB:AE004721; GB:AE004091; NCBI
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA3949
C;Superfamily: tropinesterase

Query Match 47.8%; Score 42.5; DB 2; Length 315;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 10; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
Qy 2 PRLWLNGDRG-ALDV 15
Db 249 PRLWLNGDRG-ALDV 263

Search completed: December 4, 2005, 04:53:46
Job time : 33.25 secs

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| | | | |
|--|--|----------------------|---------------------------------|
| Run on: | December 4, 2005, 04:31:36 | (without alignments) | Search time 136.875 Seconds |
| OM protein - protein search, using SW model | | | 77.318 Million cell updates/sec |
| Title: | US-10-632-706-197 | | |
| Perfect score: | 89 | | |
| Sequence: | 1 EBDWLLNGDRGALDV 15 | | |
| Scoring table: | BLOSSUM62 | | |
| Gapcp: | 10.0 , Gapext: 0.5 | | |
| Searched: | 2166443 seqs, 705528306 residues | | |
| Total number of hits satisfying chosen parameters: | 2166443 | | |
| Minimum DB seq length: | 0 | | |
| Maximum DB seq length: | 200000000 | | |
| Post-processing: | Minimum Match 0% | | |
| | Maximum Match 100% | | |
| | Listing first 45 summaries | | |
| Database : | | | |
| | 1: uniprot_50-80;* | | |
| | 2: uniprot_trembl;* | | |
| Pred. | No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | | |
| Result No. | Score | Query Length | DB ID |
| 1 | 50 | 56.2 | 441 |
| 2 | 49 | 55.1 | 208 |
| 3 | 49 | 55.1 | 405 |
| 4 | 49 | 55.1 | 779 |
| 5 | 48 | 53.9 | 217 |
| 6 | 48 | 53.9 | 262 |
| 7 | 48 | 53.9 | 426 |
| 8 | 48 | 53.9 | 448 |
| 9 | 48 | 53.9 | 775 |
| 10 | 48 | 53.9 | 874 |
| 11 | 48 | 53.9 | 793 |
| 12 | 48 | 53.9 | 804 |
| 13 | 47.5 | 53.4 | 527 |
| 14 | 47 | 52.8 | 61 |
| 15 | 47 | 52.8 | 364 |
| 16 | 47 | 52.8 | 369 |
| 17 | 47 | 52.8 | 375 |
| 18 | 47 | 52.8 | 471 |
| 19 | 47 | 52.8 | 1517 |
| 20 | 47 | 52.8 | 1547 |
| 21 | 47 | 52.8 | 1547 |
| 22 | 46 | 51.7 | 214 |
| 23 | 46 | 51.7 | 350 |
| 24 | 46 | 51.7 | 350 |
| 25 | 46 | 51.7 | 373 |
| 26 | 46 | 51.7 | 396 |
| 27 | 46 | 51.7 | 1562 |
| 28 | 45.5 | 51.1 | 266 |
| 29 | 45.5 | 51.1 | 298 |
| 30 | 45.5 | 50.6 | 91 |
| 31 | 45 | 50.6 | 141 |
| Result | Score | Query | RN |
| No. | | Length | ID |
| | | DB | Description |
| | | | |
| 1 | 50 | 56.2 | 2 QSIQ90_SILPO |
| 2 | 49 | 55.1 | 2 QSIQ90_NOCFA |
| 3 | 49 | 55.1 | 2 QSIQ90_SYNTP6 |
| 4 | 49 | 55.1 | 2 QSIQ90_FREIDI |
| 5 | 48 | 53.9 | 2 QTVJ3U3_PROMM |
| 6 | 48 | 53.9 | 2 QBEJF99_SHEON |
| 7 | 48 | 53.9 | 2 QSS550_CRYNE |
| 8 | 48 | 53.9 | 2 QSI423_SALEN |
| 9 | 48 | 53.9 | 2 QF9SA1_CANAL |
| 10 | 48 | 53.9 | 2 Q8EM13_STRGL |
| 11 | 48 | 53.9 | 2 Q9S70_CANAL |
| 12 | 48 | 53.9 | 2 Q8Z90_SALTY |
| 13 | 47.5 | 53.4 | 2 Q6ZD22_ORYSA |
| 14 | 47 | 52.8 | 2 Q6HZB_HUMAN |
| 15 | 47 | 52.8 | 2 Q7UG34_RHOB |
| 16 | 47 | 52.8 | 2 Q5KDM7_CRYNE |
| 17 | 47 | 52.8 | 2 Q5SB2_CRYNE |
| 18 | 47 | 52.8 | 2 Q4TPV5_9SPHN |
| 19 | 47 | 52.8 | 2 Q5AXP9_EMENT |
| 20 | 47 | 52.8 | 2 Q5CIA0_ASPPFU |
| 21 | 47 | 52.8 | 2 Q4WD4_ASPPFU |
| 22 | 46 | 51.7 | 2 Q4XK96_CORJK |
| 23 | 46 | 51.7 | 1 COST_PSSM |
| 24 | 46 | 51.7 | 1 Q6C182_YARLI |
| 25 | 46 | 51.7 | 2 Q50899_PYRHO |
| 26 | 46 | 51.7 | 2 Q7QGM6_CHLURB |
| 27 | 46 | 51.7 | 2 Q9Y840_MYCOBAC |
| 28 | 45.5 | 51.1 | 2 Q7D2MB_AGRITS |
| 29 | 45.5 | 51.1 | 2 Q8T680_AGRITS |
| 30 | 45.5 | 50.6 | 2 Q854E3_SCALD |
| 31 | 45 | 50.6 | 2 Q9NU66_SCALD |
| Result | Score | Match | RN |
| No. | | Length | ID |
| | | DB | Description |
| | | | |
| 1 | 50 | 56.2 | 2 QSIQ90_SILPO |
| 2 | 49 | 55.1 | 2 QSIQ90_NOCFA |
| 3 | 49 | 55.1 | 2 QSIQ90_SYNTP6 |
| 4 | 49 | 55.1 | 2 QSIQ90_FREIDI |
| 5 | 48 | 53.9 | 2 QTVJ3U3_PROMM |
| 6 | 48 | 53.9 | 2 QBEJF99_SHEON |
| 7 | 48 | 53.9 | 2 QSS550_CRYNE |
| 8 | 48 | 53.9 | 2 QSI423_SALEN |
| 9 | 48 | 53.9 | 2 QF9SA1_CANAL |
| 10 | 48 | 53.9 | 2 Q8EM13_STRGL |
| 11 | 48 | 53.9 | 2 Q9S70_CANAL |
| 12 | 48 | 53.9 | 2 Q8Z90_SALTY |
| 13 | 47.5 | 53.4 | 2 Q6ZD22_ORYSA |
| 14 | 47 | 52.8 | 2 Q6HZB_HUMAN |
| 15 | 47 | 52.8 | 2 Q7UG34_RHOB |
| 16 | 47 | 52.8 | 2 Q5KDM7_CRYNE |
| 17 | 47 | 52.8 | 2 Q5SB2_CRYNE |
| 18 | 47 | 52.8 | 2 Q4TPV5_9SPHN |
| 19 | 47 | 52.8 | 2 Q5AXP9_EMENT |
| 20 | 47 | 52.8 | 2 Q5CIA0_ASPPFU |
| 21 | 47 | 52.8 | 2 Q4WD4_ASPPFU |
| 22 | 46 | 51.7 | 2 Q4XK96_CORJK |
| 23 | 46 | 51.7 | 1 COST_PSSM |
| 24 | 46 | 51.7 | 1 Q6C182_YARLI |
| 25 | 46 | 51.7 | 2 Q50899_PYRHO |
| 26 | 46 | 51.7 | 2 Q7QGM6_CHLURB |
| 27 | 46 | 51.7 | 2 Q9Y840_MYCOBAC |
| 28 | 45.5 | 51.1 | 2 Q7D2MB_AGRITS |
| 29 | 45.5 | 51.1 | 2 Q8T680_AGRITS |
| 30 | 45.5 | 50.6 | 2 Q854E3_SCALD |
| 31 | 45 | 50.6 | 2 Q9NU66_SCALD |
| RESULT | Score | Match | RN |
| 1 | 50 | 56.2 | 2 QSIQ90_SILPO |
| 2 | 49 | 55.1 | 2 QSIQ90_NOCFA |
| 3 | 49 | 55.1 | 2 QSIQ90_SYNTP6 |
| 4 | 49 | 55.1 | 2 QSIQ90_FREIDI |
| 5 | 48 | 53.9 | 2 QTVJ3U3_PROMM |
| 6 | 48 | 53.9 | 2 QBEJF99_SHEON |
| 7 | 48 | 53.9 | 2 QSS550_CRYNE |
| 8 | 48 | 53.9 | 2 QSI423_SALEN |
| 9 | 48 | 53.9 | 2 QF9SA1_CANAL |
| 10 | 48 | 53.9 | 2 Q8EM13_STRGL |
| 11 | 48 | 53.9 | 2 Q9S70_CANAL |
| 12 | 48 | 53.9 | 2 Q8Z90_SALTY |
| 13 | 47.5 | 53.4 | 2 Q6ZD22_ORYSA |
| 14 | 47 | 52.8 | 2 Q6HZB_HUMAN |
| 15 | 47 | 52.8 | 2 Q7UG34_RHOB |
| 16 | 47 | 52.8 | 2 Q5KDM7_CRYNE |
| 17 | 47 | 52.8 | 2 Q5SB2_CRYNE |
| 18 | 47 | 52.8 | 2 Q4TPV5_9SPHN |
| 19 | 47 | 52.8 | 2 Q5AXP9_EMENT |
| 20 | 47 | 52.8 | 2 Q5CIA0_ASPPFU |
| 21 | 47 | 52.8 | 2 Q4WD4_ASPPFU |
| 22 | 46 | 51.7 | 2 Q4XK96_CORJK |
| 23 | 46 | 51.7 | 1 COST_PSSM |
| 24 | 46 | 51.7 | 1 Q6C182_YARLI |
| 25 | 46 | 51.7 | 2 Q50899_PYRHO |
| 26 | 46 | 51.7 | 2 Q7QGM6_CHLURB |
| 27 | 46 | 51.7 | 2 Q9Y840_MYCOBAC |
| 28 | 45.5 | 51.1 | 2 Q7D2MB_AGRITS |
| 29 | 45.5 | 51.1 | 2 Q8T680_AGRITS |
| 30 | 45.5 | 50.6 | 2 Q854E3_SCALD |
| 31 | 45 | 50.6 | 2 Q9NU66_SCALD |
| RESULT | Score | Match | RN |
| 1 | 50 | 56.2 | 2 QSIQ90_SILPO |
| 2 | 49 | 55.1 | 2 QSIQ90_NOCFA |
| 3 | 49 | 55.1 | 2 QSIQ90_SYNTP6 |
| 4 | 49 | 55.1 | 2 QSIQ90_FREIDI |
| 5 | 48 | 53.9 | 2 QTVJ3U3_PROMM |
| 6 | 48 | 53.9 | 2 QBEJF99_SHEON |
| 7 | 48 | 53.9 | 2 QSS550_CRYNE |
| 8 | 48 | 53.9 | 2 QSI423_SALEN |
| 9 | 48 | 53.9 | 2 QF9SA1_CANAL |
| 10 | 48 | 53.9 | 2 Q8EM13_STRGL |
| 11 | 48 | 53.9 | 2 Q9S70_CANAL |
| 12 | 48 | 53.9 | 2 Q8Z90_SALTY |
| 13 | 47.5 | 53.4 | 2 Q6ZD22_ORYSA |
| 14 | 47 | 52.8 | 2 Q6HZB_HUMAN |
| 15 | 47 | 52.8 | 2 Q7UG34_RHOB |
| 16 | 47 | 52.8 | 2 Q5KDM7_CRYNE |
| 17 | 47 | 52.8 | 2 Q5SB2_CRYNE |
| 18 | 47 | 52.8 | 2 Q4TPV5_9SPHN |
| 19 | 47 | 52.8 | 2 Q5AXP9_EMENT |
| 20 | 47 | 52.8 | 2 Q5CIA0_ASPPFU |
| 21 | 47 | 52.8 | 2 Q4WD4_ASPPFU |
| 22 | 46 | 51.7 | 2 Q4XK96_CORJK |
| 23 | 46 | 51.7 | 1 COST_PSSM |
| 24 | 46 | 51.7 | 1 Q6C182_YARLI |
| 25 | 46 | 51.7 | 2 Q50899_PYRHO |
| 26 | 46 | 51.7 | 2 Q7QGM6_CHLURB |
| 27 | 46 | 51.7 | 2 Q9Y840_MYCOBAC |
| 28 | 45.5 | 51.1 | 2 Q7D2MB_AGRITS |
| 29 | 45.5 | 51.1 | 2 Q8T680_AGRITS |
| 30 | 45.5 | 50.6 | 2 Q854E3_SCALD |
| 31 | 45 | 50.6 | 2 Q9NU66_SCALD |

OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;
 OC Corynebacterineae; Nocardiaceae; Nocardia.
 OX NCBI_TaxID:37329;
 RN [1] NUCLEOTIDE SEQUENCE.
 RP STRAIN=IFM 10152;
 RX PubMed=15666710; DOI=10.1073/pnas.0406410101;
 RA Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
 RT Shiba T., Hattori M.;
 "The complete genomic sequence of *Nocardioides farcinica* IFM 10152.";
 PROC. NATL. ACAD. SCI. U.S.A. 101:4925-4930(2004).
 RRL EMBL; AP006118; BAD09655; 1.; Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 208 AA; 22565 MW; EBE3243D9B52094E CRC64;

Query Match 55.1%; Score 49; DB 2; Length 208;
 Best Local Similarity 46.7%; Pred. No. 16;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPDWLWGDGRALDV 15
 Db 111 DEDWVYVNLNRSDIV 125

RESULT 3
 QSN4J9 SYNTP6 PRELIMINARY; PRT; 405 AA.
 ID 05N4J9 SYNTP6 PRELIMINARY; PRT; 405 AA.
 AC 05N4J9
 DT 01-FEB-2005 (TREMBLrel. 29, Created)
 DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
 DE 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
 DE Sun protein.
 GN Name=sun; OrderedLocusNames=syc0580_d;
 OS Synochococcus sp. (strain PCC 6301)-(*Anacystis nidulans*).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 RN [1] STRATN=PCC6301;

NUCLEOTIDE SEQUENCE.

Sugita M.; "Complete genome structure of the unicellular cyanobacterium *Anacystis nidulans* 6301 (Synochococcus sp. PCC6301)." Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 EMBL; AP008231; BAD0770_1.; -; Genomic DNA.
 DR GO; GO:0006364; RNA processing; IEA.
 DR IPR004573; Fmu_mifrase.
 DR InterPro; IPR001678; Fmu_NOL1 NOP2P.
 DR InterPro; IPR006027; NubB_RmbB TIM44.
 DR InterPro; IPR00174; RmbB_mifrase.
 DR InterPro; IPR000051; SAM Bind.
 DR Pfam; PF00189; Nub1_Nop2_Fmu; 1.
 DR Pfam; PF0029; NubB; 1.
 DR ProDom; PDO05242; NubB region; 1.
 DR TIGRFams; TIGR00563; rmbB; 1.
 KW Complete proteome.
 SQ SEQUENCE 405 AA; 44708 MW; 89F6C51BB86590C4 CRC64;

Query Match 55.1%; Score 49; DB 2; Length 405;
 Best Local Similarity 66.7%; Pred. No. 31;
 Matches 10; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 2 PDWLWGDGRALD 14
 Db 110 PDWLWGDGRALD 124

RESULT 4
 O6H084 FREDI PRELIMINARY; PRT; 779 AA.
 ID O6H084_FREDI PRELIMINARY; PRT; 779 AA.
 AC O6H084; 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DR Hypothetical protein (Fragment).
 OS *Premyella* diplophon (*Calothrix* PCC 7601).
 OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae.
 RN NCBI_TaxID:1577;
 RN [1] NUCLEOTIDE SEQUENCE.
 RP STRAIN=FD33;
 RC Stowe-Evans B. L., Ford J., Kehoe D.M.;
 "Genomic DNA Microarray Analysis: Identification of New Genes Regulated by Light Color in the Cyanobacterium *Premyella* diplophon";
 J. Bacteriol. 186:4338-4349 (2004).
 J2 [2]
 RN RC STRAIN=FD33;
 RC Stowe-Evans B., Ford J., Kehoe D.M.;
 DR Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY548438; AAC41885.1.; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON_TER 779
 SQ SEQUENCE 779 AA; 85897 MW; 67144DE6B472FOAD CRC64;

Query Match 55.1%; Score 49; DB 2; Length 779;
 Best Local Similarity 77.8%; Pred. No. 60;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EPDWLWGD 9
 Db 422 EPDWLWGD 430

RESULT 5
 QTV3U3 PROMM PRELIMINARY; PRT; 217 AA.
 ID QTV3U3_PROMM PRELIMINARY; PRT; 217 AA.
 AC QTV3U3
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Hypothetical protein precursor.
 GN OrderedLocusNames=PRM2247;
 OS Prochlorococcus marinus (strain MIT 9313).
 OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
 OC Prochlorococcus.
 RN [1] NCBI_TaxID:74547;
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=2282598; PubMed=12917642; DOI=10.1038/nature01947;
 RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
 RA Ahlgren N.A., Arielano A., Coleman M.M., Hauser L., Hess W.R.,
 RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
 RA Shaw S.L., Stoeck C., Sullivan M.B., Ting C.S., Tolonen A.,
 RA Webb E.A., Zinser E.R., Chisholm S.W.;
 RT "Genome divergence in two *Prochlorococcus* ecotypes reflects oceanic niche differentiation.";
 RL Nature 424:1042-1047 (2003).
 DR EMBL; BX72101; CAR22421.1.; -; Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004605; F:phosphatidate cytidylyltransferase activity; IEA.
 DR GO; GO:0008654; P:phospholipid biosynthesis; IEA.
 DR InterPro; IPR00374; PC_trans.
 DR Pfam; PF01148; CTP transf_1; 1.
 KW Complete proteome; Hypothetical protein; Signal.
 FT SIGNAL 1
 SQ SEQUENCE 217 AA; 23832 MW; 522AA449E4033FEC CRC64;

Query Match 53.9%; Score 48; DB 2; Length 217;
 Best Local Similarity 50.0%; Pred. No. 24;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 PDWLWGDGRAL 13
 Db 139 PNWLWGDGRAL 150

| RESULT 6 | | Best Local Similarity 53.3%; Pred. No. 47; Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0; | |
|--|-------------|---|--------------|
| Q8EJF9 | SHRON | Q8EJF9-SHRON PRELIMINARY; | PRT; 262 AA. |
| ID | | | |
| AC | | | |
| DT | 01-MAR-2003 | (T-EMBLrel. 23, Created) | |
| DT | 01-MAR-2003 | (T-EMBLrel. 23, Last sequence update) | |
| DT | 01-MAR-2004 | (T-EMBLrel. 26, Last annotation update) | |
| DE | | Hypothetical protein | |
| GN | | OrderedorlicusNames=SO0508; | |
| OS | | Shewanella oneidensis. | |
| OC | | Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; | |
| CC | | Shewanellaceae; Shewanella. | |
| DR | | NCBI_TaxID=70863; | |
| OX | | [1] | |
| RP | | NUCLEOTIDE SEQUENCE. | |
| RC | | STRAIN=MR_1; | |
| RX | | MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749; | |
| RA | | Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., | |
| RA | | Read T.D., Eisen J.A., Seshadri R., Ward N.L., Meche B.A., | |
| RA | | Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., | |
| RA | | Hart D.H., Kolonay J.P., Madupu R., Peterson J.D., Umayam L.A., | |
| RA | | White O., Wolf A.M., Vamathevan J.J., Impraim M., | |
| RA | | Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J., | |
| RA | | Uterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., | |
| RA | | Venter J.C., Neilson K.H., Fraser C.M., | |
| RT | | "Genome sequence of the dissimilatory metal ion-reducing bacterium | |
| RL | | Shewanella oneidensis," | |
| DR | | Nat. Biotechnol. 20:1118-1123 (2002). | |
| DR | | EMBL; AE015498; AAN53589.1; -; Genomic_DNA. | |
| DR | | TIGR; SO0508; -. | |
| DN | | Complete proteome. | |
| SQ | | SEQUENCE 262 AA; 29556 MW; 5E5B6BF4D52DC44C CRC64; | |
| Query Match 53.9%; Score 48; DB 2; Length 262; Best Local Similarity 61.5%; Pred. No. 29; Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0; | | Qy 2 PWWLWDGRGA 14 | |
| Db | 58 | PDWIAEDRGTDND 70 | |
| RESULT 7 | | Best Local Similarity 53.3%; Pred. No. 47; Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0; | |
| Q55SS0 | CRYNE | Q55SS0-CRYNE PRELIMINARY; | PRT; 426 AA. |
| ID | | | |
| AC | | | |
| DT | 13-SEP-2005 | (TREMBREL 31, Created) | |
| DT | 13-SEP-2005 | (TREMBREL 31, Last sequence update) | |
| DT | 13-SEP-2005 | (TREMBREL 31, Last annotation update) | |
| DE | | Hypothetical protein. | |
| GN | | ORFNames=CMB1140; | |
| OS | | Cryptococcus neoformans var. neoformans B-3501A. | |
| OC | | Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; | |
| OC | | Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella. | |
| OC | | NCBI_TaxID=283643; | |
| RN | | [1] | |
| RP | | NUCLEOTIDE SEQUENCE. | |
| RC | | STRAIN=B-3501A; | |
| RA | | Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M., | |
| RA | | Wickes B.L., Fu J., Davis R.W.; | |
| RT | | "Cryptococcus neoformans serotype D sequencing," | |
| RT | | Submitted (TUL-2004) to the EMBL/GenBank/DDBJ databases. | |
| CC | | -,-, CANTON: The sequence shown here is derived from an preliminary data. | |
| CC | | EMLB/GenBank/DDBJ whole genome shotgun (WGS) entry which is | |
| DR | | EMBL; AB0100024; BA120751.1; -; Genomic_DNA. | |
| KW | | Hypothetical protein. | |
| SQ | | SEQUENCE 426 AA; 47024 MW; A0F8D1F268A28310 CRC64; | |
| Query Match 53.9%; Score 48; DB 2; Length 426; | | Qy 1 EBDWLWIG 8 | |
| Db | 408 | EVDWRLWG 415 | |
| RESULT 8 | | Best Local Similarity 53.3%; Pred. No. 47; Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0; | |
| Q9S423 | SALEN | Q9S423-SALEN PRELIMINARY; | PRT; 448 AA. |
| ID | | | |
| AC | | | |
| DT | 01-MAY-2000 | (TREMBREL 13, Created) | |
| DT | 01-MAY-2000 | (TREMBREL 13, Last sequence update) | |
| DT | 01-OCT-2003 | (TREMBREL 25, Last annotation update) | |
| DE | | Hypothetical protein (Fragment). | |
| GN | | Salmonella enteritidis. | |
| OC | | Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; | |
| OC | | Enterobacteriaceae; Salmonella. | |
| OX | | NCBI_TaxID=592; | |
| RN | | [1] | |
| RP | | NUCLEOTIDE SEQUENCE. | |
| RC | | STRAIN=S1400; | |
| RX | | MEDLINE=93377131; PubMed=10447889; | |
| RA | | Pattrey T., Hernándezsteens J.-P., De Greve H., | |
| RA | | "Identification and molecular characterization of a novel Salmonella | |
| RA | | enteritidis pathogenicity island encoding an ABC transporter."; | |
| RA | | Mol. Microbiol. 33:91-805 (1999). | |
| DR | | EMBL; AP012556; AABD1877.1; -; Genomic_DNA. | |
| DR | | GO; GO_006201; Cimembrane; IEA. | |
| DR | | InterPro; IPR003838; DUF214. | |
| DR | | Pfam; PF02687; FtBX; 1. | |
| KW | | Hypothetical protein. | |
| PT | | NON_TER 1. | |
| SQ | | SEQUENCE 448 AA; 49706 MW; 389077E50235C42A CRC64; | |
| Query Match 53.9%; Score 48; DB 2; Length 448; Best Local Similarity 87.5%; Pred. No. 49; Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | | Qy 1 EBDWLWIG 8 | |
| Db | 408 | EVDWRLWG 415 | |
| RESULT 9 | | Best Local Similarity 53.3%; Pred. No. 47; Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0; | |
| Q9S411 | CANAL | Q9S411-CANAL PRELIMINARY; | PRT; 775 AA. |
| ID | | | |
| AC | | | |
| DT | 10-MAY-2005 | (TREMBREL 30, Created) | |
| DT | 10-MAY-2005 | (TREMBREL 30, Last sequence update) | |
| DT | 10-MAY-2005 | (TREMBREL 30, Last annotation update) | |
| DE | | Hypothetical protein. | |
| GN | | ORFNames=G019_10974; | |
| OS | | Candida albicans SC3314. | |
| OC | | Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; | |
| OC | | Saccharomycetales; mitosporic Saccharomycetales; Candida. | |
| OC | | NCBI_TaxID=237561; | |
| RN | | [1] | |
| RP | | NUCLEOTIDE SEQUENCE. | |
| RC | | STRAIN=SC5314; | |
| RX | | PubMed=15123810; DOI=10.1073/pnas.0401648101; | |
| RA | | Jones T., Pedersen N.A., Chibana H., Dungan J., Kalman S.,' P.T., | |
| RA | | Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T., | |
| RA | | Davis R.W., Scherer S.; | |
| RA | | "The diploid genome sequence of Candida albicans," | |
| RA | | Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004). | |
| RN | | [2] | |
| RP | | NUCLEOTIDE SEQUENCE. | |
| RC | | STRAIN=SC5314; | |
| RA | | Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O., | |
| RA | | Roberts J., Person K., Donnelly S., Favoretto S., Tzeng K.-W., | |
| RA | | Jones T., Scherer S., Agabian N.; | |
| Query Match | | 53.9%; Score 48; DB 2; Length 426; | |

RT "Annotation of the Genome of *Candida albicans*.";
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -I- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR AAC001000154; RAK93359; 1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ **SEQUENCE** 775 AA; 88474 MW; 685118C6B2C914A8 CRC64;
Best Local Similarity 54.5%; **Pred.** No. 86;
Matches 6; **Conservative** 3; **Mismatches** 2; **Indels** 0; **Gaps** 0;
RESULT 10
 QY 2 PDWLWGDRGGA 12
 ID :|||:|||:
 Db 718 PEWAVWGSQGA 728

RESULT 10
 Q8GMJ3 STRQL
 ID Q8GMJ3 STRQL PRELIMINARY; PRT; 784 AA.
 AC :|||:
 CC 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DB UVa-like drug resistance pump.
 OS Streptomyces globisporus.
 OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1908;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C-027;
 RX MEDLINE=22171413; PubMed=12183628; DOI=10.1126/science.1072110;
 RA Liu W., Christensen S.D., Standage S., Shen B.;
 RT "Biogenesis of the enediyne antitumor antibiotic C-1027.";
 RL Science 297:1170-1173 (2002).
 CC -I- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; AY08670; AL06654; 1; -; Genomic_DNA.
 GO; GO:0016020; C:membrane; IAA.
 DR GO; GO:00552; F:ATP binding; IAA.
 GO; GO:005887; F:ATPase activity; IAA.
 DR GO; GO:0016787; F:hydrolase activity; IAA.
 DR GO; GO:0006810; F:transport; IER.
 DR InterPro; IPR003439; ABC_tran; 2.
 DR Pfam; PF00005; ABC_tran; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS5083; ABC_TRANSPORTER_2; 2.
 DR ATP-binding; Membrane; Nucleoside-binding; Transport.
 KW SEQUENCE 784 AA; 83960 MW; DABC2D965720A5E7 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 784;
Best Local Similarity 53.8%; **Pred.** No. 87;
Matches 7; **Conservative** 1; **Mismatches** 5; **Indels** 0; **Gaps** 0;
RESULT 11
 QY 2 PDWLWGDRGALD 14
 ID |||| :|||:
 Db 204 PDWQIWAKSGHLD 216

RESULT 11
 Q5S700 CANAL
 ID Q5S700_CANAL PRELIMINARY; PRT; 793 AA.
 AC :|||:
 CC 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN ORFNAMES=FA019_3470;
 OS Candida albicans SC3314.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=237561;

RESULT 12
 Q8ZR90 SALTY
 ID Q8ZR90 SALTY PRELIMINARY; PRT; 804 AA.
 AC :|||:
 CC 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Putative inner membrane protein.
 GN Name=YBBP; Order=LocName=STM0508;
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=L02;
 RX MEDLINE=21534948; PubMed=1677609; DOI=10.1038/35101614;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Lettreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., MuirVancey E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoecking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 LT2.";
 RL Nature 413:859-856 (2001).
 DR EMBL; AE008719; RALL19462; 1; -; Genomic_DNA.
 GO; GO:0016020; C:membrane; IAA.
 DR InterPro; IPR003838; DUF214.
 DR Pfam; PF02687; FtBX; 2.
 KW Complete proteome.
 SQ **SEQUENCE** 804 AA; 88772 MW; 72A29069A7021F11 CRC64;
Best Local Similarity 53.9%; **Pred.** No. 89;
Matches 7; **Conservative** 0; **Mismatches** 1; **Indels** 0; **Gaps** 0;
 QY 1 EPDWLWG 8
 DB 764 EPDWLWG 771

RESULT 13
 Q6ZD22 ORYSA PRELIMINARY; PRT; 527 AA.
 AC 06ZD22-
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE Hypothetical protein P050RH12.22.
 GN Name=P050RH12.22;
 OS Oryza sativa [japonica cultivar-group].
 OC Bokaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartideae; Oryzeae; Oryza.
 OX NCBI_TaxId=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare" genomic DNA, chromosome 7, PAC
 clone P050RH12;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AP014338; BAC8311.1.; Genomic_DNA.
 DR Gramene; Q6ZD22; -
 DR GO:GO:000519; F: endonuclease activity; IEA.
 DR GO:GO:0016787; F: hydrolase activity; IEA.
 DR InterPro; IPR004843; M-peptidase.
 DR Pfam; PF00149; Metallophos; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 527 AA; 61478 MW; 2658E1451BC92EB6 CRC64;
 Query Match 53.4%; Score 47.5; DB 2; Length 527;
 Best Local Similarity 50.0%; Pred. No. 70; Gaps 1;
 Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 1;
 Qy 1 EDWIL--WGRGALDV 15
 Db 86 EPNWLLDQWGDKGTVN 103

RESULT 14
 Q6JHZC HUMAN
 ID Q6JHZC_HUMAN PRELIMINARY; PRT; 61 AA.
 AC 06JHZC-
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE HCV-E2 binding protein 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Zhang J., Cheng J., Wang L., Shao Q., Lu Y., Chen T., Hong Y.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY459390; AAC22351.; mRNA.
 SQ SEQUENCE 61 AA; 6607 MW; 4E162AA344AE7A56 CRC64;
 Query Match 52.8%; Score 47; DB 2; Length 61;
 Best Local Similarity 87.5%; Pred. No. 9.3; Gaps 0;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 WLJLGDRG 11
 Db 46 WLLWGSRG 53

RESULT 15
 OTUG34 RH0BA PRELIMINARY; PRT; 364 AA.
 ID OTUG34_RH0BA PRELIMINARY;
 AC Q7UG34;

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Om protein - protein search, using sw model

Run on: December 4, 2005, 03:59:51 ; Search time 32.1875 Seconds
(without alignments)
38.528 Million cell updates/sec

Title: US-10-632-706-197
Perfect score: 89
Sequence: 1 EPPDMLWGDRCALDV 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgn2_6/pctodata/1/iaa/5_COMB.pep:
 2: /cgn2_6/pctodata/1/iaa/6_COMB.pep:
 3: /cgn2_6/pctodata/1/iaa/H_COMB.pep:
 4: /cgn2_6/pctodata/1/iaa/PCTUS_COMB.pep:
 5: /cgn2_6/pctodata/1/iaa/RE_COMB.pep:
 6: /cgn2_6/pctodata/1/iaa/backfilest.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score or the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|------------------------|
| 1 | 48 | 53.9 | 229 | 2 US-10-489-039A-12532 |
| 2 | 45 | 50.6 | 614 | 2 US-03-543-681A-7066 |
| 3 | 49.4 | 50.6 | 2 | US-03-248-196A-22630 |
| 4 | 43 | 48.3 | 345 | 2 US-10-303-5180-194 |
| 5 | 43 | 48.3 | 363 | 2 US-03-303-518D-196 |
| 6 | 43 | 48.3 | 638 | 2 US-03-949-16-9984 |
| 7 | 43 | 48.3 | 732 | 2 US-03-902-540-13627 |
| 8 | 42.5 | 47.2 | 320 | 2 US-03-252-991A-18301 |
| 9 | 42 | 47.2 | 174 | 2 US-03-854-133-426 |
| 10 | 42 | 47.2 | 388 | 1 US-03-290-448A-80 |
| 11 | 42 | 47.2 | 1 | US-03-290-448A-80 |
| 12 | 42 | 47.2 | 388 | 1 US-03-175-069A-80 |
| 13 | 42 | 47.2 | 388 | 2 US-03-461-939B-80 |
| 14 | 42 | 47.2 | 368 | 2 US-03-464-000-80 |
| 15 | 42 | 47.2 | 493 | 2 US-03-489-039A-12903 |
| 16 | 41 | 46.1 | 588 | 4 PCT-US95-13749-4 |
| 17 | 41 | 46.1 | 611 | 2 US-03-543-681A-7786 |
| 18 | 41 | 46.1 | 884 | 2 US-03-248-196A-20574 |
| 19 | 40.5 | 45.5 | 488 | 2 US-03-311-731A-29 |
| 20 | 40 | 44.9 | 392 | 2 US-03-252-991A-2798 |
| 21 | 44.9 | 49.7 | 2 | US-03-489-039A-12027 |
| 22 | 40 | 44.9 | 576 | 2 US-03-367-206-1 |
| 23 | 40 | 44.9 | 576 | 2 US-03-367-206-21 |
| 24 | 40 | 44.9 | 576 | 2 US-03-367-206-22 |
| 25 | 40 | 44.9 | 576 | 2 US-03-367-206-23 |
| 26 | 40 | 44.9 | 576 | 2 US-03-298-404-1 |
| 27 | 44.9 | 576 | 2 | US-03-298-404-21 |

RESULT 1
US-09-489-039A-12532
Sequence 12532, Application US/09489039A
; Patent No. 6610836

; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; TITLE OF INVENTION: PNEUMONIAES FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709-2004001
 ; CURRENT APPLICATION NUMBER: US/09/489, 039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIORITY APPLICATION NUMBER: US 60/117, 747
 ; PRIORITY FILING DATE: 1999-01-29
 ; SEQ ID NO: 14342
 ; LENGTH: 229
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-12532

Query Match Similarity 53.9%; Score 48; DB 2; Length 229;
Best Local Similarity 57.1%; Pred. No. 7.8; Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EPPDMLWGDRCALDV 14
Db 32 ERSWCKNGDRFAID 45

RESULT 2
US-09-543-681A-7066
Sequence 7066, Application US/09543681A
; Sequence 7066, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709-1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543, 681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIORITY APPLICATION NUMBER: US 60/128, 706
 ; PRIORITY FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO 7066
 ; LENGTH: 614
 ; TYPE: PRT
 ; ORGANISM: Proteus mirabilis
 US-09-543-681A-7066

Query Match 50.6%; Score 45; DB 2; Length 614;

Best Local Similarity 64.3%; Pred. No. 66; Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EPDWLWGDGRALD 14
Db 452 EDGWLWGDGRALD 465

RESULT 3
US-03-248-796A-22630
; Sequence 22630, Application US/03248796A.
; Patent No. 6747137

GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-132
CURRENT APPLICATION NUMBER: US/09/248-796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 28208

Qy ;
Db ;
LENGTH: 80
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22630

Query Match 49.4%; Score 44; DB 2; Length 80;
Best Local Similarity 54.5%; Pred. No. 10; Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PDWLWGDGRGA 12
Db 12 PDWAWGSQWA 22

RESULT 4
US-03-303-518D-194
; Sequence 194, Application US/09303518D
; Patent No. 6314131

GENERAL INFORMATION:
APPLICANT: Scariato, Vincenzo
APPLICANT: Masiagnani, Vega
APPLICANT: Rappoli, Rino
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido

APPLICANT: Grandi, Guido
TITLE OF INVENTION: Neisserial Antigens
FILE REFERENCE: CHIRO160

CURRENT APPLICATION NUMBER: US/09/303,518D
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 196

Qy ;
Db ;
LENGTH: 383
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-303-518D-196

Query Match 48.3%; Score 43; DB 2; Length 383;
Best Local Similarity 70.0%; Pred. No. 72; Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PDWLWGDGR 11
Db 183 PBWLWFGYRG 192

RESULT 5
US-09-303-518D-196
; Sequence 196, Application US/09303518D

Query Match 48.3%; Score 43; DB 2; Length 638;
Best Local Similarity 85.7%; Pred. No. 1.4e+02; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPDWLW 7
Db 558 EPDWLW 564

RESULT 7
US-09-902-540-13627
; Sequence 13627, Application US/09902540
; Patent No. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkie, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B

RESULT 8
Query Match 48.3%; Score 43; DB 2; Length 732;
Best Local Similarity 63.6%; Pred. No. 1.2e+02; DB 7;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
SEQ ID NO 13627
LENGTH: 732
TYPE: PRT
ORGANISM: *Myxococcus xanthus*
US-09-902-540-13627

RESULT 9
Query Match 47.8%; Score 42.5; DB 2; Length 320;
Best Local Similarity 66.7%; Pred. No. 79; DB 10;
Matches 10; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
SEQ ID NO 18301
LENGTH: 320
TYPE: PRT
ORGANISM: *Pseudomonas aeruginosa*
US-09-252-991A-18301

RESULT 10
Query Match 47.2%; Score 42; DB 2; Length 174;
Best Local Similarity 70.0%; Pred. No. 49; DB 7;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
SEQ ID NO 5676954
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADRESSEE: LATHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,448A
FILING DATE: August 15, 1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: March 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Manatragoras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-854-133-426

RESULT 11
Query Match 47.2%; Score 42; DB 1; Length 388;
Best Local Similarity 46.7%; Pred. No. 1.2e+02; DB 7;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
SEQ ID NO 426
LENGTH: 174
TYPE: PRT
ORGANISM: *Homo sapiens*
US-09-854-133-426

RESULT 12
Query Match 47.2%; Score 42; DB 1; Length 174;
Best Local Similarity 70.0%; Pred. No. 49; DB 7;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
SEQ ID NO 124
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
US-08-290-448A-80

RESULT 13
Query Match 47.2%; Score 42; DB 1; Length 388;
Best Local Similarity 46.7%; Pred. No. 1.2e+02; DB 7;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
SEQ ID NO 323
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
US-08-290-448A-80

APPLICANT: KUO, Mei-chang
 TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
 NUMBER OF SEQUENCES: 93
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/290,448A
 FILING DATE: August 15, 1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/529, 951
 FILING DATE: May 29, 1990
 APPLICATION NUMBER: US 07/325, 365
 FILING DATE: March 17, 1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragoras
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IMI-018CN
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)227-5941
 INFORMATION FOR SEQ ID NO: 80:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 388 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-175-069A-80

Query Match 47.2%; Score 42; DB 1; length 388;
 Best Local Similarity 46.7%; Pred. No. 1.2e+02;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 EPDWLWGDGGALDV 15
 Db 323 EPENNTWNWRQNDV 337

RESULT 12
 US-08-175-069A-80
 Sequence 80, Application US/08175069A
 Patent No. 577671
 GENERAL INFORMATION:
 APPLICANT: Rogers, Bruce
 APPLICANT: Klapper, David G.
 APPLICANT: Rafnar, Thorunn
 APPLICANT: KUO, Mei-chang
 TITLE OF INVENTION: Methods For Treating Sensitivity To A
 TITER OF INVENTION: Protein Allergen Using Peptides Which Include A T Cell Epitope
 NUMBER OF SEQUENCES: 93
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/461, 939B
 FILING DATE:
 APPLICATION NUMBER: US 08/464, 000
 FILING DATE: 05-JUN-1995
 APPLICATION NUMBER: US 08/290, 448
 FILING DATE: 15-AUG-1994
 APPLICATION NUMBER: US 07/529, 951
 FILING DATE: 29-MAY-1990
 APPLICATION NUMBER: -US 07/325, 365
 FILING DATE: 17-MAR-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragoras
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IMI-018CN
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 80:

US-08-175-069A-80

Query Match 47.2%; Score 42; DB 1; length 388;
 Best Local Similarity 46.7%; Pred. No. 1.2e+02;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 EPDWLWGDGGALDV 15
 Db 323 EPENNTWNWRQNDV 337

RESULT 13
 US-08-461-939B-80
 Sequence 80, Application US/08461939B
 Patent No. 6335019
 GENERAL INFORMATION:
 APPLICANT: Rogers, Bruce
 APPLICANT: Klapper, David G.
 APPLICANT: Rafnar, Thorunn
 APPLICANT: KUO, Mei-chang
 TITLE OF INVENTION: Methods For Treating Sensitivity To A
 TITER OF INVENTION: Protein Allergen Using Peptides Which Include A T Cell Epitope
 NUMBER OF SEQUENCES: 93
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/461, 939B
 FILING DATE:
 APPLICATION NUMBER: US 08/464, 000
 FILING DATE: 05-JUN-1995
 APPLICATION NUMBER: US 08/290, 448
 FILING DATE: 15-AUG-1994
 APPLICATION NUMBER: US 07/529, 951
 FILING DATE: 29-MAY-1990
 APPLICATION NUMBER: -US 07/325, 365
 FILING DATE: 17-MAR-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragoras
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IMI-018CN
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 80:

RESULT 15
; SEQUENCE CHARACTERISTICS:
; LENGTH: 388 amino acids
; TYPE: amino acid
; MOLECULE TYPE: protein
; US-08-461-939B-80

Query Match 47.2%; Score 42; DB 2; Length 388;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPDWLWDRGALDV 15
Db 323 EPENMTNWRQNDV 337

RESULT 14
US-08-464-000-80
; Sequence 80, Application US/08464000
; Patent No. 6335020
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce
; APPLICANT: Klapper, David G.
; APPLICANT: Rafnar, Thorunn
; APPLICANT: Kuo, Mei-chang
; TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,000
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/290,448
; FILING DATE: 15-AUG-1994
; APPLICATION NUMBER: US 07/529,951
; FILING DATE: 29-MAY-1990
; APPLICATION NUMBER: US 07/325,365
; FILING DATE: 17-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REFERENCE/DOCKET NUMBER: IMI-018CN2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 388 amino acids
; TYPE: amino acid
; MOLECULE TYPE: protein
; US-08-464-000-80

Query Match 47.2%; Score 42; DB 2; Length 388;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPDWLWDRGALDV 15
Db 323 EPENMTNWRQNDV 337

RESULT 15
US-09-489-039A-12903
; Sequence 12903, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 1442
; SEQ ID NO 12903
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-12903

Query Match 47.2%; Score 42; DB 2; Length 493;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 WLWLGDRGAL 13
Db 463 WLWCGERGV 472

Search completed: December 4, 2005, 04:09:44
Job time : 33.1875 Secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 4, 2005, 04:07:28 ; Search time 107.5 seconds

(without alignments) 58.302 Million cell updates/sec

Title: US-10-632-706-197

Perfect score: 89

Sequence: 1 EBDWLWGDGALDV 15

Scoring table: BLOSUM62

Gappop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 41729326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : Published Applications AA_Main:*

1: /cgn2_6/ptodata/1/pupbaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pupbaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pupbaa/US10_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pupbaa/US10_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pupbaa/US10_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pupbaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|---|
| 1 | 89 | 100.0 | 15 | 4 US-10-632-706-129 Sequence 129, APP |
| 2 | 89 | 100.0 | 15 | 4 US-10-632-706-130 Sequence 130, APP |
| 3 | 89 | 100.0 | 15 | 4 US-10-632-706-131 Sequence 131, APP |
| 4 | 89 | 100.0 | 15 | 4 US-10-632-706-134 Sequence 194, APP |
| 5 | 89 | 100.0 | 15 | 4 US-10-632-706-134 Sequence 195, APP |
| 6 | 89 | 100.0 | 15 | 4 US-10-632-706-197 Sequence 200, APP |
| 7 | 75 | 84.3 | 15 | 4 US-10-632-706-203 Sequence 203, APP |
| 8 | 51 | 57.3 | 33 | 5 US-10-450-763-50690 Sequence 50690, APP |
| 9 | 48 | 53.9 | 201 | 4 US-10-634-548-27 Sequence 27, APP |
| 10 | 48 | 53.9 | 775 | 4 US-10-159-257A-60 Sequence 160, APP |
| 11 | 47.5 | 53.4 | 992 | 4 US-10-437-963-134365 Sequence 134365, APP |
| 12 | 47 | 52.8 | 455 | 4 US-10-450-563-52883 Sequence 52883, APP |
| 13 | 47 | 52.8 | 904 | 4 US-10-369-493-12420 Sequence 12420, APP |
| 14 | 45 | 50.6 | 159 | 4 US-10-425-115-240160 Sequence 240160, APP |
| 15 | 45 | 50.6 | 372 | 4 US-10-282-122A-68332 Sequence 68332, APP |
| 16 | 44.5 | 50.0 | 203 | 4 US-10-767-701-42189 Sequence 42189, APP |
| 17 | 44.5 | 50.0 | 394 | 4 US-10-425-115-24524 Sequence 424524, APP |
| 18 | 44 | 49.4 | 472 | 4 US-10-017-161-1674 Sequence 1674, APP |
| 19 | 44 | 49.4 | 472 | 4 US-10-292-798-1334 Sequence 1334, APP |
| 20 | 44 | 49.4 | 505 | 4 US-10-437-963-179634 Sequence 179634, APP |
| 21 | 44 | 49.4 | 687 | 4 US-10-369-493-2076 Sequence 20876, APP |
| 22 | 43.5 | 48.9 | 77 | 4 US-10-125-115-268892 Sequence 268892, APP |
| 23 | 43 | 48.3 | 264 | 4 US-10-156-761-11420 Sequence 11420, APP |
| 24 | 43 | 48.3 | 368 | 4 US-10-137-963-115853 Sequence 115853, APP |
| 25 | 43 | 48.3 | 439 | 4 US-10-156-761-11497 Sequence 11497, APP |
| 26 | 43 | 48.3 | 615 | 4 US-10-808-532-8 Sequence 8, APP |
| 27 | 43 | 48.3 | 1975 | 4 US-10-137-963-140079 Sequence 140079, APP |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-10-632-706-129
Sequence 129, Application US/10632706
Publication No. US20040175385A1

GENERAL INFORMATION:

APPLICANT: MARKS, JAMES D.

TITLE OF INVENTION: THERAPEUTIC MONOClonal ANTIBODIES THAT NEUTRALIZE BOTULINUM TOXINS

TITLE OF INVENTION: NEUROTOXINS

FILE REFERENCE: 407T-895120US

CURRENT APPLICATION NUMBER: US/10/632,706

CURRENT FILING DATE: 2003-08-01

CURRENT FILING NUMBER: 2003-08-01

PRIOR APPLICATION NUMBER: US 60/400,721

PRIOR FILING DATE: 2002-08-01

PRIOR FILING NUMBER: US 09/144,806

NUMBER OF SEQ ID NOS: 278

SOFTWARE: Patentin version 3.2

SEQ ID NO 129

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial

FEATURE: OTHER INFORMATION: single chain antibody fragment

US-10-632-706-129

Query Match Score: 100.0%; Score: 89; DB: 4; Length: 15;
Best Local Similarity: 100.0%; Pred. No.: 2.8e-06;
Matches: 15; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Qy Db

1 EBDWLWGDGALDV 15
1 EBDWLWGDGALDV 15

RESULT 2
US-10-632-706-130
Sequence 130, Application US/10632706
Publication No. US20040175385A1

GENERAL INFORMATION:

APPLICANT: MARKS, JAMES D.

APPLICANT: AMERSDORFER, PETER

TITLE OF INVENTION: THERAPEUTIC MONOClonal ANTIBODIES THAT NEUTRALIZE BOTULINUM TOXINS

TITLE OF INVENTION: NEUROTOXINS

FILE REFERENCE: 407T-895120US

CURRENT APPLICATION NUMBER: US/10/632,706

CURRENT FILING DATE: 2003-08-01

CURRENT FILING NUMBER: 2003-08-01

PRIOR APPLICATION NUMBER: US 60/400,721

PRIOR FILING DATE: 2002-08-01

PRIOR FILING NUMBER: US 09/144,806

SEQUENCE 45388, APP
SEQUENCE 922, APP
SEQUENCE 206981, APP
SEQUENCE 45666, APP
SEQUENCE 26, APP
SEQUENCE 426, APP
SEQUENCE 426, APP
SEQUENCE 31629, APP
SEQUENCE 34131, APP
SEQUENCE 3798, APP
SEQUENCE 108592, APP
SEQUENCE 66625, APP
SEQUENCE 50322, APP
SEQUENCE 20944, APP
SEQUENCE 17, APP
SEQUENCE 97, APP

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; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 130
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: single chain antibody fragment
; FEATURE: OTHER INFORMATION: single chain antibody fragment
; US-10-632-706-130

Query Match          100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 EPDWLWLGDRGALDV 15
Db      1 EPDWLWLGDRGALDV 15

RESULT 3
US-10-632-706-131
; Sequence 131, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; ATTORNEY OR AGENT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOClonAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROToXINS
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIORITY APPLICATION NUMBER: US 6/0/400,721
; PRIORITY FILING DATE: 2002-08-01
; PRIORITY APPLICATION NUMBER: US 09/144,806
; PRIORITY FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SEQ ID NO: 131
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: Patentin version 3.2
; FEATURE: OTHER INFORMATION: single chain antibody fragment
; US-10-632-706-131

Query Match          100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 EPDWLWLGDRGALDV 15
Db      1 EPDWLWLGDRGALDV 15

RESULT 4
US-10-632-706-194
; Sequence 194, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; ATTORNEY OR AGENT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOClonAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROToXINS
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIORITY APPLICATION NUMBER: US 6/0/400,721
; PRIORITY FILING DATE: 2002-08-01
; PRIORITY APPLICATION NUMBER: US 09/144,806
; PRIORITY FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SEQ ID NO: 131
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: Patentin version 3.2
; FEATURE: OTHER INFORMATION: single chain antibody fragment
; US-10-632-706-194

Query Match          100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 EPDWLWLGDRGALDV 15
Db      1 EPDWLWLGDRGALDV 15

RESULT 5
US-10-632-706-197
; Sequence 197, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; ATTORNEY OR AGENT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOClonAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROToXINS
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIORITY APPLICATION NUMBER: US 6/0/400,721
; PRIORITY FILING DATE: 2002-08-01
; PRIORITY APPLICATION NUMBER: US 09/144,806
; PRIORITY FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SEQ ID NO: 131
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: Patentin version 3.2
; FEATURE: OTHER INFORMATION: single chain antibody fragment
; US-10-632-706-197

Query Match          100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 EPDWLWLGDRGALDV 15
Db      1 EPDWLWLGDRGALDV 15

RESULT 6
US-10-632-706-200
; Sequence 200, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; ATTORNEY OR AGENT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOClonAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROToXINS
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIORITY APPLICATION NUMBER: US 6/0/400,721
; PRIORITY FILING DATE: 2002-08-01
; PRIORITY APPLICATION NUMBER: US 09/144,806
; PRIORITY FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SEQ ID NO: 200
; LENGTH: 15
; TYPE: PRT

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FEATURE: OTHER INFORMATION: single chain antibody fragment
; OTHER INFORMATION: sodium:neurotransmitter symporter family proteins domain
; OTHER INFORMATION: identified by eMATRIX, accession number B00610D, p-value=2.00e-00
; OTHER INFORMATION: Best Local Similarity 100.0%; Score 89; DB 4; Length 15;
; OTHER INFORMATION: Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; OTHER INFORMATION: Qy 1 EPDWLWGDGALDV 15
; OTHER INFORMATION: Db 1 EPDWLWGDGALDV 15

RESULT 7
US-10-632-706-203
; Sequence 203, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARIS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS
; FILE REFERENCE: 407T-895J20US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-06-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 203
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment

RESULT 8
US-10-632-706-203
; Sequence 203, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARIS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS
; FILE REFERENCE: 407T-895J20US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 203
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment

RESULT 9
US-10-634-548-27
; Sequence 27, Application US/10634548
; Publication No. US20040045051A1
; GENERAL INFORMATION:
; APPLICANT: No. US20040045051A1 is, Susan R
; APPLICANT: Lincoln, Kim
; APPLICANT: Abad, Mark Scott
; APPLICANT: Eilers, Robert
; APPLICANT: Hartcuylker, Karen Kindle
; APPLICANT: Hirshberg, Joseph
; APPLICANT: Karunandaa, Balasuloujini
; APPLICANT: Moshiri, Farhad
; APPLICANT: Stein, Joshua C.
; APPLICANT: Valentin, Henry E.
; APPLICANT: Venkatesh, Tyamagondlu V.
; TITLE OF INVENTION: Tocopherol biosynthesis related genes and used thereof
; FILE REFERENCE: Ren-01-125
; CURRENT APPLICATION NUMBER: US/10/634,548
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: US 60/400,689
; PRIOR FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Prochlorococcus marinus-MT9313

RESULT 10
US-10-159-257A-160
; Sequence 160, Application US/10159257A
; Publication No. US2004016182A1
; GENERAL INFORMATION:
; APPLICANT: SHEN, BEN
; APPLICANT: LIU, WEN
; APPLICANT: CHRISTENSEN, STEVEN D.
; APPLICANT: CHANDRASEKARAN, SCOTT
; TITLE OF INVENTION: GENE CLUSTER FOR PRODUCTION OF THE ENDIENE ANTITUMOR
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Xaa = X or * as defined in Table 2

RESULT 11
US-10-450-763-50690
; Sequence 27, Application US/10450763
; Publication No. US20040045051A1
; GENERAL INFORMATION:
; APPLICANT: No. US20040045051A1 is, Susan R
; APPLICANT: Lincoln, Kim
; APPLICANT: Abad, Mark Scott
; APPLICANT: Eilers, Robert
; APPLICANT: Hartcuylker, Karen Kindle
; APPLICANT: Hirshberg, Joseph
; APPLICANT: Karunandaa, Balasuloujini
; APPLICANT: Moshiri, Farhad
; APPLICANT: Stein, Joshua C.
; APPLICANT: Valentin, Henry E.
; APPLICANT: Venkatesh, Tyamagondlu V.
; TITLE OF INVENTION: Tocopherol biosynthesis related genes and used thereof
; FILE REFERENCE: Ren-01-125
; CURRENT APPLICATION NUMBER: US/10/634,548
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: US 60/400,689
; PRIOR FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Prochlorococcus marinus-MT9313

RESULT 12
US-10-634-548-27
; Sequence 27, Application US/10634548
; Publication No. US20040045051A1
; GENERAL INFORMATION:
; APPLICANT: No. US20040045051A1 is, Susan R
; APPLICANT: Lincoln, Kim
; APPLICANT: Abad, Mark Scott
; APPLICANT: Eilers, Robert
; APPLICANT: Hartcuylker, Karen Kindle
; APPLICANT: Hirshberg, Joseph
; APPLICANT: Karunandaa, Balasuloujini
; APPLICANT: Moshiri, Farhad
; APPLICANT: Stein, Joshua C.
; APPLICANT: Valentin, Henry E.
; APPLICANT: Venkatesh, Tyamagondlu V.
; TITLE OF INVENTION: Tocopherol biosynthesis related genes and used thereof
; FILE REFERENCE: Ren-01-125
; CURRENT APPLICATION NUMBER: US/10/634,548
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: US 60/400,689
; PRIOR FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Xaa = X or * as defined in Table 2

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; TITLE OF INVENTION: ANTIBIOTIC C-107
; FILE REFERENCE: 407T-896020US
; CURRENT APPLICATION NUMBER: US/10/159,257A
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 09/478,188
; PRIOR FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 60/115,434
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO: 160
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Streptomyces globisporus
; FEATURE:
; OTHER INFORMATION: off(-1)
; US-10-159-257A-160

Query Match      53.9%; Score 48; DB 4; Length 775;
Best Local Similarity 53.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy   2 PDWILWGDGALD 14
Db   195 PDWQIWAKSGRLD 207

RESULT 11
US-10-437-963-134365
; Sequence 134365, Application US/10437963
; Publication No. US20040123343A1
GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbezuk, Brad

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO: 134365
LENGTH: 992
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_36146C.1.pep
; US-10-437-963-134365

Query Match      53.4%; Score 47.5; DB 4; Length 992;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 1;
Qy   1 EPPDWL1--KDGDRGALD 15
Db   551 EPNWLWDWYMDKTKGNV 568

RESULT 12
US-10-450-763-52883
; Sequence 52883, Application US/10450763
; Publication No. US20050196754A1
GENERAL INFORMATION:
; APPLICANT: Rysaq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790C13/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11

Query Match      52.8%; Score 47; DB 4; Length 904;
Best Local Similarity 70.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy   4 WLWLGDRGAL 13
Db   460 WLWLGDKTSL 469

RESULT 14
US-10-425-115-240160
; Sequence 240160, Application US/10425115
; Publication No. US20040214272A1
GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115

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CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 369326
 SEQ ID NO: 240160
 LENGTH: 159
 TYPE: PRT
 ORGANISM: Zea mays
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)..(159)
 OTHER INFORMATION: unsure at all Xaa locations

; OTHER INFORMATION: Clone ID: MRT4577_150607C.1.pep
 US-10-425-115-240160

| Query | Match | Score | DB | Length |
|-------|--------------|-------|----|--------|
| Qy | PDWLWGDGRGAL | 50.6% | 4 | 159 |
| Db | PGRLLWGRGAL | 75.0% | 83 | 46 |

Best Local Similarity 75.0%; Pred. No. 83; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Query Match 50.6%; Score 45; DB 4; Length 372;
 Best Local Similarity 70.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Db 221 PDWLWTPAG 230

Search completed: December 4, 2005, 04:37:43
 Job time : 121.5 secs

RESULT 15

US-10-282-122A-68332

; Sequence 68332, Application US/10282122A
 ; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Lianggu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haslbeck, Robert

; APPLICANT: Ohlsen, Karl

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELTRA_034A

CURRENT APPLICATION NUMBER: US/10/282,122A

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 6/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 6/0207,727

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 6/0/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 6/0/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 6/0/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 6/0/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 6/0/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 6/0/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 6/0/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 68332

LENGTH: 372

TYPE: PRT

ORGANISM: Pseudomonas putida

US-10-282-122A-68332

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 4, 2005, 04:08:08 ; Search time 4.375 seconds
 (without alignments)
 16.417 Million cell updates/sec

Title: US-10-632-706-197
 perfect score: 89
 Sequence: 1 EPPWLWDRGALDV 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications All_New,*

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 2: /cggn_2_6/ptodata/1/pubpaal/US06 NEW PUB.PEP.*
 3: /cggn_2_6/ptodata/1/pubpaal/US07 NEW PUB.PEP.*
 4: /cggn_2_6/ptodata/1/pubpaal/US08 NEW PUB.PEP.*
 5: /cggn_2_6/ptodata/1/pubpaal/PCT NEW PUB.PEP.*
 6: /cggn_2_6/ptodata/1/pubpaal/US10 NEW PUB.PEP.*
 7: /cggn_2_6/ptodata/1/pubpaal/US60 NEW PUB.PEP.*
 8: /cggn_2_6/ptodata/1/pubpaal/US61 NEW PUB.PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|--------------------|--------------------|
| 1 | 43 | 48.3 | 383 | US-10-467-557-5602 |
| 2 | 41 | 46.1 | 251 | US-11-054-515-1084 |
| 3 | 40.5 | 45.5 | 125 | US-10-821-234-1277 |
| 4 | 38.5 | 43.3 | 1075 | US-11-174-150-34 |
| 5 | 38.5 | 43.3 | 1114 | US-11-174-150-35 |
| 6 | 38 | 42.7 | 248 | US-11-054-515-1679 |
| 7 | 37 | 42.7 | 251 | US-11-054-515-944 |
| 8 | 37 | 41.6 | 344 | US-10-967-527A-24 |
| 9 | 36 | 40.4 | 225 | US-10-821-234-1116 |
| 10 | 36 | 40.4 | 322 | US-10-467-567-1006 |
| 11 | 36 | 40.4 | 428 | US-10-793-626-484 |
| 12 | 36 | 40.4 | 1857 | US-11-057-058-60 |
| 13 | 36 | 40.4 | 7 | US-11-057-058-61 |
| 14 | 35.5 | 39.9 | 158 | US-10-510-386-128 |
| 15 | 35.5 | 39.9 | 247 | US-10-793-626-1466 |
| 16 | 35.5 | 39.9 | 344 | US-10-821-234-923 |
| 17 | 35.5 | 39.9 | 380 | US-10-624-932-20 |
| 18 | 35 | 39.3 | 239 | US-10-957-569-54 |
| 19 | 35 | 39.3 | 350 | US-10-467-567-5824 |
| 20 | 35 | 39.3 | 401 | US-10-510-386-68 |
| 21 | 35 | 39.3 | 530 | US-10-820-388-62 |
| 22 | 35 | 39.3 | 551 | US-10-793-626-1668 |
| 23 | 34.5 | 38.8 | 1613 | US-11-108-528-84 |
| 24 | 34.5 | 38.8 | 1613 | US-11-108-528-86 |
| 25 | 34.2 | 38.2 | US-11-054-515-1079 | |

ALIGNMENTS

RESULT 1
 US-10-467-557-5602
 ; Sequence 5602, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SPA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabettra
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467-657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIORITY FILING DATE: 2001-02-12
 ; PRIORITY APPLICATION NUMBER: GB-0103424.8
 ; SOFTWARE: SeqWing9, version 1.04
 ; SEQ ID NO: 5602
 ; LENGTH: 383
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-557-5602
 Query Match Score 43; DB 6; Length 383;
 Best Local Similarity 48.3%; Pred. No. 3.8;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PWLWLWDRG 11
 |||||
 181 PWLWLWDRG 190

RESULT 2
 US-11-054-515-1084
 ; Sequence 1084, Application US/11054515
 ; Publication No. US2005025552A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
 ; FILE REFERENCE: P1952P3
 ; CURRENT APPLICATION NUMBER: US/11/054,515
 ; CURRENT FILING DATE: 2005-02-10
 ; PRIOR APPLICATION NUMBER: 60/543,296
 ; PRIOR FILING DATE: 2004-02-11
 ; PRIORITY APPLICATION NUMBER: 60/580,347
 ; PRIORITY FILING DATE: 2004-06-18
 ; PRIORITY APPLICATION NUMBER: 10/293,418
 ; PRIORITY APPLICATION NUMBER: 10/054-515-1079

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; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/195,603
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/199,417
; PRIOR FILING DATE: 2000-04-24
; PCT/US01/11797
; FILE REFERENCE: GP50022
; CURRENT APPLICATION NUMBER: US/11/174,150
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/257,174
; PRIOR FILING DATE: 2002-10-10
; SEQ ID NO: 1084
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-1084

RESULT 3
Query Match 46.1%; Score 41; DB 7; Length 251;
Best Local Similarity 46.2%; Pred. No. 5.1; Mismatches 3; Indels 4; Gaps 0;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 2 PDWLJWGDGRGALD 14
Db 45 PEWMGWNINRGGSDB 57

; US-10-821-234-1277
; Sequence 35, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Staché-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PR SEQ_Genes Version 1.0
; SEQ ID NO: 1277
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-1277

RESULT 3
Query Match 46.1%; Score 40.5; DB 6; Length 125;
Best Local Similarity 63.6%; Pred. No. 3.1; Mismatches 0; Indels 1; Gaps 1;
Matches 7; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
Qy 1 EPDWLJWGDRG 11
Db 101 DPDWLJ-GERG 110

; US-11-174-150-34
; Sequence 34, Application US/11174150
; Publication No. US20050260714A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50022
; CURRENT APPLICATION NUMBER: US/11/174,150
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/257,174
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: PCT/US01/11797
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/196,603
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/199,417
; PRIOR FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 35
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-174-150-35

RESULT 5
Query Match 43.3%; Score 38.5; DB 7; Length 1114;
Best Local Similarity 53.8%; Pred. No. 53; Mismatches 1; Indels 3; Gaps 1;
Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;
Qy 3 DWLWGG--DRGA 12
Db 961 EWSVWMSWYDRGA 973

; US-11-054-515-1679
; Sequence 1679, Application US/11054515
; Publication No. US2005025532A1

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; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BuYS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/275,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO: 1679
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-1679

Query Match Score 38; DB 7; Length 248;
Best Local Similarity 42.7%; Pred. No. 15; Mismatches 6; Conservative 4; Indels 0; Gaps 0;

Qy 1 EPDWLWGDGRGALD 14
Db 44 EPEWNGWINGGSGD 57

RESULT 7

US-11-054-515-944
; Sequence 944, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BuYS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/331,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/275,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO: 1679
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-944

Query Match Score 38; DB 7; Length 251;
Best Local Similarity 42.9%; Pred. No. 15; Mismatches 6; Conservative 4; Indels 0; Gaps 0;

Qy 1 EPDWLWGDGRGALD 14
Db 44 EPEWNGWINGGSGD 57

RESULT 8

US-10-967-527A-24
; Sequence 24, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 24
; LENGTH: 344
; TYPE: PRT
; ORGANISM: mus musculus
; US-10-967-527A-24

Query Match Score 37; DB 6; Length 344;
Best Local Similarity 41.6%; Pred. No. 29; Mismatches 5; Conservative 0; Indels 0; Gaps 0;

Qy 2 PDWLW 7
Db 3 PSWLLW 8

RESULT 9

US-10-821-234-1116
; Sequence 1116, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC SEQ_Sgenes version 1.0
; SEQ ID NO: 1116
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-1116

Query Match Score 36; DB 6; Length 225;

Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 10
US-10-467-657-1006
; Sequence 1006, Application US/10467657
; Publication No. US20050260581A1
GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI ElisaBetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
PRIORITY FILING DATE: 2003-08-11
PRIORITY APPLICATION NUMBER: GB-0103424.8
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 1006
LENGTH: 322
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1006

Query Match 40.4%; Score 36; DB 6; Length 322;
Best Local Similarity 63.6%; Pred. No. 38; Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 PDWLWGDGRGA 12
Db 251 PDWLFWLDRSA 261

RESULT 11
US-10-793-626-484
; Sequence 484, Application US/10793626
; Publication No. US20050255478A1
GENERAL INFORMATION:
; APPLICANT: KIMMELLI, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS SPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIORITY FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 484
LENGTH: 428
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-484

Query Match 40.4%; Score 36; DB 6; Length 428;
Best Local Similarity 62.5%; Pred. No. 50; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 WGDRGALD 14
Db 333 WGDKGKWD 340

RESULT 12
US-11-057-058-60
; Sequence 60, Application US/11057058
; Publication No. US20050244400A1
GENERAL INFORMATION:
; APPLICANT: Maga, John
; TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
FILE REFERENCE: SYM-011
CURRENT APPLICATION NUMBER: US/11/057,058
CURRENT FILING DATE: 2005-02-10
PRIORITY FILING DATE: 2004-02-10
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn version 3.3
SEQ ID NO 60
LENGTH: 1857
TYPE: PRT
ORGANISM: Homo sapiens
US-11-057-058-60

Query Match 40.4%; Score 36; DB 7; Length 1857;
Best Local Similarity 45.5%; Pred. No. 2.1e+02; Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 WLLWGDGRGA 14
Db 1749 WLFWDDGQSID 1759

RESULT 13
US-11-057-058-61
; Sequence 61, Application US/11057058
; Publication No. US20050244400A1
GENERAL INFORMATION:
; APPLICANT: LeBowitz, Jonathan
; APPLICANT: Maga, John
TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
FILE REFERENCE: SYM-011
CURRENT APPLICATION NUMBER: US/11/057,058
CURRENT FILING DATE: 2005-02-10
PRIORITY FILING DATE: 2004-02-10
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn version 3.3
SEQ ID NO 61
LENGTH: 1857
TYPE: PRT
ORGANISM: Homo sapiens
US-11-057-058-61

Query Match 40.4%; Score 36; DB 7; length 1857;
Best Local Similarity 45.5%; Pred. No. 2.1e+02; Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 WLLWGDGRGA 14
Db 1749 WLFWDDGQSID 1759

RESULT 14
US-10-510-386-128
; Sequence 128, Application US/10510386
; Publication No. US20050244922A1
GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjørke
; APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: Improved Bacillus Host Cell
FILE REFERENCE: 10294.201-US
CURRENT APPLICATION NUMBER: US/10/510,386

; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 128
; LENGTH: 158
; TYPE: PRT
; ORGANISM: *Bacillus licheniformis*
US-10-510-386-128

Query Match 39.9%; Score 35.5; DB 6; Length 158;
Best Local Similarity 72.7%; Pred. No. 23; Mismatches 2; Indels 1; Gaps 1;
Matches 8; Conservative 0; Db 65 LWGDDGKLD 75

Qy 5 LWGDDGAL 14

Db 65 LWGDDGKLD 75

RESULT 15

US-10-793-626-1466

; Sequence 1466, Application US/10793626

; Publication No. US200505055478A1

; GENERAL INFORMATION:

; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

; FILE REFERENCE: PUS480US

; CURRENT APPLICATION NUMBER: US/10/793,626

; CURRENT FILING DATE: 2004-03-04

; PRIORITY APPLICATION NUMBER: 60/164,258

; PRIORITY FILING DATE: 1999-11-09

; NUMBER OF SEQ ID NOS: 4472

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1466

; LENGTH: 247

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: amino acid sequence

US-10-793-626-1466

Query Match 39.9%; Score 35.5; DB 6; Length 247;
Best Local Similarity 63.6%; Pred. No. 35; Mismatches 1; Indels 1; Gaps 1;
Matches 7; Conservative 2; Db 186 WMNLWGNVGA 196

Qy 4 WL-LWGDDGAL 13

Db 186 WMNLWGNVGA 196

Search completed: December 4, 2005, 04:37:50
Job time : 5.375 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:09:54 ; Search time 95.5625 Seconds
(without alignment)
50.576 Million cell updates/sec

Title: US-10-632-706-198
Perfect score: 59
Sequence: 1 WGGCTTVTVSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
A_Geneseq_21: *
1: geneseqP1990s: **
2: geneseqP2000s: **
3: geneseqP2000s: **
4: geneseqP2002s: **
5: geneseqP2002s: **
6: geneseqP2003as: **
7: geneseqP2003bs: **
8: geneseqP2004s: **
9: geneseqP2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|---------------------|
| 1 | 59 | 100.0 | 11 2 | AAR85166 |
| 2 | 59 | 100.0 | 11 2 | AAR97333 Humanized |
| 3 | 59 | 100.0 | 11 4 | AAU07452 Synthetic |
| 4 | 59 | 100.0 | 11 5 | AEE28561 scFv anti |
| 5 | 59 | 100.0 | 11 5 | AUT0517 Mouse |
| 6 | 59 | 100.0 | 11 5 | AUT0501 Mouse |
| 7 | 59 | 100.0 | 11 5 | AUT0485 Mouse |
| 8 | 59 | 100.0 | 11 5 | AUT0477 Mouse |
| 9 | 59 | 100.0 | 11 6 | ABO1719 Desimmunis |
| 10 | 59 | 100.0 | 11 6 | ABR1463 Murine J4 |
| 11 | 59 | 100.0 | 11 7 | ABO13904 Anti-GPI- |
| 12 | 59 | 100.0 | 11 7 | ADG75671 Peptide O |
| 13 | 59 | 100.0 | 11 8 | ADH17960 Human mod |
| 14 | 59 | 100.0 | 11 8 | ADH18011 Human mod |
| 15 | 59 | 100.0 | 11 8 | ADQ90791 Artificial |
| 16 | 59 | 100.0 | 11 8 | ADR12645 Mammalian |
| 17 | 59 | 100.0 | 11 8 | ADR18796 Mouse |
| 18 | 59 | 100.0 | 11 8 | ADR18793 Mouse |
| 19 | 59 | 100.0 | 11 8 | ADR18802 Mouse |
| 20 | 59 | 100.0 | 11 8 | ADR18799 Mouse |
| 21 | 59 | 100.0 | 11 8 | ADU8427 Mouse |
| 22 | 59 | 100.0 | 11 8 | ADU67919 Mouse |
| 23 | 59 | 100.0 | 11 9 | ADW07403 Heavy cha |
| 24 | 59 | 100.0 | 11 9 | ADW07419 Heavy cha |

ALIGNMENTS

RESULT 1
ID AAR85166 standard; protein; 11 AA.
XX
AAR85166;
XX
18-JAN-1996 (first entry)
DE Human ONS-M21 antibody heavy variable region FR 4.
XX Human; ONS-M21 antibody; heavy variable region; chimeric protein;
KW framework region; FR 4; medulloblastoma; brain tumour; treatment;
KW diagnosis.
XX Homo sapiens.
OS XX
RN WO9514041-A1.
XX
PD 26-MAY-1995.
XX
PF 19-OCT-1994; 94WO-JP001763.
PR XX
19-NOV-1993; 93JP-00291078.
XX
(CHUS) CHUGAI SEIYAKU KK.
XX
PI Ohtomo T, Sato K, Tsuchiya M;
DR XX
WPI; 1995-200347/26.
XX
Reconstituted antibody against human medulloblastoma cells - contains
PT high proportion of human antibody origin and has low antigenicity.
XX
Claim 18; Page 102; 120pp; Japanese.
CC
AAR85163-R05166 are human antibody ONS-M21 heavy variable region
framework regions (FRs). They were used in the construction of a
human/murine chimeric antibody, reactive with human medulloblastoma (a
CC brain tumour) cells. The chimeric antibody can be used in the diagnosis
and treatment of this disease
XX
Sequence 11 AA;

Query Match 100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Miatches 0; Indels 0; Gaps 0;

Qy 1 WGGQTIVTVSS 11
 XX |||||||
 ID AAR97333 standard; peptide; 11 AA.
 Db 1 WGQGTTVTVSS 11
 AC AAR97333;
 XX
 DT 15-OCT-1996 (first entry)
 XX
 DB Humanised monoclonal antibody heavy chain framework region.
 XX
 KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
 KW complementary determining region; anti-carcinoembryonic antigen; CEA;
 KW diagnosis; imaging; therapy; immune response.
 OS
 OS Homo sapiens.
 OS
 OS WO9611013-A1.
 PN
 XX
 PD 18-APR-1996.
 XX
 PR 28-SEP-1995; 95WO-US011964.
 XX
 DR 05-OCT-1994; 94US-0031157.
 XX
 PA (IMMU-) IMMUNOMEDICS INC.
 XX
 PI Hansen HJ, Armour KL;
 XX
 DR WPI; 1996-209653/21.
 XX
 PT New humanised anti-CEA monoclonal antibody - having engrafted murine
 CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
 XX
 PS Claim 7; Page 40; 62pp; English.

New humanised monoclonal antibodies (Mabs) comprising the complementary determining regions (CDRs) of a parental murine class III anti-carcinoembryonic (CEA) Mab grafted to the framework regions (FRs) of a heterologous antibody which can be derived from any species including human, retain the anti-CEA binding specificity of the parental murine Mab but are less immunogenic in a human subject than the parental Mab. The humanised antibodies can be used in diagnosis, imaging and therapy of CEA-producing cancers and patients receiving the humanised antibodies and conjugates show improved therapeutic results, decreased immune responses and decreased immune-mediated adverse effects compared to the parent antibody. This sequence corresponds to the fourth framework region of the heavy chain of the humanised Mab. See AAR97313-97333

SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGQTIVTVSS 11
 Db 1 WGQGTTVTVSS 11

RESULT 3
 AAU07452 standard; peptide; 11 AA.
 ID AAU07452;
 XX
 AC AAU07452;
 DT 24-OCT-2001 (first entry)
 XX
 DE Synthetic peptide H-FR4-FB.

Qy 1 WGGQTIVTVSS 11
 Db 1 WGQGTTVTVSS 11

RESULT 4
 AAE28561
 ID AAB28561 standard; peptide; 11 AA.
 XX
 AC AAE28561;
 XX
 DT 27-DEC-2002 (first entry)
 XX
 DB scFv antibody heavy chain frame work region 4 from S18 clone.
 XX
 KW Human; sugar-nucleic acid interaction; single chain human antibody; scFv;
 KW L-peptide binder; D-nucleic acid binder; sugar-protein interaction; FR4;

KW frame work region 4.
 XX
 OS Homo sapiens.
 XX
 PN WO200367860-A2.
 XX PD 06-SEP-2002.
 XX PP 22-FEB-2002; 2002WO-US005193.
 XX PR 22-FEB-2001; 2001US-027137P.
 XX PA (SCRIPPS RES INST.
 XX PI Wong C;
 XX DR WPI; 2002-691633/74.

Disclosure: Fig 6B; 46pp; English.

XX CC The present invention relates to a novel method of selecting L-peptide or D-nucleic acid binders that bind to enantiomers of naturally occurring sugar or carbohydrate. The method involves providing enantiomers of naturally occurring sugar or carbohydrate employable for screening the library and then screening the library against the enantiomers for identifying a L-peptide binder or D-nucleic acid binder having binding activity with respect to enantiomers. The method is useful for selecting L-peptide binder or D-nucleic acid binder that binds to enantiomer of naturally occurring sugar or carbohydrate. It is useful for selecting L-peptide binders and/or L-nucleic acid binders that are resistant to enzymatic degradation due to their non-naturally occurring chirality, for blocking or activating the biological function of the naturally occurring sugar or carbohydrate to which they are targeted. The naturally occurring sugars and carbohydrates include bacterial or viral cell surface sugars or carbohydrates, heparin sulphates involved in viral entry, thrombosis and angiogenesis. The method is useful for identifying D-peptides, for studying sugar-protein and sugar-nucleic acid interaction and for designing high-affinity and hydrolase resistant molecules as artificial receptor capable of binding natural carbohydrate. The immobilised enantiomers are useful for screening phage expressing a peptide library on the coat proteins to identify specific clones. This sequence is used to illustrate the method of the invention

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGTTTVVSS 11
 Db 1 WGQTTTVVSS 11

RESULT 5

ID AAU70517
 ID AAU70517 standard; peptide; 11 AA.

Db 1 WGQTTTVVSS 11

RESULT 6

ID AAU70501
 ID AAU70501 standard; peptide; 11 AA.

AC AAU70501;
 XX DT 14-FEB-2002 (first entry)

DB Mouse heavy chain immunoglobulin framework region 4 #7.

XX KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarity determining region; framework region; IgBP;
 KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
 KW IgD; IgE; IgY; IgM; kappa; lambda; CHBP.

XX DE Mouse heavy chain immunoglobulin framework region 4 #11.

XX KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarity determining region; framework region; IgBP;
 KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
 KW IgD; IgE; IgY; IgM; kappa; lambda; CHBP.

OS Mus musculus.

PN WO200183806-A1.

KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
 KW IgD; IgE; IgY; IgM; kappa; lambda; CHBP.

XX OS Mus musculus.

XX PN 02-MAY-2000; 2000US-00563222.

XX PR (EPIC-) EPICYTE PHARM INC.

XX PI Hiatt AC, Hein MB;

XX DR WPI; 2002-055482/07.

XX PT Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynucleotides encoding binding protein polypeptides specific to ligand, selecting plant cells for preparing array.

XX PS Disclosure; Fig 1B; 129PP; English.

XX CC The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polynucleotides encoding different immunoglobulin binding protein (IgBP) polypeptides that specifically bind to a ligand or form one or more disulphide bonds with polypeptides in transfected cells, to generate an IgBP that binds to a ligand, and transformed plant cells are selected, and preparing an IgBP array in plant cells. At least one Peptide sequence has at least 75% sequence identity to a framework region (FR) of a native IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is useful for preparing an immunoglobulin binding protein array, preferably heavy chain binding protein (CHBP) array in eukaryotic cells especially plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic cells (e.g. insect cells or mammal cells). The CHBP is useful for discovery of e.g. screening assays of IgBPs having desired characteristics. The present sequence is a mammalian immunoglobulin derived peptide that may be incorporated into an IgBP of the invention

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGTTTVVSS 11
 Db 1 WGQTTTVVSS 11

PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array.
 XX
 Disclosure: Fig 1B; 129pp; English.

CC The invention relates to transforming a population of cells (e.g. plant
 CC cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IgBP) polypeptides
 CC that specifically bind to a ligand or form one or more disulphide bonds
 CC with polypeptides in transfected cells, to generate an IgBP that binds to
 CC a ligand, and transformed plant cells are selected and preparing an IgBP
 CC array in plant cells. At least one peptide sequence has at least 75%
 CC sequence identity to a framework region (FPR) of a native IgM, IgG, IgA,
 CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
 CC useful for preparing an immunoglobulin binding protein array, preferably
 CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
 CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
 CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
 CC discovery of e.g. screening assays of IgBPs having desired
 CC characteristics. The present sequence is a mammalian immunoglobulin
 CC derived peptide that may be incorporated into an IgBP of the invention
 XX
 SQ sequence 11 AA;

Query Match 100.0%; Score 59; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0;
 Matches 11; Conservative 0; Indels 0; Gaps 0;
 Qy 1 WQGQTIVVSS 11
 Db 1 WQGQTIVVSS 11

RESULT 9

ID ABO10719
 ID ABO10719 standard; peptide; 11 AA.
 XX
 AC ABO10719;
 DT 20-AUG-2003 (first entry)

XX Deimmunised murine J415-4 antibody framework sequence VHFR4.
 XX Modified antibody; deimmunised antibody; anti-PSMA antibody;
 KW prostate specific membrane antigen; immunogenic; CDR; murine;
 KW complementarity determining region; J415; J533; E99; mouse;
 KW prostatic disorder; cancerous disorder; genitourinary inflammation;
 KW prostatitis; benign enlargement; prostatic cancer; testicular cancer;
 KW solid tumour; soft tissue tumour; metastatic lesion; pain; analgesic;
 KW antiinflammatory; cytostatic; framework region; variable heavy chain;
 KW variable light chain; VH; VL; variable region; mutant; mutein.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 WO2002029897-A2.

XX
 PN
 XX
 PD 12-DEC-2002.
 XX
 PP 30-MAY-2002; 2002WO-US017068.
 XX
 PR 01-JUN-2001; 2001US-0295214P.
 PR 20-SEP-2001; 2001US-0323585P.
 PR 08-MAR-2002; 2002US-0362810P.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Bander N;
 XX DR WPI; 2003-313319/30.
 XX
 PT Ablating/killing aberrant prostate specific membrane antigen-expressing
 PT cells for treating skin disorders, by contacting the cell with an
 PT antibody that binds to the extracellular domain of prostate specific
 PT membrane antigen.
 XX
 RS Disclosure; Page 68; 225pp; English.

CC New modified anti-prostate specific membrane antigen (PSMA)
 CC immunoglobulins, useful for treating or preventing a prostatic or

PT cancerous disorder, e.g. genitourinary inflammation, prostatitis, or
 PT prostatic or testicular cancer.
 XX
 Disclosure: Page 21; 254pp; English.

CC The present invention relates to modified (e.g. deimmunised) antibodies
 CC to prostate specific membrane antigen (PSMA). The modified anti-PSMA
 CC antibodies are less immunogenic compared to the unmodified anti-PSMA
 CC antibodies. The modified antibodies comprise complementarity determining
 CC regions (CDRs) from a non-human antibody (e.g. murine antibody J591,J15,
 CC J533 or E99), and framework sequences that are less immunogenic in humans
 (e.g. less antigenic than the murine frameworks in which a murine CDR
 CC naturally occurs). The modified antibodies bind with PSMA, preferably
 CC human PSMA, with high affinity and specificity. The anti-PSMA antibodies
 CC are useful for treating or preventing a prostatic or cancerous disorder,
 e.g. genitourinary inflammation, prostatitis, benign enlargement,
 CC prostatic cancer or testicular cancer, or solid tumours, soft tissue
 CC tumours or metastatic lesions, and its associated pain. The present
 CC sequence represents a deimmunised murine framework region
 XX Sequence 11 AA;

Query Match 100.0%; Score 59; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0;
 Matches 11; Conservative 0; Indels 0; Gaps 0;
 Qy 1 WQGQTIVVSS 11
 Db 1 WQGQTIVVSS 11

RESULT 10

ID ABR44663
 ID ABR44663 standard; peptide; 11 AA.
 XX
 AC ABR44663;
 XX
 DT 25-JUL-2003 (first entry)

XX Murine J415-4 antibody VH FR4 amino acid sequence SEQ ID NO:40.
 XX Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytoblastic;
 KW prostate specific membrane antigen; antipsoriatic; antiarthritic;
 KW dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;
 KW epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;
 KW neoplastic disorder.
 XX OS Mus musculus.
 OS Synthetic.
 XX PN WO2003024388-A2.

XX
 DD 27-MAR-2003.
 XX
 PF 30-MAY-2002; 2002WO-US017064.
 XX
 PR 20-SEP-2001; 2001US-032410P.
 PR 08-MAR-2002; 2002US-0362612P.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Bander N;
 XX DR WPI; 2003-313319/30.
 XX
 PT Ablating/killing aberrant prostate specific membrane antigen-expressing
 PT cells for treating skin disorders, by contacting the cell with an
 PT antibody that binds to the extracellular domain of prostate specific
 PT membrane antigen.
 XX
 RS Disclosure; Page 68; 225pp; English.

CC The present invention describes a method (M1) for ablating or killing an

CC aberrant prostate specific membrane antigen (PSMA)-expressing cell (e.g. CC an epidermal and a dermal cell). MI comprises contacting the cell, or a CC vascular endothelial cell proximate to the cell, with an antibody (or its CC antigen-binding fragment), which binds specifically to the extracellular CC domain of PSMA in an amount sufficient to ablate or kill the cell. The CC antibodies have anti-psoriatic, antiarthritic, dermatotoxic, cytotstatic, CC antiinflammatory and antiallergic activities, and can be used in CC vaccines. MI is useful for treating a skin disorder in a subject, by CC administering to the subject an amount of an antibody which binds CC specifically to the extracellular domain of PSMA (the subject is a CC mammal, preferably human and is having, or at risk of, a skin disorder). CC The skin disorder is a dermal or an epidermal disorder, and is selected CC from psoriasis (preferably chronic, stationary psoriasis, psoriasis vulgaris, eruptive (glutamate) psoriasis, psoriatic erythroderma, generalised pustular psoriasis (Von Zumbusch), annular psoriasis, psoriasis, and localised pustular psoriasis), psoriatic arthritis, exfoliative dermatitis, pityriasis rubra pilaris, pityriasis rosea, parapsoriasis, pityriasis lichenoides, lichen planus, lichen nitidus, ichthyosiform dermatosis, keratodermas, dermatosis, and prokeratosis, preferably psoriasis. MI is useful for treating a skin disorder such as an inflammatory or neoplastic disorder of the epidermis or dermis, preferably an epidermal precancerous or cancerous lesion. MI is also useful to treat or prevent disorders involving aberrant activity of PSMA-expressing cell, e.g., kidney, liver or brain cell. ACC69816 to ACC69837 and ABR44613 to ABR44733 represent sequences used in the exemplification of the present invention

XX SQ Sequence 11 AA;

Query Match Best Local Similarity 100.0%; Score 59; DB 6; Length 11; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WQGQTIVVSS 11

Db 1 WQGQTIVVSS 11

RESULT 11

ID ADG75671

ID ADG75671 standard; peptide; 11 AA.

XX AC ADG75671;

XX DT 11-MAR-2004 (first entry)

XX DB Peptide of the human heavy chain framework region 4 seqID135.

XX KW interleukin-9; IL-9; anti-IL-9; antibody; MH9A3; MH9D1; MH9L1;

XX KW bronchial hyperresponsiveness; asthma; atopic allergy;

XX KW mucin overproduction; chronic obstructive pulmonary disorder;

XX KW cystic fibrosis; chronic obstructive pulmonary disorder; antiallergic;

XX KW antiasthmatic; cytostatic; human.

XX OS Homo sapiens.

XX PN WO2003086458-A1.

XX PD 23-OCT-2003.

XX PP 11-APR-2003; 2003WO-US011113.

XX PR 12-APR-2002; 2002US-0371683P.

XX PR 12-APR-2002; 2002US-0371728P.

XX PA (MEDI-) MEDIMMUNE INC.

PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Reed JL, Dall'acqua W, Van Snick J, Renaud J, Cormont R;

PI Uttenhoff C;

XX DR

XX WPI; 2003-845267/78.

XX

PD 10-OCT-2002.

XX 06-APR-2001; 2001US-00828708.

PR 06-APR-2001; 2001US-00828708.

XX (DITZ/) DITZEL H.

PA (BURT/) BURTON D R.

PA (SCHA/) SCHALLER M.

XX Ditzel H, Burton DR, Schaller M;

XX WPI; 2003-521517/49.

PT Immunopolypeptide for diagnosis and treatment of human autoimmune disease, e.g., human rheumatoid arthritis, comprises a polypeptide that

PT binds to human glucose-6-phosphate isomerase.

XX Claim 6; FIG 4B; 47pp; English.

The invention describes an immunopolypeptide comprising a polypeptide that binds to human glucose-6-phosphate isomerase (GPI). The methods and compositions are used for diagnosis and treatment of human autoimmune disease, e.g., human rheumatoid arthritis. This is the amino acid sequence of human anti-GPI-antibody heavy chain variable region framework region

XX SQ Sequence 11 AA;

Query Match Best Local Similarity 100.0%; Score 59; DB 7; Length 11; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WQGTTVTVSS 11

Db 1 WQGTTVTVSS 11

RESULT 12

ID ADG75671

ID ADG75671 standard; peptide; 11 AA.

XX AC ADG75671;

XX DT 11-MAR-2004 (first entry)

XX DB Peptide of the human heavy chain framework region 4 seqID135.

XX KW interleukin-9; IL-9; anti-IL-9; antibody; MH9A3; MH9D1; MH9L1;

XX KW bronchial hyperresponsiveness; asthma; atopic allergy;

XX KW mucin overproduction; chronic obstructive pulmonary disorder;

XX KW cystic fibrosis; chronic obstructive pulmonary disorder; antiallergic;

XX KW antiasthmatic; cytostatic; human.

XX OS Homo sapiens.

XX PN WO2003086458-A1.

XX PD 23-OCT-2003.

XX PP 11-APR-2003; 2003WO-US011113.

XX PR 12-APR-2002; 2002US-0371683P.

XX PR 12-APR-2002; 2002US-0371728P.

XX PA (MEDI-) MEDIMMUNE INC.

PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Reed JL, Dall'acqua W, Van Snick J, Renaud J, Cormont R;

PI Uttenhoff C;

XX DR

XX WPI; 2003-845267/78.

XX

PT New antibody or antibody fragment that specifically binds to IL-9, useful for preparing a composition for preventing or treating e.g., atopic allergy, asthma, mucin overproduction, chronic obstructive pulmonary disorder or cystic fibrosis.

XX Disclosure: SEQ ID NO 135; 206pp; English.

XX

This invention relates to novel humanised and chimeric antibody molecules, and functional fragments thereof, which have specificity for human interleukin-9 (IL-9), specifically, it refers to recombinant antibodies derived from several mouse anti-IL-9 monoclonal antibodies, namely MH9A3, MH9D1 and MH9L1. The present invention describes using the humanised and chimeric antibody molecules to treat, prevent and/or ameliorate disorders including bronchial hyperresponsiveness, asthma, atopic allergy, mucin overproduction, chronic obstructive pulmonary disorder, cystic fibrosis, chronic obstructive pulmonary disorder,

CC excessive T cell or neutrophil activity. Accordingly, these IL-9
CC antagonists exhibit antiallergic, antiarrhythmic and cytotatic
CC activities. This peptide sequence is a peptide from the human heavy chain
CC framework region 4, used in an exemplification of the invention.

SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WQGTTTVSS 11
Db 1 WQGTTTVSS 11

RESULT 13

ADH17960 Human modified 15H12/19D12 HCA framework region 4 peptide.

ID ADH17960 standard; peptide; 11 AA.

XX AC ADH17960;

XX DT 11-MAR-2004 (first entry)

XX DE Human modified 15H12/19D12 HCA framework region 4 peptide.

XX KW insulin-like growth factor receptor 1; IGFR1; cytostatic; osteopathic;
KW antiatherosclerotic; antipsoriatic; vasoconstrictive; antidiarrhoeal;
KW acromegaly; bladder cancer; Wilms' tumour; ovarian; pancreatic;
KW benign prostatic hyperplasia; breast; prostate; bone; lung; colorectal;
KW cervical; synovial sarcoma; diarrhoea; carcinoid syndrome;
KW vasoactive intestinal peptide; gigantism; psoriasis; atherosclerosis;
KW smooth muscle restenosis; blood vessel; microvascular proliferation;
KW gene therapy; human; 15H12/19D12; heavy chain A; HCA; framework region.
XX OS Synthetic.
OS Homo sapiens.
XX PN WO2003100008-A2.
XX PD 04-DEC-2003.
XX PP 22-MAY-2003; 2003WO-US016283.
XX PR 24-MAY-2002; 2002US-0383459P.
PR 02-JUL-2002; 2002US-0393214P.
PR 23-DEC-2002; 2002US-0436254P.
XX PA (SCHE) SCHERRING CORP.
XX PT Wang Y, Greenberg R, Presta L, Pachter JA, Hailey J, Brams P;
PT Williams D, Srinivasan M, Feingersh D;
XX DR WPI; 2004-042807/04.
DR N-PSDB; ADH17959.

New binding composition that specifically binds to insulin-like growth factor receptor 1, useful for treating or preventing a medical condition that is mediated by elevated expression or activity of IGFR1.

PS Disclosure: SEQ ID NO 69; 144pp; English.

XX PT The invention relates to a novel binding composition that specifically binds to insulin-like growth factor receptor 1 (IGFR1). The composition of the invention demonstrates cytostatic, osteopathic, antiatherosclerotic, antipsoriatic, vasoconstrictive and antidiarrhoeal activities and may be useful for preventing or treating a medical condition selected from acromegaly, bladder cancer, Wilms' cancer, ovarian cancer, pancreatic cancer, benign prostatic hyperplasia, breast cancer, prostate cancer, bone cancer, lung cancer, colorectal cancer, cervical cancer, synovial sarcoma, diarrhoea associated with carcinoid syndrome, vasoactive intestinal peptide secreting tumours, gigantism, psoriasis, atherosclerosis, smooth muscle restenosis of blood vessels and

CC inappropriate microvascular proliferation. The composition may also have
CC gene therapy applications. The current sequence is that of the human
CC 15H12/19D12 heavy chain A (HCA) framework region peptide of the
CC invention.

SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WQGTTTVSS 11
Db 1 WQGTTTVSS 11

RESULT 14

ADH18011 Human modified 15H12/19D12 HCB framework region 4 peptide.

ID ADH18011 standard; peptide; 11 AA.

XX AC ADH18011;

XX DT 11-MAR-2004 (first entry)

XX DE Human modified 15H12/19D12 HCB framework region 4 peptide.

XX KW insulin-like growth factor receptor 1; IGFR1; cytostatic; osteopathic;
KW antiatherosclerotic; antipsoriatic; vasoconstrictive; antidiarrhoeal;
KW acromegaly; bladder cancer; Wilms' tumour; ovarian; pancreatic;
KW benign prostatic hyperplasia; breast; prostate; bone; lung; colorectal;
KW cervical; synovial sarcoma; diarrhoea; carcinoid syndrome;
KW vasoactive intestinal peptide; gigantism; psoriasis; atherosclerosis;
KW smooth muscle restenosis; blood vessel; microvascular proliferation;
KW gene therapy; human; 15H12/19D12; heavy chain B; LCB; framework region.
XX OS Synthetic.
OS Homo sapiens.
XX PN WO2003100008-A2.
XX PD 04-DEC-2003.
XX PP 22-MAY-2003; 2003WO-US016283.
XX PR 24-MAY-2002; 2002US-0383459P.
PR 02-JUL-2002; 2002US-0393214P.
PR 23-DEC-2002; 2002US-0436254P.
XX PA (SCHE) SCHERRING CORP.
XX PT Wang Y, Greenberg R, Presta L, Pachter JA, Hailey J, Brams P;
PT Williams D, Srinivasan M, Feingersh D;
XX DR WPI; 2004-042807/04.
DR N-PSDB; ADH18010.

XX PT New binding composition that specifically binds to insulin-like growth factor receptor 1, useful for treating or preventing a medical condition that is mediated by elevated expression or activity of IGFR1.

PS Disclosure: SEQ ID NO 120; 144pp; English.

CC The invention relates to a novel binding composition that specifically binds to insulin-like growth factor receptor 1 (IGFR1). The composition of the invention demonstrates cytostatic, osteopathic, antiatherosclerotic, antipsoriatic, vasoconstrictive and antidiarrhoeal activities and may be useful for preventing or treating a medical condition selected from acromegaly, bladder cancer, Wilms' cancer, ovarian cancer, pancreatic cancer, benign prostatic hyperplasia, breast cancer, prostate cancer, bone cancer, lung cancer, colorectal cancer, cervical cancer, synovial sarcoma, diarrhoea associated with carcinoid syndrome, vasoactive intestinal peptide secreting tumours, gigantism, psoriasis, atherosclerosis, smooth muscle restenosis of blood vessels and

CC inappropriate microvascular proliferation. The composition may also have
 CC gene therapy applications. The current sequence is that of the human
 CC 15H12/19D12 heavy chain B (HCB) framework region peptide of the
 CC invention.

SQ Sequence 11 AA;
 Query Match 100.0%; Score 59; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.011; 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX

QY 1 WGGQTIVTVSS 11
 Db 1 WGGQTIVTVSS 11

RESULT 15
 ID ADQ90791
 XX ADQ90791 standard; protein; 11 AA.
 AC ADQ90791;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Artificially desimmunised framework sequence #14.
 XX
 KW insulin-related disorder; prostate specific membrane antigen; PSMA;
 KW obesity; hyperglycaemia; hypoglycaemia; hyperinsulinaemia;
 KW insulin-resistance; impaired glucose tolerance; impaired fasting glucose;
 KW Type 1 diabetes mellitus; Type 2 diabetes mellitus; gestational diabetes.
 XX
 OS Synthetic.
 XX
 PN US2004136398-A1.
 XX
 PD 15-JUN-2004.
 XX
 PP 17-OCT-2003; 2003US-00688015.
 XX
 PR 30-OCT-2002; 2002US-0422396P.
 XX
 PA (BAND/) BANDER N H.
 XX
 PI Bander NH;
 XX
 DR WPI; 2004-533338/51.
 XX
 PT Use of anti-prostate specific membrane antigen antibodies for treating or
 PT preventing insulin-related disorders, e.g. obesity, hyperglycemia,
 PT hypoglycemia, hyperinsulinemia, insulin-resistance, or Type 1 or 2
 PT diabetes mellitus.
 XX
 PS Disclosure; SEQ ID NO 40; 89pp; English.
 XX
 CC The invention relates to a method of treating or preventing an insulin-
 CC related disorder in a subject which comprises administering an antibody
 CC or its antigen-binding portion specific for prostate specific membrane
 CC antigen (PSMA). The method is useful for treating an insulin-related
 CC disorder, including obesity, hyperglycaemia, hypoglycaemia, hyperinsulinaemia,
 CC hyperinsulinaemia, insulin-resistance, impaired glucose tolerance,
 CC impaired fasting glucose, Type 1 diabetes mellitus, Type 2 diabetes
 CC mellitus, and gestational diabetes. The present sequence represents an
 CC artificially deimmunised framework sequence.
 XX
 Sequence 11 AA;

Search completed: December 4, 2005, 04:45:01
 Job time : 97.5625 sec

Query Match 100.0%; Score 59; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.011; 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX

QY 1 WGGQTIVTVSS 11
 Db 1 WGGQTIVTVSS 11

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On protein - protein search, using bw model

Run on: December 4, 2005, 04:31:45 ; Search time 15.5833 Seconds
(without alignment) 67.918 Million cell updates/sec

Title: US-10-632-706-198
Perfect score: 59
Sequence: 1 WGQGTTVTVSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80,*
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description |
|------------|-------|-------|--------|-----------|---------------------------------|
| 1 | 59 | 100.0 | 74 | 2 S26793 | Ig heavy chain V region - human |
| 2 | 59 | 100.0 | 110 | 2 PH1655 | Ig heavy chain V |
| 3 | 59 | 100.0 | 113 | 2 S5533 | Ig heavy chain V |
| 4 | 59 | 100.0 | 113 | 2 S5535 | Ig heavy chain V |
| 5 | 59 | 100.0 | 113 | 2 S5530 | Ig heavy chain V |
| 6 | 59 | 100.0 | 113 | 2 S5534 | Ig heavy chain V |
| 7 | 59 | 100.0 | 113 | 2 S5538 | Ig heavy chain V |
| 8 | 59 | 100.0 | 113 | 2 S5532 | Ig heavy chain V |
| 9 | 59 | 100.0 | 113 | 2 S5531 | Ig heavy chain V |
| 10 | 59 | 100.0 | 114 | 2 S46392 | Ig heavy chain V |
| 11 | 59 | 100.0 | 114 | 2 S20707 | Ig heavy chain V |
| 12 | 59 | 100.0 | 115 | 2 S20706 | Ig heavy chain V |
| 13 | 59 | 100.0 | 116 | 2 S15672 | Ig heavy chain V |
| 14 | 59 | 100.0 | 116 | 2 S5542 | Ig heavy chain V |
| 15 | 59 | 100.0 | 117 | 2 S5541 | Ig heavy chain V |
| 16 | 59 | 100.0 | 118 | 2 PH1666 | Ig heavy chain V |
| 17 | 59 | 100.0 | 118 | 2 PH1660 | Ig heavy chain V |
| 18 | 59 | 100.0 | 118 | 2 S37286 | Ig heavy chain (an |
| 19 | 59 | 100.0 | 119 | 2 PH061 | Ig heavy chain V |
| 20 | 59 | 100.0 | 120 | 2 PH1650 | Ig heavy chain V |
| 21 | 59 | 100.0 | 120 | 2 BE49390 | Ig heavy chain V |
| 22 | 59 | 100.0 | 120 | 2 PD00308 | Ig heavy chain V |
| 23 | 59 | 100.0 | 120 | 2 S55338 | Ig heavy chain V |
| 24 | 59 | 100.0 | 120 | 2 S55339 | Ig heavy chain V |
| 25 | 59 | 100.0 | 120 | 2 S5533 | Ig heavy chain V |
| 26 | 59 | 100.0 | 120 | 2 S55336 | Ig heavy chain V |
| 27 | 59 | 100.0 | 120 | 2 S12953 | Ig heavy chain V |
| 28 | 59 | 100.0 | 121 | 2 S3110 | Ig heavy chain - h |
| 29 | 59 | 100.0 | 121 | 2 S55340 | Ig heavy chain V |

ALIGNMENTS

RESULT 1

S26793 Ig heavy chain V region - human

C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26793
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Bur. J. Immunol. 22, 241-245, 1992

A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family

A;Reference number: S26786; MUID:9211632; PMID:1730251

A;Status: Preliminary

A;Molecule type: mRNA

A;Residues: 1-74 <MOR>

A;Cross-references: UNIPARC:UPI0000115EC, EMBL:X61019, NID:932787, PIDN:CAA43353.1; PID: C;Superfamily: Immunoglobulin V region; Immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match Best Local Similarity 100.0%; Score 59; DB 2; Length 74;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
Db 64 WGQGTTVTVSS 74

RESULT 2

PH1655 Ig heavy chain V region (clone 2E8) - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1655
R;Hillson, J.L.; Karr, N.S.; Opliger, I.R.; Mannik, M.; Sabo, E.H.
J. Exp. Med. 178, 311-336, 1993

J;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A: Reference number: PH1642; MUID:93301610; PMID:8315388

A;Accession: PH1655
A;Molecule type: mRNA
A;Residues: 1-110 <HIL>

A;Cross-references: UNIPARC:UPI0000176BPC

A;Experimental source: B cell
A;Source: Cell

C;Superfamily: Immunoglobulin V region; Immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F,7-90/Domin, Immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 110;

Best Local Similarity 100.0%; Pred. No.0032; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
Db 64 WGQGTTVTVSS 74

Db 100 WGQGTTVTVSS 110

RESULT 3

S55533 Ig heavy chain V region pε25 - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C;Accession: S55533 R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using mutations in the variable region genes.
A;Reference number: S55528; MUID:95239763; PMID:7536850
A;Accession: S55533
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <BOE>
A;Cross-references: UNIPARC:UPI0000116205; EMBL:X82594; NID:9854314; PIDN:CAA57930.1; PI
S55535 C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin F;14-97/Domain: immunoglobulin homology <IMM>
F;14-97/Domain: immunoglobulin homology <IMM>
Query Match 100.0%; Score 59; DB 2; Length 113;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WGQGTTVTVSS 11
Db 103 WGQGTTVTVSS 113

RESULT 4

S55535 Ig heavy chain V region pε23 - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Accession: S55535 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using mutations in the variable region genes.
A;Reference number: S55528; MUID:95239763; PMID:7536850
A;Accession: S55535
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <BOE>
A;Cross-references: UNIPARC:UPI00001161FC; EMBL:X82584; NID:9854292; PIDN:CAA57928.1; PI
S55535 C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin F;14-97/Domain: immunoglobulin homology <IMM>
Query Match 100.0%; Score 59; DB 2; Length 113;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WGQGTTVTVSS 11
Db 103 WGQGTTVTVSS 113

RESULT 5

S55530 Ig heavy chain V region pε17 - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Accession: S55530 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using mutations in the variable region genes.
A;Reference number: S55528; MUID:95239763; PMID:7536850
A;Accession: S55530
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <BOE>
A;Cross-references: UNIPARC:UPI00001161FB; EMBL:X82585; NID:9854294; PIDN:CAA57921.1; PI
S55530 C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin F;14-97/Domain: immunoglobulin homology <IMM>
Query Match 100.0%; Score 59; DB 2; Length 113;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
Db 103 WGQGTTVTVSS 113

RESULT 8

Ig heavy chain V region *pel19* - mouse (fragment)

C;Species: *Mus musculus* (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C;Accession: S5532
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using mutations in the variable region genes.
A;Reference number: S5528; MUID:95239763; PMID:7536850
A;Accession: S5532
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <BOE>
A;Cross-references: UNIPARC:UPI00001161FF; EMBL:X82588; NID:9854300; PIDN:CAA57924.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.0033; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
Db 103 WGQGTTVTVSS 113

RESULT 9

S5531

Ig heavy chain V region *pel18* - mouse (fragment)

C;Species: *Mus musculus* (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C;Accession: S5531
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using mutations in the variable region genes.
A;Reference number: S5528; MUID:95239763; PMID:7536850
A;Accession: S5531
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <BOE>
A;Cross-references: UNIPARC:UPI00001161FE; EMBL:X82587; NID:9854298; PIDN:CAA57923.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin <IMM>

Query Match 100.0%; Score 59; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0033; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
Db 104 WGQGTTVTVSS 114

RESULT 10

S43392

Ig heavy chain V region (VH-28) - human

C;Species: *Homo sapiens* (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46392
R;Friggin, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994

Query Match 100.0%; Score 59; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.0033; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
Db 103 WGQGTTVTVSS 113

RESULT 10

S43392

Ig heavy chain V region (VH-28) - human

C;Species: *Homo sapiens* (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46392
R;Friggin, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994

Query Match 100.0%; Score 59; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.0033; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
Db 104 WGQGTTVTVSS 114

A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46392
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <IG>
A;Cross-references: UNIPARC:UPI00001137D6; EMBL:Z31688; NID:9499306; PIDN:CAA83493.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0033; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
Db 104 WGQGTTVTVSS 114

A;Title: Binding specificity and variable region sequences of two monoclonal antibodies A;Reference number: S20706
A;Accession: S20707
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-14 <BE>
A;Cross-references: UNIPARC:UPI00001176B37; EMBL:Z11916
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin F;12-95/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0033; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
Db 104 WGQGTTVTVSS 114

RESULT 12

S20706

Ig heavy chain V region - mouse

C;Species: *Mus musculus* (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S20706
R;Brennan, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Osi
submitted to the EMBL Data Library, April 1992
A;Description: Binding specificity and variable region sequences of two monoclonal anti- A;Reference number: S20706
A;Accession: S20706
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-15 <BB>
A;Cross-references: UNIPROT:QB33V9; UNIPARC:UPI00001176C45; EMBL:Z11914
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin F;12-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.0033; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTTVTVSS 11
Db 104 WGQGTTVTVSS 114

Db 105 WQGTTTVVSS 115
RESULT 13
 Ig heavy chain V region - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C;Accession: S15672
 R;Tempest, P.R.; Bremer, P.; Lambert, M.; Taylor, G.; Purze, J.M.; Carr, P.J.; Harris, Bio/Technology 9, 266-271, 1991
 A;Reference number: S15672; MUID:91337412; PMID:1367535
 A;Accession: S15672
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-116 <TEN>
 A;Cross-references: UNIPARC:UPI00001161F8; EMBL:X82580; NID:9854286; PIDN:CAA57916.1; PIDC;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 C;Keywords: heterotetramer; immunoglobulin F;14-97/bdomain: immunoglobulin homology <IMM>
 Query Match 100.0%; Score 59; DB 2; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.0034; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WQGTTTVVSS 11
 Db 106 WQGTTTVVSS 116

RESULT 14
 S55542
 Ig heavy chain V region pε2 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
 C;Accession: S55542
 R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
 J. Mol. Biol. 247, 932-946, 1995
 A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin
 A;Reference number: S55528; MUID:9233973; PMID:7336850
 A;Accession: S55542
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-116 <BOB>
 A;Cross-references: UNIPARC:UPI00001161F9; EMBL:X82581; NID:9854302; PIDN:CRA57917.1; PI
 C;Supergroup: immunoglobulin V region; immunoglobulin homology <IMM>
 C;Keywords: heterotetramer; immunoglobulin F;14-97/Domain: immunoglobulin homology <IMM>
 Query Match 100.0%; Score 59; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.0033; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WQGTTTVVSS 11
 Db 106 WQGTTTVVSS 116

RESULT 15
 S55541
 Ig heavy chain V region pε1 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
 C;Accession: S55541
 R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
 J. Mol. Biol. 247, 932-946, 1995
 A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin
 A;Reference number: S55528; MUID:9233973; PMID:7336850
 A;Accession: S55541
 A;Status: preliminary

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:36 ; Search time 100.375 seconds

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Scoring table: BLASTUME2
Gapop 10.0 , Gapext 0.5

Searched: US-10-632-706-198
Sequence: 1 WGGTTTVVSS 11

Perfect score: 59

Score: 2166443 seqs, 705528306 residues

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|----------------|
| 1 | 59 | 100.0 | 119 | 2 Q9GYZ2_MOUSE |
| 2 | 59 | 100.0 | 121 | 2 Q8CGS2_MOUSE |
| 3 | 59 | 100.0 | 145 | 1 HV2I_HUMAN |
| 4 | 59 | 100.0 | 147 | 1 HVIC_HUMAN |
| 5 | 59 | 100.0 | 147 | 2 Q92533_MOUSE |
| 6 | 59 | 100.0 | 159 | 2 Q96QSO_HUMAN |
| 7 | 59 | 100.0 | 170 | 2 Q92582_MOUSE |
| 8 | 59 | 100.0 | 218 | 2 Q92531_MOUSE |
| 9 | 59 | 100.0 | 241 | 2 Q92146_MOUSE |
| 10 | 59 | 100.0 | 348 | 2 Q6PYX1_HUMAN |
| 11 | 59 | 100.0 | 416 | 2 Q9NP96_HUMAN |
| 12 | 59 | 100.0 | 472 | 2 Q6NO99_HUMAN |
| 13 | 59 | 100.0 | 573 | 2 Q8WU88_HUMAN |
| 14 | 59 | 100.0 | 576 | 2 Q6P418_HUMAN |
| 15 | 59 | 100.0 | 595 | 2 Q8WU44_HUMAN |
| 16 | 59 | 100.0 | 597 | 2 Q9B088_HUMAN |
| 17 | 59 | 100.0 | 597 | 2 Q9GMX5_HUMAN |
| 18 | 59 | 100.0 | 597 | 2 Q9GMX5_HUMAN |
| 19 | 59 | 100.0 | 606 | 2 Q6GM72_HUMAN |
| 20 | 59 | 100.0 | 625 | 2 Q96A46_HUMAN |
| 21 | 59 | 98.3 | 455 | 2 Q6PJ22_MOUSE |
| 22 | 58 | 98.3 | 468 | 2 Q569WQ_MOUSE |
| 23 | 58 | 98.3 | 468 | 2 Q505N9_MOUSE |
| 24 | 58 | 98.3 | 471 | 2 Q6K0D4_MOUSE |
| 25 | 58 | 98.3 | 472 | 2 Q6PJA7_MOUSE |
| 26 | 58 | 98.3 | 473 | 2 Q91205_MOUSE |
| 27 | 58 | 98.3 | 475 | 2 Q569X1_MOUSE |
| 28 | 58 | 98.3 | 477 | 2 Q98E5C_MOUSE |
| 29 | 58 | 98.3 | 486 | 2 Q91207_MOUSE |
| 30 | 58 | 98.3 | 487 | 2 Q99KA4_MOUSE |
| 31 | 56 | 94.9 | 109 | 2 Q9JL75_MOUSE |

SUMMARIES

RESULT 1

Q9GYZ2_MOUSE PRELIMINARY; PRT; 119 AA.

ID Q9GYZ2; AC Q9GYZ2; DT 01-MAR-2001 (TREMBLrel. 16, Created)

DR AF282822; ARG01452.1; -; mRNA.

DR SRK; Q9GYZ2; 1-119.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR SMART; SMO006; IgV; 1.

DR PROSITE; PSS0835; IG_LIKE; 1.

FT NON_TER 1

FT NON_TER 119 119

SEQUENCE 119 AA; 13567 MW; BA893873FD5FAGAB CRC64;

Query Match Best Local Similarity 100.0%; Pred. No. 0.0053; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 WGGTTTVVSS 11

Db 109 WGGTTTVVSS 119

RESULT 2

Q8CGS2_MOUSE

ID Q8CGS2_MOUSE PRELIMINARY; PRT; 121 AA.

AC Q8CGS2; DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE (Fragment)

DE Anti-deoxynivalenol scfv lambda heavy chain variable region

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

ALIGNMENTS

OX NCBI_TAXID=10030;
 RN [1]
 RP NUCLEOTIDE_SEQUENCE.
 RC STRAIN=BAB/C;
 RA Wang Z., Munshi K., Osawa F., Pestka J.J., Hart L.P.;
 RL Submitted (2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY151140; AAN75452.1; -; mRNA.
 DR HSSP; P0151; INQB.
 DR Ensemble; ENSMUSG0000021155; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SMD0406; IgV; 1.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 FT NON_TER 1
 FT 121 121
 SQ SEQUENCE 121 AA; 13475 MW; 84F56CFAB053F5D6 CRC64;
 Query Match Best Local Similarity 100.0%; Score 59; DB 1; Length 146;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WQGQTIVTVSS 11
 Db 111 WQGQTIVTVSS 121
 RESULT 3
 HV2I_HUMAN STANDARD; PRT: 146 AA.
 ID HV2I_HUMAN
 AC P06331;
 DT 01-JAN-1988 (Rel. 05, Created)
 DT 01-JAN-1988 (Rel. 05, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V-II region ARH-77 precursor.
 OS Homo sapiens (Human)
 OC Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 RN [1]
 RP NUCLEOTIDE_SEQUENCE.
 RX MEDLINE=8320532; PubMed=6815656;
 RA Kenten J.H., Nolgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
 RA Bell L.O., Gould H.J.;
 RT "Cloning and sequence determination of the gene for the human
 RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
 RN [2]
 RP PROTEIN_SEQUENCE_OF_20-147;
 RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.,
 RL (In) Bach M.K. (eds.);
 RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
 RL Marcel Dekker, New York (1978).
 CC -I- MISCELLANEOUS: This epsilon chain was isolated from a myeloma
 CC protein.
 CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR HSSP; P0125; INQB.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR SMART; SMD0406; IgV; 1.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 DR Direct protein sequencing; Immunoglobulin domain;
 DR KW Immunoglobulin V region; Pyrolydine carboxylic acid; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 147
 FT DOMAIN 20 131
 FT MOD_RES 20 20
 FT DISTIFID 41 115
 FT CONFLICT 21 21
 FT CONFLICT 53 54
 FT CONFLICT 67 68
 FT CONFLICT 125 125
 FT NON_TER 147 147
 SQ SEQUENCE 147 AA; 16296 MW; 948F9FT2A536C20 CRC64;
 Query Match Best Local Similarity 100.0%; Score 59; DB 1; Length 147;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|-----------------------|---|--|--------------|
| DB | 137 | WGQGTTVTVSS | 147 |
| RESULT 5 | | | |
| ID | Q925S3 | MOUSE PRELIMINARY; | PRT; 147 AA. |
| AC | Q925S3; | | |
| DT | 01-DEC-2001 | (TREMBrel. 19, Created) | |
| DR | 01-DEC-2001 | (TREMBrel. 19, Last sequence update) | |
| DT | 01-OCT-2003 | (TREMBrel. 25, Last annotation update) | |
| DE | Mkp3; | | |
| OS | Mus musculus (Mouse). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus. | | |
| OX | NCBI_TaxID=10090; | | |
| RP | NUCLEOTIDE SEQUENCE. | | |
| RC | STRAIN=BALB/c; | | |
| RX | Cui, D.X., Zeng, G.Y., Wang, F., Xu, J.R., Ren, D.Q., Guo, Y.H., Tian, F.R., Yan, X.J., Hou, Y., Su, C.Z.; -; mRNA. | | |
| RA | "Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after gamma-irradiation in mice."; | | |
| RT | World J. Gastroenterol. 6:709-717(2000). [2] | | |
| RN | NUCLEOTIDE SEQUENCE. | | |
| RC | STRAIN=BALB/c; | | |
| RT | "Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same strain."; | | |
| RT | Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001). | | |
| DR | EMBL; AF240166; AAK43731.1; -; mRNA. | | |
| DR | HSPB; P01751; 1AGW. | | |
| DR | SMR; Q925S3; 3-139. | | |
| DR | InterPro; IPR007110; Ig-like. | | |
| DR | InterPro; IPR003586; Ig_v. | | |
| DR | SMART; SM00466; IgV; 1. | | |
| DR | PROSITE; PS00835; Ig_LIKE; 1. | | |
| KW | immunoglobulin domain. | | |
| SQ | SEQUENCE 147 AA; 1674 MW; 800594A12B97191F CRC64; | | |
| RESULT 6 | Q9QSO0 HUMAN | | |
| Query Match | 100.0% | Score 59; DB 2; Length 147; | |
| Best Local Similarity | 100.0% | Pred. No. 0.0067; | |
| Matches | 11; | Conservative 0; Mismatches 0; | |
| Indels | 0; | Gaps 0; | |
| DR | InterPro; IPR007110; Ig-like. | | |
| DR | InterPro; IPR003596; Ig_v. | | |
| DR | SMART; SM00466; IgV; 1. | | |
| DR | PROSITE; PS00835; Ig_LIKE; 1. | | |
| KW | immunoglobulin domain. | | |
| SQ | SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64; | | |
| RESULT 7 | Q925S2 MOUSE | | |
| Query Match | 100.0% | Score 59; DB 2; Length 159; | |
| Best Local Similarity | 100.0% | Pred. No. 0.0073; | |
| Matches | 11; | Conservative 0; Mismatches 0; | |
| Indels | 0; | Gaps 0; | |
| DR | InterPro; IPR003596; IgV; 1. | | |
| DR | SMART; SM00466; IgV; 1. | | |
| DR | PROSITE; PS00835; Ig_LIKE; 1. | | |
| KW | immunoglobulin domain. | | |
| SQ | SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64; | | |
| RESULT 8 | Q925S1 MOUSE | | |
| Query Match | 100.0% | Score 59; DB 2; Length 170; | |
| Best Local Similarity | 100.0% | Pred. No. 0.0078; | |
| Matches | 11; | Conservative 0; Mismatches 0; | |
| Indels | 0; | Gaps 0; | |
| DR | InterPro; IPR007110; Ig-like. | | |
| DR | InterPro; IPR003596; Ig_v. | | |
| DR | SMART; SM00466; IgV; 1. | | |
| DR | PROSITE; PS00835; Ig_LIKE; 1. | | |
| KW | immunoglobulin domain. | | |
| SQ | SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64; | | |
| RESULT 9 | Q925S1 MOUSE | | |
| Query Match | 100.0% | Score 59; DB 2; Length 149; | |
| Best Local Similarity | 100.0% | Pred. No. 0.0073; | |
| Matches | 11; | Conservative 0; Mismatches 0; | |
| Indels | 0; | Gaps 0; | |
| DR | InterPro; IPR003596; IgV; 1. | | |
| DR | SMART; SM00466; IgV; 1. | | |
| DR | PROSITE; PS00835; Ig_LIKE; 1. | | |
| KW | immunoglobulin domain. | | |
| SQ | SEQUENCE 149 AA; 17497 MW; 5D29537E881FAF02 CRC64; | | |

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buteria; Buarchontoglires; Gires; Rodentia; Sciuromorpha;
 OC Muridae; Murinae; Mus.
 OX NCBI_TAXID=1090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/C;
 RX PubMed=11819679;
 RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,
 RA Yan X.J., Hou Y., Su C.Z.;
 RT Mechanism of exogenous nucleic acids and their precursors improving
 the repair of intestinal epithelium after gamma-irradiation in mice.";
 RL World J. Gastroenterol. 6:709-717(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/C;
 RA Cui D., Zeng G., Yan X., Li X., Su C.;
 RT "Cloning of mouse genes related to repairing of intestinal RNA of mice of
 RT the same strain.";
 RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
 DR EMBL; AF20168; AAK43733.1; -; mRNA.
 DR Ensemble; ENSMUSG00000058040; Mus musculus.
 DR Interpro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PSS0835; Ig_LIKE; 1.
 FT NON_TER 218 AA; 218 MW; 52784FA8F7982817 CRC64;
 SQ SEQUENCE 218 AA; |||||||
 Query Match 100.0%; Score 59; DB 2; Length 218;
 Best Local Similarity 100.0%; Pred. No. 0.012; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0;
 QY 1 WQGQTIVTVSS 11
 Db 110 WQGQTIVTVSS 120

RESULT 9
 Q921A6_MOUSE
 ID Q921A6_MOUSE PRELIMINARY; PRT; 241 AA.
 AC 0921A6;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Anti-CEA_79 single chain Fv (fragment).
 OS Mus musculus (Mouse).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buteria; Buarchontoglires; Gires; Rodentia; Sciuromorpha;
 OC Muridae; Murinae; Mus.
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=8170165; PubMed=9509426;
 RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
 RA Yi K.S., Sun P.G., Ryu S.H., Chung H.K.;
 RT "cloning and characterization of cDNAs encoding VH and VL of a
 monoclonal anti-CEA antibody (CEA-79) cross-reactive with NCA-95 and
 generation of a single-chain Fv molecule (scFv).";
 RL Mol. Cells 7:816-819(1997).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=1341421; PubMed=1908510; DOI=10.1084/jem.174.3.613;
 RA Stark S.E., Caton A.J.;
 RT "Antibodies that are specific for a single amino acid interchange in a
 protein epitope use structurally distinct variable regions.";
 RL J. Exp. Med. 174:613-624(1991).
 DR EMBL; U88057; RAB48044.1; -; mRNA.
 DR PIR; S1965; S1995;
 DR PIR; S1967; S1997.
 DR PIR; S19968; S19968.

RESULT 10
 Q6PYX1_HUMAN
 ID Q6PYX1_HUMAN PRELIMINARY; PRT; 348 AA.
 AC Q6PYX1;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hepatitis B virus receptor binding protein (Fragment).
 OS Homo sapiens (Human).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buteria; Buarchontoglires; Primates; Catarrhini; Hominidae;
 OX Homo.
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Zhu N.-S., Chen Y.-Y.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY507031; ARB88328.1; -; mRNA.
 DR PDB; 1T89; X-ray; A/B=-.
 DR SMR; Q6PYX1; 3-348.
 DR GO; GO:0004872; F:receptor activity; IFA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR0031006; Ig_MHC.
 DR Pfam; PF01654; Cl-set; 3.
 DR SMART; SM00007; Ig1; 3.
 DR PROSITE; PSS0835; Ig_LIKE; 3.
 DR PROSITE; PS00290; Ig_MHC; UNKNOWN_2.
 KW Receptor.
 FT NON_TER 1 AA; 1 MW; 38162 MN; DD96C3D7E0B8E5845 CRC64;
 SQ SEQUENCE 348 AA; |||||||
 Query Match 100.0%; Score 59; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 0.017; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0;
 QY 1 WQGQTIVTVSS 11
 Db 8 WQGQTIVTVSS 18

RESULT 11
 Q9NP86_HUMAN
 ID Q9NP86_HUMAN PRELIMINARY; PRT; 416 AA.
 AC Q9NP86;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Immunoglobulin heavy chain variant (Fragment).
 OS Homo sapiens (Human).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buteria; Buarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.

OX NCBI_TaxID=9606;
 RN [1] NUCLEOTIDE SEQUENCE.
 RP Nucleotide sequence submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 RA Lehrach H., Poustka A., Lundeberg J.;
 RA Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 RL RN
 RP NUCLEOTIDE SEQUENCE.
 RA Puvinet R., Estivill X., Bacarceller M., Sumoy L.;
 RA Submitter (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL389978; CAB97534.1; -; mRNA.
 DR HSPP; P01876; IgM.
 DR SNR; Q9NPP6; 186-394.
 DR InterPro; IPR07110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003066; Ig_MHC.
 DR InterPro; IPR03596; Ig_v.
 DR Pfam; PF07654; Cl-Bet; 2.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig_LIKE; 3.
 DR PROSITE; PS00290; Ig_MHC; UNKNOWN_2.
 FT NON_TER; 1
 SQ SEQUENCE 416 AA; 44786 MW; 8C4170BBBABA4687 CRC64;
 Query Match Score 59; DB 2; Length 416;
 Best Local Similarity 100.0%; Pred. No. 0.021; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0;
 Qy 1 WQGQTTVYSS 11
 Db 66 WGQGTTVYSS 76
 RESULT 12
 ID Q9N089_HUMAN PRELIMINARY; PRT; 472 AA.
 AC Q9N089;
 DT 05-JUL-2004 (TREMBREL_27, Created)
 DT 05-JUL-2004 (TREMBREL_27, Last sequence update)
 DT 05-JUL-2004 (TREMBREL_27, Last annotation update)
 DE Hypothetical protein DKFZp686P15220.
 Name=DKFZp686P15220;
 OS Homo sapiens (Human).
 OC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
 OC NEBI_TAXID=9606;
 RN [1] NUCLEOTIDE SEQUENCE.
 RP TISSUE=Primary B-Cells;
 RN MEDLINE2288257; PubMed1247932; DOI=10.1073/pnas.242603899;
 RX Straubhaar R.L., Feingold E.A., Grouse L.H., Berger J.G., Klauser R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhattacharya S., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heilek P., Diatchenko L., Marsusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Ronald M.F., Casavant T.L., Schatz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Kettman M., Madan R., Rodrigues S., Sanchez A., Blakely R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.B., Schnech A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL RN [2] NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RA Director MGC Project;
 RP RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
 RN RN [3] PROTEIN SEQUENCE.
 RP PUBMED1555592;
 RA Makiya R., Stigbrand T.; "Placental alkaline phosphatase has a binding site for the human immunoglobulin G Fc portion"; Eur. J. Biochem. 205:341-345 (1992).
 RL DR EMBL; BC021276; ARH21276.1; -; mRNA.
 DR PIR; S21205; S21205.
 DR PIR; S20532; S30532.
 DR HSPP; P18522; IgA.
 DR Ensembl; ENSG00000196122; Homo sapiens.
 DR InterPro; IPR07110; Ig-like.
 DR InterPro; IPR03597; Ig-cl.
 DR InterPro; IPR003066; Ig_MHC.
 DR InterPro; IPR03596; Ig_v.
 DR Pfam; PF07654; Cl-Bet; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig_LIKE; 4.
 DR PROSITE; PS00290; Ig_MHC; UNKNOWN_2.
 SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;
 Query Match Score 59; DB 2; Length 472;
 Best Local Similarity 100.0%; Pred. No. 0.024; Indels 0; Gaps 0; Mismatches 11; Conservative 0; Mismatches 0;

Mon Dec 5 13:15:03 2005

usb-10-632-706-198.rup

Page 7

Query Match 100.0%; Score 59; DB 2; Length 595;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WGGTTTVVSS 11
Db 141 WGGTTTVVSS 151

Search completed: December 4, 2005, 04:52:27
Job time : 102.375 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 03:59:51 ; Search time 23.6042 Seconds
 (without alignments) 38.528 Million cell updates/sec

Title: US-10-632-706-198
 Perfect score: 59
 Sequence: 1 WGGGTTTVVSS 11

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AAI:
 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:/*
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 3: /cgn2_6/ptodata/1/iaaH_COMB.pep:/*
 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:/*
 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:/*
 6: /cgn2_6/ptodata/1/iaa/batchfile1.pep:/*

Pred. No.: is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|---------------------------|--------------------|
| 1 | 59 | 100.0 | 11 1 US-08-471-780C-120 | Sequence 120, App |
| 2 | 59 | 100.0 | 11 1 US-08-467-282B-120 | Sequence 120, App |
| 3 | 59 | 100.0 | 11 1 US-08-471-780C-120 | Sequence 120, App |
| 4 | 59 | 100.0 | 11 1 US-08-318-157B-40 | Sequence 40, App |
| 5 | 59 | 100.0 | 11 1 US-08-466-710C-120 | Sequence 120, App |
| 6 | 59 | 100.0 | 11 2 US-08-468-230C-120 | Sequence 120, App |
| 7 | 59 | 100.0 | 11 2 US-08-616-265A-114 | Sequence 114, App |
| 8 | 59 | 100.0 | 11 2 US-08-253-129 | Sequence 129, App |
| 9 | 59 | 100.0 | 11 2 US-09-253-94-40 | Sequence 40, App |
| 10 | 59 | 100.0 | 11 2 US-09-563-230C-146 | Sequence 146, App |
| 11 | 59 | 100.0 | 11 2 US-09-563-222C-169 | Sequence 169, App |
| 12 | 59 | 100.0 | 11 2 US-09-263-921-137 | Sequence 137, App |
| 13 | 59 | 100.0 | 11 2 US-09-293-769A-120 | Sequence 120, App |
| 14 | 59 | 100.0 | 13 6 S189147-14 | Patent No. 5189147 |
| 15 | 59 | 100.0 | 15 1 US-08-765-179B-8 | Sequence 8, Appl |
| 16 | 59 | 100.0 | 15 6 S189147-20 | Patent No. 5189147 |
| 17 | 59 | 100.0 | 16 4 PCT-US91-02942-91 | Sequence 91, Appl |
| 18 | 59 | 100.0 | 20 2 PCT-US91-194-975-107 | Sequence 107, Appl |
| 19 | 59 | 100.0 | 22 4 PCT-US91-02942-100 | Sequence 100, Appl |
| 20 | 59 | 100.0 | 29 1 US-08-053-3173 | Sequence 73, Appl |
| 21 | 59 | 100.0 | 29 1 US-08-643-641-73 | Sequence 73, Appl |
| 22 | 59 | 100.0 | 29 1 US-07-853-408B-73 | Sequence 73, Appl |
| 23 | 59 | 100.0 | 29 1 US-08-956-762-73 | Sequence 73, Appl |
| 24 | 59 | 100.0 | 29 1 US-08-308-865-73 | Sequence 73, Appl |
| 25 | 59 | 100.0 | 29 2 US-09-042-353-270 | Sequence 270, Appl |
| 26 | 59 | 100.0 | 29 2 US-08-758-417A-118 | Sequence 118, Appl |
| 27 | 59 | 100.0 | 4 PCT-US92-10983-73 | Sequence 73, Appl |

ALIGNMENTS

RESULT 1
 US-08-471-780C-120
 Sequence 120, Application US/08471780C
 Patent No. 5759808
 GENERAL INFORMATION:
 APPLICANT: Casterman, Cecile
 ATTORNEY: Haners, Raymond
 TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
 NUMBER OF SEQUENCES: 130
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3315
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MG-DOS
 SOFTWARE: PatentIn Release #1.0, Version #11.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/471,780C
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/7106,944
 FILING DATE: 17-AUG-1993
 APPLICATION NUMBER: FR 92402326.0
 FILING DATE: 21-AUG-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 93401310.3
 FILING DATE: 21-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Porter, Jane E.R.
 REGISTRATION NUMBER: 33,332
 PERFORMANCE/DECET NUMBER: 04958.0008-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-405-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 120:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-471-780C-120

Query Match Similarity 100.0%; Score 59; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0017;

| Matches | 11 | Conservative | 0 | Mismatches | 0 | Indels | 0 | Gaps | 0 |
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| Qy | 1 | WGQGTTVTVSS | 11 | | | | | | |
| Db | 1 | WGQGTTVTVSS | 11 | | | | | | |
| RESULT² US-08-467-282B-120 | | | | | | | | | |
| ; Sequence 120, Application US/08467282B | | | | | | | | | |
| ; Patent No. 5840853 | | | | | | | | | |
| ; GENERAL INFORMATION: | | | | | | | | | |
| ; APPLICANT: Casterman, Cecile | | | | | | | | | |
| ; CITY: Washington | | | | | | | | | |
| ; COUNTRY: D.C. | | | | | | | | | |
| ; CORRESPONDENCE ADDRESS: | | | | | | | | | |
| ; ADDRESSEE: Finegan, Henderson, Farabow, Garrett & Dunner | | | | | | | | | |
| ; STREET: 1300 I Street, N.W. | | | | | | | | | |
| ; CITY: Washington | | | | | | | | | |
| ; COUNTRY: USA | | | | | | | | | |
| ; ZIP: 20005-3315 | | | | | | | | | |
| ; COMPUTER READABLE FORM: | | | | | | | | | |
| ; MEDIUM TYPE: Floppy disk | | | | | | | | | |
| ; COMPUTER: IBM PC compatible | | | | | | | | | |
| ; OPERATING SYSTEM: PC-DOS/MS-DOS | | | | | | | | | |
| ; SOFTWARE: PatentIn Release #1.0, Version #1.25 | | | | | | | | | |
| ; CURRENT APPLICATION DATA: | | | | | | | | | |
| ; APPLICATION NUMBER: US 08/106,944 | | | | | | | | | |
| ; FILING DATE: 17-AUG-1993 | | | | | | | | | |
| ; APPLICATION NUMBER: FR 92402326.0 | | | | | | | | | |
| ; FILING DATE: 06-JUN-1995 | | | | | | | | | |
| ; CLASSIFICATION: 536 | | | | | | | | | |
| ; PRIORITY APPLICATION DATA: | | | | | | | | | |
| ; APPLICATION NUMBER: US 08/467-282B | | | | | | | | | |
| ; FILING DATE: 21-AUG-1992 | | | | | | | | | |
| ; ATTORNEY/AGENT INFORMATION: | | | | | | | | | |
| ; NAME: Potter, Jane E. R. | | | | | | | | | |
| ; REGISTRATION NUMBER: 33,332 | | | | | | | | | |
| ; REFERENCE/DOCKET NUMBER: 04958.0008-00000 | | | | | | | | | |
| ; TELECOMMUNICATION INFORMATION: | | | | | | | | | |
| ; TELEPHONE: 202-408-4000 | | | | | | | | | |
| ; TELEFAX: 202-408-4400 | | | | | | | | | |
| ; INFORMATION FOR SEQ ID NO: 120: | | | | | | | | | |
| ; SEQUENCE CHARACTERISTICS: | | | | | | | | | |
| ; LENGTH: 11 amino acids | | | | | | | | | |
| ; TYPE: amino acid | | | | | | | | | |
| ; TOPOLogy: linear | | | | | | | | | |
| ; MOLECULE TYPE: peptide | | | | | | | | | |
| ; US-08-471-282A-120 | | | | | | | | | |
| ; Query Match 100.0%; Score 59; DB 1; Length 11; | | | | | | | | | |
| ; Best Local Similarity 100.0%; Pred. No. 0.0017; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | |
| ; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | |
| ; INFORMATION FOR SEQ ID NO: 120: | | | | | | | | | |
| ; SEQUENCE CHARACTERISTICS: | | | | | | | | | |
| ; LENGTH: 11 amino acids | | | | | | | | | |
| ; TYPE: amino acid | | | | | | | | | |
| ; TOPOLogy: linear | | | | | | | | | |
| ; MOLECULE TYPE: peptide | | | | | | | | | |
| ; US-08-467-282B-120 | | | | | | | | | |
| ; Query Match 100.0%; Score 59; DB 1; Length 11; | | | | | | | | | |
| ; Best Local Similarity 100.0%; Pred. No. 0.0017; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | |
| ; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | |
| ; RESULT ³ US-08-318-157B-40 | | | | | | | | | |
| ; Sequence 40, Application US/08318157B | | | | | | | | | |
| ; Patent No. 5874540 | | | | | | | | | |
| ; GENERAL INFORMATION: | | | | | | | | | |
| ; APPLICANT: HANSEN, Hans J. | | | | | | | | | |
| ; CITY: Copenhagen | | | | | | | | | |
| ; COUNTRY: Denmark | | | | | | | | | |
| ; CORRESPONDENCE ADDRESS: | | | | | | | | | |
| ; ADDRESSEE: Folev & Lardner | | | | | | | | | |
| ; STREET: 3000 K Street, N.W., Suite 500 | | | | | | | | | |
| ; CITY: Washington | | | | | | | | | |
| ; COUNTRY: USA | | | | | | | | | |
| ; ZIP: 20007-5109 | | | | | | | | | |
| ; COMPUTER READABLE FORM: | | | | | | | | | |
| ; MEDIUM TYPE: Floppy disk | | | | | | | | | |
| ; COMPUTER: IBM PC compatible | | | | | | | | | |
| ; OPERATING SYSTEM: PC-DOS/MS-DOS | | | | | | | | | |
| ; SOFTWARE: PatentIn Release #1.0, Version #1.30 | | | | | | | | | |
| ; CURRENT APPLICATION DATA: | | | | | | | | | |
| ; APPLICATION NUMBER: US/08/318.157B | | | | | | | | | |
| ; FILING DATE: 05-OCT-1994 | | | | | | | | | |

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:

NAME: Saxe, Bernhard D.

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 18733/464

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-318-157B-40

Query Match Score 59; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 WGQGTTVTVSS 11
Db 1 WGQGTTVTVSS 11

RESULT 5

US-08-466-710C-120

Sequence 120 Application US/08466710C

Patent No. 5,745,41

GENERAL INFORMATION:

APPLICANT: Casterman, Cecile

APPLICANT: Hamers, Raymond

TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains

NUMBER OF SEQUENCES: 130

CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES: 130

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finegan, Henderson, Farabow, Garrett & Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent-in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,739C

FILING DATE: 06-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/106,944

FILING DATE: 17-AUG-1993

APPLICATION NUMBER: FR 92402326.0

FILING DATE: 21-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/106,944

FILING DATE: 17-AUG-1993

APPLICATION NUMBER: FR 92402326.0

FILING DATE: 21-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 93401310.3

FILING DATE: 21-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Potter, Jane E. R.

REGISTRATION NUMBER: 33,332

REFERENCE/DOCKET NUMBER: 04958.0008-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

TELEX: 904136

INFORMATION FOR SEQ ID NO: 120:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-466-710C-120

Query Match Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 WGQGTTVTVSS 11
Db 1 WGQGTTVTVSS 11

RESULT 6

US-08-468-739C-120

Sequence 120 Application US/08468739C

Patent No. 6015635

GENERAL INFORMATION:

APPLICANT: Casterman, Cecile

APPLICANT: Hamers, Raymond

TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains

NUMBER OF SEQUENCES: 130

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finegan, Henderson, Farabow, Garrett & Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent-in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,739C

FILING DATE: 06-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 93401310.3

FILING DATE: 21-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Potter, Jane E. R.

REGISTRATION NUMBER: 33,332

REFERENCE/DOCKET NUMBER: 04958.0008-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

TELEX: 904136

INFORMATION FOR SEQ ID NO: 120:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-468-739C-120

Query Match Score 59; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 WGQGTTVTVSS 11
Db 1 WGQGTTVTVSS 11

RESULT 7

US-08-646-265A-114

Sequence 114 Application US/08646265A

Patent No. 6214973

GENERAL INFORMATION:

APPLICANT: OHTOMO, Toshihiko
 APPLICANT: SATO, Koh
 APPLICANT: TSUCHIYA, Masayuki.
 TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
 TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
 NUMBER OF SEQUENCES: 132

CORRESPONDENCE ADDRESS:
 ADDRESSE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,265A
 FILING DATE: 09-SEP-1996
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/JP94/01763
 FILING DATE: 19-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 5-291078
 FILING DATE: 09-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: WEGNER, Harold C.
 REGISTRATION NUMBER: 25,258
 REFERENCE/DOCKET NUMBER: 53466/184
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5300
 TELEFAX: (202) 672-5399
 TELEX: 904136
 INFO: 19-NOV-1993
 INFORMATION FOR SEQ ID NO: 129:
 ATTORNEY NUMBER: WO PCT/JP94/01763
 FILING DATE: 19-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: WEGNER, Harold C.
 REGISTRATION NUMBER: 25,258
 REFERENCE/DOCKET NUMBER: 53466/184
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5300
 TELEFAX: (202) 672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 114:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-646-265A-114

RESULT 8
 US-08-646-265A-129
 Sequence 129 Application US/08646265A
 Patent No. 6214973
 GENERAL INFORMATION:
 APPLICANT: OHTOMO, Toshihiko
 APPLICANT: SATO, Koh
 APPLICANT: TSUCHIYA, Masayuki.
 TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
 TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
 NUMBER OF SEQUENCES: 132

CORRESPONDENCE ADDRESS:
 ADDRESSE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/253,794
 FILING DATE: 22-Feb-1999
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/318,157
 FILING DATE: 05-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: SAXE, Bernhard D.
 REGISTRATION NUMBER: 28,665
 REFERENCE/DOCKET NUMBER: 18733/464
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 40:
 ;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 40:
 US-09-253-794-40

Query Match 100.0%; Score 59; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WGQGTTVVS 11
 Db 1 WGQGTTVVS 11

RESULT 10
 US-09-563-222C-146
 Sequence 146, Application US/09563222C
 Patent No. 6596620
 GENERAL INFORMATION:
 APPLICANT: EPICTYE PHARMACEUTICALS, INC.
 APPLICANT: HEIN, MICH B.
 APPLICANT: HIATT, ANDREW C.
 TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
 CURRENT APPLICATION NUMBER: US/09/563,222C
 CURRENT FILING DATE: 2000-05-02
 PRIOR APPLICATION NUMBER: PCT/US01/14349
 PRIOR FILING DATE: 2001-05-02
 PRIOR APPLICATION NUMBER: 09/563,222
 PRIOR FILING DATE: 2000-05-02
 NUMBER OF SEQ ID NOS: 182
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 146
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Mus musculus

Query Match 100.0%; Score 59; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WGQGTTVVS 11
 Db 1 WGQGTTVVS 11

RESULT 11
 US-09-563-222C-169
 Sequence 169, Application US/09563222C
 Patent No. 6596620
 GENERAL INFORMATION:
 APPLICANT: EPICTYE PHARMACEUTICALS, INC.
 APPLICANT: HEIN, MICH B.
 APPLICANT: HIATT, ANDREW C.
 TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
 CURRENT APPLICATION NUMBER: US/09/563,222C
 CURRENT FILING DATE: 2000-05-02
 PRIOR APPLICATION NUMBER: PCT/US01/14349
 PRIOR FILING DATE: 2001-05-02
 NUMBER OF SEQ ID NOS: 182
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 169

Query Match 100.0%; Score 59; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WGQGTTVVS 11
 Db 1 WGQGTTVVS 11

RESULT 12
 US-09-269-921-137
 Sequence 137, Application US/09269921
 Patent No. 6599974
 GENERAL INFORMATION:
 APPLICANT: Ono, Koichiro
 APPLICANT: Ohtomo, Toshihiko
 APPLICANT: Yoshimura, Masayuki
 APPLICANT: Kojihara, Yasuo
 TITLE OF INVENTION: RESHADED HUMAN ANTI-HM 1.24 ANTIBODY
 FILE REFERENCE: 35029-20007.00
 CURRENT APPLICATION NUMBER: US/09/269, 921
 CURRENT FILING DATE: 1999-04-01
 EARLIER APPLICATION NUMBER: PCT/JP97/03553
 EARLIER FILING DATE: 1997-10-03
 EARLIER APPLICATION NUMBER: JP 8-264756
 EARLIER FILING DATE: 1996-10-04
 NUMBER OF SEQ ID NOS: 137
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 137
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: Description of Unknown Organism: JHG
 PUBLICATION INFORMATION:
 AUTHORS: Revetch, J. et al.
 JOURNAL: CELL
 VOLUME: 27
 PAGES: 583-591
 DATE: 1981
 US-09-269-921-137

Query Match 100.0%; Score 59; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WGQGTTVVS 11
 Db 1 WGQGTTVVS 11

RESULT 13
 US-09-293-769A-120
 Sequence 120, Application US/09293769A
 Patent No. 6765087
 GENERAL INFORMATION:
 APPLICANT: CASTREMAN, CECILE
 APPLICANT: HAMERS, RAYMOND
 TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
 CURRENT APPLICATION NUMBER: 094958 0008-07000
 CURRENT FILING DATE: 1999-04-19
 PRIOR APPLICATION NUMBER: 08/471,284
 PRIOR FILING DATE: 1995-06-06
 PRIOR APPLICATION NUMBER: 07/106,944
 PRIOR FILING DATE: 1997-10-15
 PRIOR APPLICATION NUMBER: B60 92402326.0
 SEQ ID NO 169.

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; PRIOR FILING DATE: 1992-08-21
; PRIOR APPLICATION NUMBER: EPO 93401310.3
; PRIOR FILING DATE: 1993-05-21
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 120
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-05-293-769A-120

Query Match          100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy   1 WGQGTTVTVSS 11
Db   1 WGQGTTVTVSS 11

RESULT 14
5189147-14
;Patent No. 5189147
; APPLICANT: SAITO, HARUO; KRAZ, DAVID M.; JELSEN, HERMAN N. ;
; TONIGAWA, SUSumu
TITLE OF INVENTION: METERODIMERIC T LYMPHOCYTE RECEPTOR
;ANTIBODY
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/271,216
; FILING DATE: 14-NOV-1988
; PRIOR APPLICATION DATA:
APPLICATION NUMBER: 666,988
; FILING DATE: 31-OCT-1984
APPLICATION NUMBER: 620,122
; FILING DATE: 13-JUN-1984
;SEQ ID NO:14:
;SEQ ID NO:14:
; LENGTH: 13
5189147-14

Query Match          100.0%; Score 59; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0027; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy   1 WGQGTTVTVSS 11
Db   3 WGQGTTVTVSS 13

RESULT 15
US-06-765-179B-8
; Sequence 8, Application US/08765179B
; Patent No. 554027
; GENERAL INFORMATION:
; APPLICANT: STILPE, Boris
; APPLICANT: STEINBACHER, Stefan
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
; TITLE OF INVENTION: OF ANTIBODIES
NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Nikaldo, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/165,179B

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 4, 2005, 04:07:28 ; Search time 78.8333 Seconds
 (Without alignments)
 58.302 Million cell updates/sec

Title: US-10-632-706-198

Perfect score: 59
 Sequence: 1 WGGITTVVSS 11

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications RA_Main:
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 2: /cggn2_6/ptodata/1/pubpa/us08_PUBCOMB.pep:
 3: /cggn2_6/ptodata/1/pubpa/us09_PUBCOMB.pep:
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 6: /cggn2_6/ptodata/1/pubpa/us11_PUBCOMB.pep:
 *;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|-------------------|
| 1 | 59 | 100.0 | 11 3 | US-09-233-794-40 |
| 2 | 59 | 100.0 | 11 3 | US-09-748-705-78 |
| 3 | 59 | 100.0 | 11 3 | US-09-749-811-114 |
| 4 | 59 | 100.0 | 11 3 | US-09-749-73-129 |
| 5 | 59 | 100.0 | 11 3 | US-09-239-921-137 |
| 6 | 59 | 100.0 | 11 3 | US-09-563-221-157 |
| 7 | 59 | 100.0 | 11 3 | US-09-563-222-165 |
| 8 | 59 | 100.0 | 11 3 | US-09-563-222-181 |
| 9 | 59 | 100.0 | 11 3 | US-09-563-222-197 |
| 10 | 59 | 100.0 | 11 3 | US-09-569-98-179 |
| 11 | 59 | 100.0 | 11 4 | US-10-218-253-137 |
| 12 | 59 | 100.0 | 11 4 | US-10-163-351-4 |
| 13 | 59 | 100.0 | 11 4 | US-10-160-505-40 |
| 14 | 59 | 100.0 | 11 4 | US-10-310-13-126 |
| 15 | 59 | 100.0 | 11 4 | US-10-310-13-147 |
| 16 | 59 | 100.0 | 11 4 | US-10-310-13-148 |
| 17 | 59 | 100.0 | 11 4 | US-10-310-13-149 |
| 18 | 59 | 100.0 | 11 4 | US-10-310-13-150 |
| 19 | 59 | 100.0 | 11 4 | US-10-310-13-151 |
| 20 | 59 | 100.0 | 11 4 | US-10-310-13-152 |
| 21 | 59 | 100.0 | 11 4 | US-10-310-13-153 |
| 22 | 59 | 100.0 | 11 4 | US-10-310-13-154 |
| 23 | 59 | 100.0 | 11 4 | US-10-310-13-155 |
| 24 | 59 | 100.0 | 11 4 | US-10-310-13-156 |
| 25 | 59 | 100.0 | 11 4 | US-10-310-13-157 |
| 26 | 59 | 100.0 | 11 4 | US-10-310-13-158 |
| 27 | 59 | 100.0 | 11 4 | US-10-310-13-159 |

ALIGNMENTS

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| 28 | 59 | 100.0 | 11 4 | US-10-412-703A-135 | Sequence 135, App |
| 29 | 59 | 100.0 | 11 4 | US-10-443-466A-69 | Sequence 69, App |
| 30 | 59 | 100.0 | 11 4 | US-10-443-466A-120 | Sequence 120, App |
| 31 | 59 | 100.0 | 11 4 | US-10-449-379-40 | Sequence 40, App |
| 32 | 59 | 100.0 | 11 4 | US-10-688-015-40 | Sequence 40, App |
| 33 | 59 | 100.0 | 11 4 | US-10-632-706-195 | Sequence 198, App |
| 34 | 59 | 100.0 | 11 4 | US-10-632-706-198 | Sequence 201, App |
| 35 | 59 | 100.0 | 11 4 | US-10-632-706-201 | Sequence 413, App |
| 36 | 59 | 100.0 | 11 4 | US-10-632-706-204 | Sequence 40, App |
| 37 | 59 | 100.0 | 11 4 | US-10-783-950-146 | Sequence 146, App |
| 38 | 59 | 100.0 | 11 4 | US-10-783-950-146 | Sequence 40, App |
| 39 | 59 | 100.0 | 11 4 | US-10-160-505-40 | Sequence 120, App |
| 40 | 59 | 100.0 | 11 5 | US-10-751-826-120 | Sequence 78, App |
| 41 | 59 | 100.0 | 11 5 | US-10-932-068-413 | Sequence 40, App |
| 42 | 59 | 100.0 | 11 5 | US-10-630-009-78 | Sequence 9, App |
| 43 | 59 | 100.0 | 11 5 | US-10-755-382-40 | Sequence 45, App |
| 44 | 59 | 100.0 | 11 5 | US-10-984-960A-9 | Sequence 45, App |
| 45 | 59 | 100.0 | 11 5 | US-10-984-960A-45 | Sequence 45, App |

SEQUENCE DESCRIPTION

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| SEQUENCE TYPE: protein | SEQUENCE ID NO: 40: |
| SEQUENCE DESCRIPTION: SEQ ID NO: 40: | |
| SEQUENCE LENGTH: 11 amino acids | |
| TYPE: amino acid | |
| STRANDEDNESS: <Unknown> | |
| TOPOLOGY: linear | |
| MOLECULE TYPE: protein | |
| SEQUENCE: 159, APP | |
| SEQUENCE: 159, APP | |

SEQUENCE DESCRIPTION

| | |
|--------------------------------------|---------------------|
| SEQUENCE TYPE: protein | SEQUENCE ID NO: 40: |
| SEQUENCE DESCRIPTION: SEQ ID NO: 40: | |
| SEQUENCE LENGTH: 11 amino acids | |
| TYPE: amino acid | |
| STRANDEDNESS: <Unknown> | |
| TOPOLOGY: linear | |
| MOLECULE TYPE: protein | |
| SEQUENCE: 159, APP | |
| SEQUENCE: 159, APP | |

SEQUENCE DESCRIPTION

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|--------------------------------------|---------------------|
| SEQUENCE TYPE: protein | SEQUENCE ID NO: 40: |
| SEQUENCE DESCRIPTION: SEQ ID NO: 40: | |
| SEQUENCE LENGTH: 11 amino acids | |
| TYPE: amino acid | |
| STRANDEDNESS: <Unknown> | |
| TOPOLOGY: linear | |
| MOLECULE TYPE: protein | |
| SEQUENCE: 159, APP | |
| SEQUENCE: 159, APP | |

QY 1 WGGQTIVTVSS 11
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 1 WGGQTIVTVSS 11

RESULT 2
 US-09-828-708-78
 Sequence 78, Application US/09828708
 Patent No. US2002146753A1
 GENERAL INFORMATION:
 APPLICANT: Burton, D.
 APPLICANT: Schaller, M.
 TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their participation in autoimmune disease
 FILE REFERENCE: 1361_005US1
 CURRENT APPLICATION NUMBER: US/09/828,708
 CURRENT FILING DATE: 2001-09-24
 NUMBER OF SEQ ID NOS: 123
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 78
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-828-708-78

Query Match 100.0%; Score 59; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.01; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Type: amino acid
 QY 1 WGGQTIVTVSS 11
 Db 1 WGGQTIVTVSS 11

RESULT 3
 US-09-749-873-114
 Sequence 114, Application US/09749873
 Publication No. US20030023045A1
 GENERAL INFORMATION:
 APPLICANT: OHTOMO, Toshihiko
 SATO, Koh
 TSUCHIYA, Masayuki
 TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN MEDULLOBLASTOMA CELLS
 NUMBER OF SEQUENCES: 132
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/749,873
 FILING DATE: 29-Dec-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/646,265
 FILING DATE: 1966-09-09
 APPLICATION NUMBER: JP 5-291078
 FILING DATE: 19-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: WEGNER, Harold C.
 REGISTRATION NUMBER: 25,258
 REFERENCE/DOCKET NUMBER: 53466/184
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5399
 TELEFAX: (202) 672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 129:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 129:
 Query Match 100.0%; Score 59; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.01; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Type: amino acid
 US-09-749-873-114

QY 1 WGGQTIVTVSS 11
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 1 WGGQTIVTVSS 11

RESULT 4
 US-09-749-873-129
 Sequence 129, Application US/09749873
 Publication No. US20030023045A1
 GENERAL INFORMATION:
 APPLICANT: OHTOMO, Toshihiko
 SATO, Koh
 TSUCHIYA, Masayuki
 TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN MEDULLOBLASTOMA CELLS
 NUMBER OF SEQUENCES: 132
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/749,873
 FILING DATE: 29-Dec-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/646,265
 FILING DATE: 1966-09-09
 APPLICATION NUMBER: JP 5-291078
 FILING DATE: 19-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: WEGNER, Harold C.
 REGISTRATION NUMBER: 25,258
 REFERENCE/DOCKET NUMBER: 53466/184
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5399
 TELEFAX: (202) 672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 129:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 129:
 Query Match 100.0%; Score 59; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.01; Indels 0; Gaps 0;

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/646,265
 FILING DATE: 1966-09-09
 FILING DATE: 19-Nov-1993
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: WEGNER, Harold C.
 REGISTRATION NUMBER: 25,258
 REFERENCE/DOCKET NUMBER: 53466/184
 TELECOMMUNICATION INFORMATION:

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; Mon Dec 5 13:15:01 2005
; us-10-632-706-198.rapbm
; Page 3

; RESULT 5
; US-09-269-921-137
; Sequence 137, Application US/09269921
; Publication No. US20030045691A1
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshihiko
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuhi
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
FILE REFERENCE: 35029/2007.00
CURRENT APPLICATION NUMBER: US/09/269,921
CURRENT FILING DATE: 1999-04-01
EARLIER APPLICATION NUMBER: PCT/JP97/03553
EARLIER FILING DATE: 1997-10-03
EARLIER APPLICATION NUMBER: JP 8-264756
EARLIER FILING DATE: 1996-10-04
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 137
LENGTH: 11
TYPE: PRT
ORGANISM: Unknown
FEATURE: OTHER INFORMATION: Description of Unknown Organism: JH6
PUBLICATION INFORMATION:
AUTHORS: Ravetch, J. et al.
JOURNAL: CELL
VOLUME: 27
PAGES: 583-591
DATE: 1981
US-09-269-921-137

; RESULT 6
; US-09-563-222-157
; Sequence 157, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
FILE REFERENCE: 310098.406
CURRENT APPLICATION NUMBER: US/09/563,222
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 181
LENGTH: 11
TYPE: PRT
ORGANISM: Mus musculus
US-09-563-222-157

; RESULT 7
; US-09-563-222-165
; Sequence 165, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
FILE REFERENCE: 310098.406
CURRENT APPLICATION NUMBER: US/09/563,222
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 165
LENGTH: 11
TYPE: PRT
ORGANISM: Mus musculus
US-09-563-222-165

; RESULT 8
; US-09-563-222-181
; Sequence 181, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
FILE REFERENCE: 310098.406
CURRENT APPLICATION NUMBER: US/09/563,222
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 181
LENGTH: 11
TYPE: PRT
ORGANISM: Mus musculus
US-09-563-222-181

; RESULT 9
; US-09-563-222-197
; Sequence 197, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
FILE REFERENCE: 310098.406
TITLE OF INVENTION: EUKARYOTIC CELLS
FILE REFERENCE: 310098.406

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; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 197
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-563-222-197

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WGQGTTVTVSS 11
Db 1 WGQGTTVTVSS 11

RESULT 10
US-09-509-098-179
; Sequence 179, Application US/09509098
; Publication No. US20030103970A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
; FILE REFERENCE: 053468/0274
; CURRENT APPLICATION NUMBER: US/09/509,098
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/JP98/04469
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: JP 9-271726
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 179
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: Sequence of the H chain V region JH6
US-09-509-098-179

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WGQGTTVTVSS 11
Db 1 WGQGTTVTVSS 11

RESULT 11
US-10-218-253-137
; Sequence 137, Application US/10218253
; Publication No. US20030129185A1
; GENERAL INFORMATION:
; APPLICANT: OMO, KOICHIRO
; APPLICANT: Ontomo, Toshihiko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishikawa, Yasuo
; TITLE OF INVENTION: RSHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; CURRENT FILING DATE: 2002-11-21
; CURRENT APPLICATION NUMBER: US/10/218,253
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/269,921
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: PCT/JP97/03553
; PRIOR FILING DATE: 1997-10-03
; PRIOR APPLICATION NUMBER: JP 8-264756
; PRIOR FILING DATE: 1996-10-04

Query Match 100.0%; Score 59; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WGQGTTVTVSS 11
Db 1 WGQGTTVTVSS 11

RESULT 12
US-10-163-351-4
; Sequence 4, Application US/10169351
; Publication No. US20030157090A1
; GENERAL INFORMATION:
; APPLICANT: BENVENTO, EUGENIO
; APPLICANT: FRANCONI, ROSELLA
; APPLICANT: DESIDERIO, ANGELA
; APPLICANT: TAVLADOKI, PARASKEVI
; TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES
; FILE REFERENCE: 4161-4
; CURRENT APPLICATION NUMBER: US/10/169,351
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/IT00/00554
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: IT RM99A000803
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-169-351-4

Query Match 100.0%; Score 59; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WGQGTTVTVSS 11
Db 1 WGQGTTVTVSS 11

RESULT 13
US-10-160-506-40
; Sequence 40, Application US/10160506
; Publication No. US20030161832A1
; GENERAL INFORMATION:
; APPLICANT: Bandar, Neil H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
; TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR
; TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
; FILE REFERENCE: 10448-162001

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CURRENT APPLICATION NUMBER: US/10/660,506
 CURRENT FILING DATE: 2002-05-30
 PRIORITY APPLICATION NUMBER: 60/324,100
 PRIORITY FILING DATE: 2001-05-20
 PRIORITY APPLICATION NUMBER: 60/342,612
 PRIORITY FILING DATE: 2002-03-08
 NUMBER OF SEQ ID NOS: 128
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 40
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: deimmunized heavy chain J415-4
 ; US-10-160-506-40

Query Match 100.0%; Score 59; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WGQGTTVTVSS 11
 Db 1 WGQGTTVTVSS 11

RESULT 14
 US-10-310-113-26
 Sequence 26, Application US/10310113
 Publication No. US2003017664A1
 GENERAL INFORMATION:
 APPLICANT: JIAO, JIN-AN
 APPLICANT: WONG, HING C.
 APPLICANT: NIENES, ESPERANZA LILIANA
 APPLICANT: MOSQUERA, LUTIS A.
 TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
 TITLE OF INVENTION: THROMBOSES
 FILE REFERENCE: 58122(71758)
 CURRENT APPLICATION NUMBER: US/10/310,113
 CURRENT FILING DATE: 2002-12-04
 PRIORITY APPLICATION NUMBER: 09/990,586
 PRIORITY FILING DATE: 2001-11-21
 PRIORITY APPLICATION NUMBER: 60/343,306
 PRIORITY FILING DATE: 2001-10-29
 PRIORITY APPLICATION NUMBER: 09/293,854
 PRIORITY FILING DATE: 1999-04-16
 PRIORITY APPLICATION NUMBER: 08/814,806
 PRIORITY FILING DATE: 1997-03-10
 NUMBER OF SEQ ID NOS: 169
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 26
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-310-113-26

Query Match 100.0%; Score 59; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WGQGTTVTVSS 11
 Db 1 WGQGTTVTVSS 11

Search completed: December 4, 2005, 04:37:44
 Job time : 79.8333 secs

TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
 TITLE OF INVENTION: THROMBOSES
 FILE REFERENCE: 58122(71758)
 CURRENT APPLICATION NUMBER: US/10/310,113
 CURRENT FILING DATE: 2002-12-04
 PRIORITY APPLICATION NUMBER: 09/990,586
 PRIORITY FILING DATE: 2001-11-21
 PRIORITY APPLICATION NUMBER: 60/343,306
 PRIORITY FILING DATE: 2001-10-29
 PRIORITY APPLICATION NUMBER: 09/293,854
 PRIORITY FILING DATE: 1999-04-16
 PRIORITY APPLICATION NUMBER: 08/814,806
 PRIORITY FILING DATE: 1997-03-10
 NUMBER OF SEQ ID NOS: 169
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 147
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Humanized HC-01 FR4 amino acid sequence
 ; US-10-310-113-147

Query Match 100.0%; Score 59; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WGQGTTVTVSS 11
 Db 1 WGQGTTVTVSS 11

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